Supplementary Information for *Folivory elicits a strong defense reaction in Catharanthus roseus: metabolomic and transcriptomic analyses reveal distinct local and systemic responses*

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This pdf file contains internal links which will help you browsing the present Supplementary Information.

Content of the Supplementary Information:

Supplemental Figure S1: M. sexta is able to feed on C. roseus. A, preferential choice assay. Caterpillars were laid besides N. tabacum (Nta) and C. roseus (Cro) leaf discs. Pictures were taken 5' (left) and 120' (right) after the beginning of the experiment. B, Larval weights obtained 24h, 48h et and 72h after continuous feeding on N. tabacum and C. roseus. Pictures on the right show typical consumed areas on each plant after 2h (top) and 24h (down). C, Left panel, M. sexta larvae dissected after 24h of feeding on N. tabacum (left) or C. roseus (right) showing the presence of plant tissues in the intestinal tract. Right panel, dissection of caterpillar after 72h feeding on C. roseus showing intense browning of the intestinal tract. D, Targeted LC-MS analysis of catharanthine, vindoline and anhydrovinblastine in leaf tissues and caterpillar intestinal tract (sampled on the larva shown in right panel of C).

Supplemental Figure S2: Experimental design to test MIA accumulation in leaves of C. roseus during herbivory. a, design for metabolic analysis. b, comparison of caterpillar and mechanical wounding effects – During 2 hours, leaves were subjected to caterpillar attack or to mechanical wounding (performed with a clamp every 10 min to mimic the chewing effect – similar area of leaves were removed). 48h and 72h post-treatment, leaves were collected and strictosidine quantified. c, design for transcriptomic analyses.

Supplemental Figure S3: PFAM classification of transcripts significantly modulated in leaves of C. roseus fed by M. sexta. Lists of differentially expressed transcripts were obtained for individual experiments (Figure 4). The number of transcripts is indicated for each domain by a dot which diameter is proportional to the p-value of enrichment testing (Hypergeometric distribution). Only PFAM attributed to more than 4 transcripts are represented. a, classification of up-regulated transcripts. b, classification of down-regulated transcripts.

Supplemental Figure S4: Motifs significantly enriched in the 300bp promoters in up-regulated transcripts. Motifs were discovered with DREME from MEME suite. a, enrichment of GCCGCC box in transcripts commonly up-regulated in at least 3 samples. b, enrichment of CACGTG box in the core set of up-regulated transcripts. For each motif, gene ontology (GO) term represented among Arabidopsis genes containing the corresponding motif are reported (processed with GOMO).

Supplemental Table S1: Description of transcripts up-regulated upon challenge with M. sexta found in the intersections between lists of each experiment.

Supplemental Table S2: Description of transcripts down-regulated upon challenge with M. sexta found in the intersections between lists of each experiment.

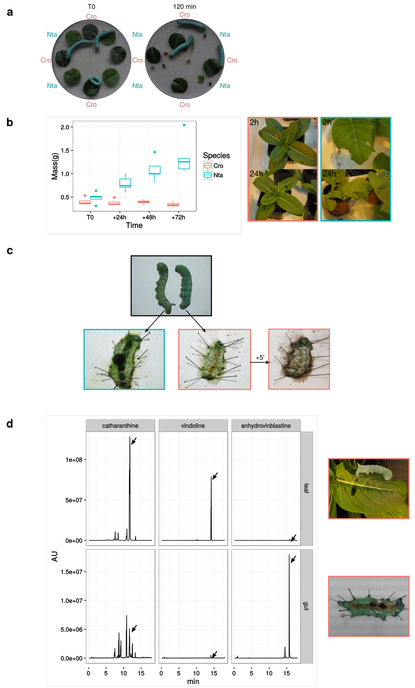
Supplemental Table S3: Most represented Uniprot keywords in transcripts modulated upon challenge with M. sexta. Enrichment tests were performed by comparison with a hypergeometric distribution.

Supplemental Table S4: Most represented PFAM domains Uniprot keywords in transcripts modulated upon challenge with M. sexta. Enrichment tests were performed by comparison with a hypergeometric distribution.

Supplemental Table S5: Primers used in this study.

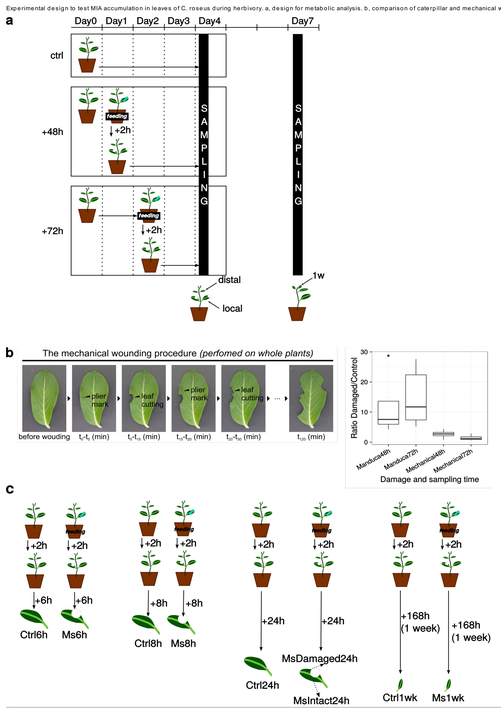
Supplemental Figure S1

M. sexta is able to feed on C. roseus. A, preferential choice assay. Caterpillars were laid besides N. tabacum (Nta) and C. roseus (Cro) leaf discs. Pictures were taken 5' (left) and 120' (right) after the beginning of the experiment. B, Larval weights obtained 24h, 48h et and 72h after continuous feeding on N. tabacum and C. roseus. Pictures on the right show typical consumed areas on each plant after 2h (top) and 24h (down). C, Left panel, M. sexta larvae dissected after 24h of feeding on N. tabacum (left) or C. roseus (right) showing the presence of plant tissues in the intestinal tract. Right panel, dissection of caterpillar after 72h feeding on C. roseus showing intense browning of the intestinal tract. D, Targeted LC-MS analysis of catharanthine, vindoline and anhydrovinblastine in leaf tissues and caterpillar intestinal tract (sampled on the larva shown in right panel of C).



Supplemental Figure S2

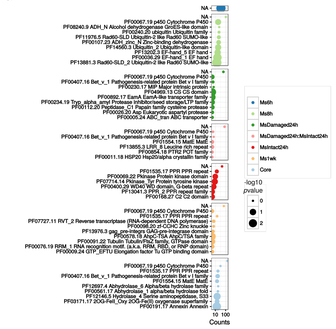
Experimental design to test MIA accumulation in leaves of C. roseus during herbivory. a, design for metabolic analysis. b, comparison of caterpillar and mechanical wounding effects – During 2 hours, leaves were subjected to caterpillar attack or to mechanical wounding (performed with a clamp every 10 min to mimic the chewing effect – similar area of leaves were removed). 48h and 72h post-treatment, leaves were collected and strictosidine quantified. c, design for transcriptomic analyses.



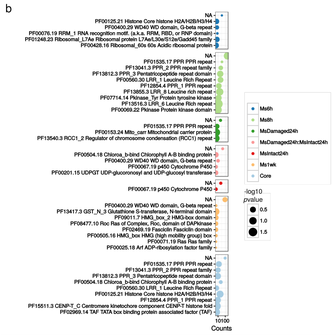
Supplemental Figure S3

PFAM classification of transcripts significantly modulated in leaves of C. roseus fed by M. sexta. Lists of differentially expressed transcripts were obtained for individual experiments (Figure 4). The number of transcripts is indicated for each domain by a dot which diameter is proportional to the p-value of enrichment testing (Hypergeometric distribution). Only PFAM attributed to more than 4 transcripts are represented. a, classification of up-regulated transcripts, b, classification of down-regulated transcripts

a



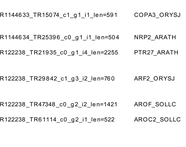
b



Supplemental Figure S4

Motifs significantly enriched in the 300bp promoters in up-regulated transcripts. Motifs were discovered with DREME from MEME suite. a, enrichment of GCCGCC box in transcripts commonly up-regulated in at least 3 samples. b, enrichment of CACGTG box in the core set of up-regulated transcripts. For each motif, gene ontology (GO) term represented among Arabidopsis genes containing the corresponding motif are reported (processed with GOMO).

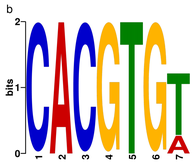
a



Positives	53/443
Negatives	12/443
P-value	5.1e-008
E-Value	1.9e-003
Unerased E-value	1.9e-003

GO term	GO:0080008	
score	2.274e-02	
p-value	1.671e-05	
q-value	6.959e-03	
Specificity	75%	
GO name	CUL4 RING ubiquitin ligase complex	

b



Positives	48/707	
Negatives	2/707	
P-value	5.3e-013	
E-Value	2e-008	
Unerased E-value	2e-008	
GO term	GO:0009753	GO:0009611
score	1.506e-02	7.333e-03
p-value	2.652e-06	2.652e-07
q-value	2.326e-03	3.323e-04
Specificity	45%	2%
GO name	Response to jasmonic acid stimulus	Response to wounding

Supplemental Table S1

Description of transcripts up-regulated upon challenge with M. sexta found in the intersections between lists of each experiment.

Core
Ms1wk
Meth
Meth
MsDamaged24h
MsDamaged24h_MsIntact24h
MsIntact24h

Core

Transcript (CDF97)	Uniprot homolog	BLAST X Position	BLAST X %Identity	BLAST X evalue	Uniprot descr	Pfam	PValue_Ms6h	logFC_Ms6h	PValue_Ms8h	logFC_Ms8h	PValue_MsDamaged24h	logFC_MsDamaged24h	PValue_MsIntact24h	logFC_MsIntact24h	PValue_Ms1wk	logFC_Ms1wk	Entry.name	Protein names	Gene names	Organism	Pathway	Keywords
SRR342017_TR6167_c0_g1_i1_len=1094	PNAE_RAUSE	Q:129-881,H:12-262	45.74%ID	E:1e-63	Polyneuridine-aldehyde esterase	PF12146.5*Hydrolase_4*Serine aminopeptidase, S33*10-119*E:6e-07*PF00561.17*Abhydrolase_1*alpha/beta hydrolase fold*14-123*E:3.2e-09*PF12697.4*Abhydrolase_6*Alpha/beta hydrolase family*15-255*E:1.4e-14	0	1,723	0,003	-1,574	0,007	-0,964	0,08	0,528	0	7,349	PNAE_RAUSE	Polyneuridine-aldehyde esterase (EC 3.1.1.78) (Polyneuridine aldehyde esterase)	PNAE	Rauvolfia serpentina (Serpentine wood) (Ophioxylon serpentinum)	PATHWAY: Alkaloid biosynthesis; ajmaline biosynthesis.	3D-structure; Alkaloid metabolism; Direct protein sequencing; Hydrolase; Serine esterase
SRR646604_TR17021_c2_g3_i5_len=1249	NA	NA	NA	NA	NA	.	0	2,047	0,681	-0,086	0,939	0,017	0,487	0,147	0	5,706	.	.	.	.	.	.
SRR648707_TR16521_c0_g2_i1_len=3328	LOX6_ARATH	Q:407-3222,H:37-917	65.72%ID	E:0	Lipoxygenase 6, chloroplastic	PF01477.20*PLAT/LH2 domain*159-221*E:2.4e-05*PF00305.16*Lipoxygenase*Lipoxygenase*234-803*E:0	0,001	1,536	0,007	1,569	0,935	0,026	0,485	0,168	0	1,733	LOX6_ARATH	Lipoxygenase 6, chloroplastic (AtLOX6) (EC 1.13.11.12)	LOX6 At1g67560 F12B7.11	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Lipid metabolism; oxylipin biosynthesis. (ECO:0000255|PROSITE-ProRule:PRU00726).	Chloroplast; Complete proteome; Dioxygenase; Fatty acid biosynthesis; Fatty acid metabolism; Iron; Lipid biosynthesis; Lipid metabolism; Metal-binding; Oxidoreductase; Oxylipin biosynthesis; Plastid; Reference proteome; Transit peptide
SRR1144633_TR15074_c1_g1_i1_len=591	COPA3_ORYSJ	Q:4-591,H:106-301	95.41%ID	E:3e-132	Coatomer subunit alpha-3	PF00400.29*WD40*WD domain, G-beta repeat*2-17*E:0.0028*PF00400.29*WD40*WD domain, G-beta repeat*22-59*E:1.4e-08*PF00400.29*WD40*WD domain, G-beta repeat*94-127*E:3.7e-03*PF12894.4*ANAPC4_WD40*Anaphase-promoting complex subunit 4 WD40 domain*107-187*E:2.8e-05*PF00400.29*WD40*WD domain, G-beta repeat*136-172*E:1.6e-06	0,326	-0,356	0,001	1,996	0,09	-0,703	0,721	-0,151	0	1,831	COPA3_ORYSJ	Coatomer subunit alpha-3 (Alpha-coat protein 3) (Alpha-COP 3)	Os09g0127800 LOC_Os09g04110 Osj_027299	Oryza sativa subsp. japonica (Rice)		Complete proteome; Cytoplasm; Cytoplasmic vesicle; ER-Golgi transport; Golgi apparatus; Membrane; Protein transport; Reference proteome; Repeat; Transport; WD repeat
SRR1144634_TR25396_c0_g1_i1_len=504	NRP2_ARATH	Q:144-485,H:1-107	70.18%ID	E:1e-44	NAP1-related protein 2	PF00956.15*NAP*Nucleosome assembly protein (NAP)*33-77*E:2.3e-07	0	-8,412	0	6,758	1	0	1	2,591	0	6,924	NRP2_ARATH	NAP1-related protein 2 (Nucleosome/chromatin assembly factor group AS) (Protein SET homolog 2)	NRP2 NFA5 At1g18600 F6A14.10	Arabidopsis thaliana (Mouse-ear cress)		Alternative splicing; Chaperone; Coiled coil; Complete proteome; Cytoplasm; Nucleus; Reference proteome
SRR122238_TR21935_c0_g1_i4_len=2255	PTR27_ARATH	Q:208-591,H:1-555	77.35%ID	E:0	Protein NRT1/ PTR FAMILY 6.2	PF00854.18*PTR2*POT family*96-630*E:1.7e-104	0,283	0,625	0	3,033	0,653	0,115	0,019	0,572	0	2,319	PTR27_ARATH	Protein NRT1/ PTR FAMILY 6.2 (AINPF6.2) (Nitrate transporter 1.4)	NPF6.2 NRT1.4 NTP2 At2g26690 F18A8.6	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Membrane; Nitrate assimilation; Reference proteome; Symport; Transmembrane; Transmembrane helix; Transport
SRR122238_TR29842_c1_g3_i2_len=760	ARF2_ORYSJ	Q:152-694,H:1-181	98.9%ID	E:3e-130	ADP-ribosylation factor 2	PF00025.18*Arf*ADP-ribosylation factor family*5-177*E:3.1e-80*PF09439.7*SRPRB*Signal recognition particle receptor beta subunit*16-143*E:8.8e-14*PF08477.10*Roc*Ras of Complex, Roc, domain of DAPKinase*19-129*E:1.1e-13*PF04670.9*Gtr1_RagA*Gtr1/RagA G protein conserved region*19-142*E:2.5e-10*PF01926.20*MMR_HSR1*50S ribosome-binding GTPase*19-122*E:4.9e-05*PF00071.19*Ras*Ras family*20-172*E:1.1e-12	0,464	-0,237	0	1,178	1	0,001	0,751	0,114	0	0,903	ARF2_ORYSJ	ADP-ribosylation factor 2	ARF Os05g0489600 LOC_Os05g41060 OJ1119_H02.17	Oryza sativa subsp. japonica (Rice)		Complete proteome; ER-Golgi transport; GTP-binding; Golgi apparatus; Lipoprotein; Myristate; Nucleotide-binding; Protein transport; Reference proteome; Transport
SRR122238_TR47348_c0_g2_i2_len=1421	AROF_SOLLC	Q:1205-18,H:27-407	80.56%ID	E:0	Phospho-2-dehydro-3-deoxyheptonate aldolase 1, chloroplastic	PF01474.13*DAHP_synth_2*Class-II DAHP synthetase family*72-418*E:1.3e-145	0,028	0,542	0	3,799	0,034	0,58	0,101	0,464	0	2,336	AROF_SOLLC	Phospho-2-dehydro-3-deoxyheptonate aldolase 1, chloroplastic (EC 2.5.1.54) (3-deoxy-D-arabino-heptulosonate 7-phosphate synthase 1) (DAHP synthase 1) (Phospho-2-keto-3-deoxyheptonate aldolase 1)		Solanum lycopersicum (Tomato) (Lycopersicon esculentum)	PATHWAY: Metabolic intermediate biosynthesis; chorismate biosynthesis; chorismate from D-erythrose 4-phosphate and phosphoenolpyruvate: step 1/7.	Amino-acid biosynthesis; Aromatic amino acid biosynthesis; Chloroplast; Complete proteome; Plastid; Reference proteome; Transferase; Transit peptide
SRR122238_TR61114_c0_g2_i1_len=522	AROC2_SOLLC	Q:93-520,H:1-139	76.06%ID	E:3e-63	Chorismate synthase 2, chloroplastic	PF01264.18*Chorismate_synt*Chorismate synthase*91-172*E:1e-32	0,429	-0,515	0	7,813	0,623	0,42	0,52	0,463	0	7,752	AROC2_SOLLC	Chorismate synthase 2, chloroplastic (EC 4.2.3.5) (5-enolpyruvylshikimate-3-phosphate phospholyase 2)	CS2	Solanum lycopersicum (Tomato) (Lycopersicon esculentum)	PATHWAY: Metabolic intermediate biosynthesis; chorismate biosynthesis; chorismate from D-erythrose 4-phosphate and phosphoenolpyruvate: step 7/7.	Amino-acid biosynthesis; Aromatic amino acid biosynthesis; Chloroplast; Complete proteome; Lyase; Plastid; Reference proteome; Transit peptide

SRR122238_TR73954_c0_g1_i3_len=839	NA	NA	NA	NA	NA	.	0,129	0,829	0	1,586	0,012	0,858	0,175	0,488	0	7,872	.	.	.	.	.	.
SRR122238_TR77156_c0_g1_i2_len=836	UEV1C_ARATH	Q:697-260,H:1-145	89.73%ID	E:2e-88	Ubiquitin-conjugating enzyme E2 variant 1C	PF00179.23^UQ_con^Ubiquitin-conjugating enzyme^89-182^E:2e-14	1	-0,022	0	1,866	0,579	0,204	0,005	-1,123	0	8,434	UEV1C_ARATH	Ubiquitin-conjugating enzyme E2 variant 1C (Ubc enzyme variant 1C) (Protein MMS ZWEI HOMOLOG 3)	UEV1C MMZ3 At2g36060 F11F19.3	Arabidopsis thaliana (Mouse-ear cress)		Alternative splicing; Complete proteome; Reference proteome
SRR1271857_TR2593_c0_g2_i3_len=1500	GOLS2_ARATH	Q:176-1168,H:14-335	72.81%ID	E:1e-175	Galactinol synthase 2	PF01501.17^Glyco_transf_8^Glycosyl transferase family 8^28-272^E:1.8e-41	0,01	1,772	0	2,345	0,004	0,753	0,098	0,447	0,001	0,996	GOLS2_ARATH	Galactinol synthase 2 (AtGolS2) (GolS-2) (EC 2.4.1.123)	GOLS2 At1g56600 F25P12.95	Arabidopsis thaliana (Mouse-ear cress)		Carbohydrate metabolism; Complete proteome; Cytoplasm; Galactose metabolism; Glycosyltransferase; Manganese; Metal-binding; Reference proteome; Transferase
SRR1271857_TR26829_c0_g1_i1_len=2197	RFS2_ARATH	Q:248-2032,H:1-586	77.98%ID	E:0	Probable galactinol--sucrose galactosyltransferase 2	PF05691.9^Raffinose_syn^Raffinose synthase or seed imbibition protein Sip1^7-576^E:4.1e-269	0,333	0,616	0	3,977	0,224	0,367	0,206	0,386	0	2,405	RFS2_ARATH	Probable galactinol--sucrose galactosyltransferase 2 (EC 2.4.1.82) (Protein SEED IMBIBITION 2) (Raffinose synthase 2)	RFS2 RS2 SIP2 At3g57520 T8H10.120	Arabidopsis thaliana (Mouse-ear cress)		Alternative splicing; Carbohydrate metabolism; Complete proteome; Glycosyltransferase; Reference proteome; Transferase
SRR1271857_TR40399_c0_g1_i1_len=2792	TMN9_ARATH	Q:2432-558,H:16-644	82.83%ID	E:0	Transmembrane 9 superfamily member 9 {ECO:0000305}	PF02990.13^EMP70^Endomembrane protein 70^61-598^E:3.4e-220	0,568	0,182	0	1,93	0,504	0,219	0,144	0,456	0,001	1,311	TMN9_ARATH	Transmembrane 9 superfamily member 9 (Endomembrane protein 2) (Transmembrane nine protein 9) (AtTMN9)	TMN9 EMP2 At5g25100 T11H3_110	Arabidopsis thaliana (Mouse-ear cress)		Alternative splicing; Complete proteome; Endosome; Golgi apparatus; Membrane; Reference proteome; Signal; Transmembrane; Transmembrane helix
SRR1271858_TR3401_c0_g2_i1_len=2902	CDC48_SOYBN	Q:2755-341,H:1-807	94.18%ID	E:0	Cell division cycle protein 48 homolog	PF02359.15^CDC48_N^Cell division protein 48 (CDC48), N-terminal domain^30-111^E:3.9e-23`PF02933.14^CDC48_2^Cell division protein 48 (CDC48), domain 2^132-195^E:6.2e-12`PF00004.26^AAA^ATPase family associated with various cellular activities (AAA)^245-374^E:2.8e-48`PF05496.9^RuvB_N^Holliday junction DNA helicase ruvB N-terminus^245-320^E:5.8e-06`PF07724.11^AAA_2^AAA domain (Cdc48 subfamily)^245-338^E:4e-06`PF07728.11^AAA_5^AAA domain (dynein-related subfamily)^245-363^E:5.7e-05`PF05496.9^RuvB_N^Holliday junction DNA helicase ruvB N-terminus^517-552^E:1.1e-05`PF00004.26^AAA^ATPase family associated with various cellular activities (AAA)^518-651^E:6.6e-47	0,44	-0,254	0	2,945	1	-0,032	0,085	0,609	0	2,23	CDC48_SOYBN	Cell division cycle protein 48 homolog (Valosin-containing protein homolog) (VCP)	CDC48	Glycine max (Soybean) (Glycine hispida)		ATP-binding; Cell cycle; Cell membrane; Complete proteome; Membrane; Nucleotide-binding; Reference proteome; Repeat
SRR1271858_TR19224_c0_g2_i1_len=607	NA	NA	NA	NA	NA	PF11744.5^ALMT^Aluminium activated malate transporter^57-111^E:3.2e-21	0,034	0,824	0	6,802	0,005	1,32	0,005	1,319	0,001	1,788	.	.	.	.	.	.
SRR1271858_TR58701_c1_g1_i1_len=1833	E1313_ARATH	Q:1567-212,H:24-456	42.86%ID	E:7e-125	Glucan endo-1,3-beta-glucosidase 13	PF00332.15^Glyco_hydro_17^Glycosyl hydrolases family 17^39-355^E:3.4e-99`PF07983.10^X8^X8 domain^399-470^E:7.5e-22	0,632	0,249	0	2,781	0,01	2,133	0,517	0,767	0	4,389	E1313_ARATH	Glucan endo-1,3-beta-glucosidase 13 (EC 3.2.1.39) ((1->3)-beta-glucan endohydrolase 13) ((1->3)-beta-glucanase 13) (Beta-1,3-endoglucanase 13) (Beta-1,3-glucanase 13)	At5g56590 MIK19.3	Arabidopsis thaliana (Mouse-ear cress)		Cell membrane; Cell wall; Cell wall biogenesis/degradation; Complete proteome; Disulfide bond; GPI-anchor; Glycoprotein; Glycosidase; Hydrolase; Lipoprotein; Membrane; Plant defense; Reference proteome; Secreted; Signal
SRR1271859_TR815_c0_g1_i1_len=855	NA	NA	NA	NA	NA	.	0,399	-0,187	0	1,483	0,866	0,041	0,052	-0,448	0	11,959	.	.	.	.	.	.
SRR1271859_TR10523_c2_g1_i2_len=689	C71A8_MENPI	Q:108-674,H:284-472	48.68%ID	E:6e-58	Cytochrome P450 71A8	PF00067.19^p450^Cytochrome P450^18-203^E:5.5e-51	0,778	-0,083	0	2,354	0,016	0,762	0	-1,79	0	2,112	C71A8_MENPI	Cytochrome P450 71A8 (EC 1.14.-.-)	CYP71A8	Mentha piperita (Peppermint) (Mentha aquatica ? Mentha spicata)		Heme; Iron; Membrane; Metal-binding; Monooxygenase; Oxidoreductase; Transmembrane; Transmembrane helix
SRR1271859_TR28455_c0_g1_i2_len=1369	EF1A_SOLLC	Q:189-1367,H:1-393	97.96%ID	E:0	Elongation factor 1-alpha	PF00009.24^GTP_EFTU^Elongation factor Tu GTP binding domain^6-221^E:7.2e-53`PF03144.22^GTP_EFTU_D2^Elongation factor Tu domain 2^248-313^E:5.9e-15`PF03143.14^GTP_EFTU_D3^Elongation factor Tu C-terminal domain^322-392^E:1.2e-17	0,014	-0,7	0	1,142	0,636	0,186	1	-0,027	0	1,376	EF1A_SOLLC	Elongation factor 1-alpha (EF-1-alpha)		Solanum lycopersicum (Tomato) (Lycopersicon esculentum)		Complete proteome; Cytoplasm; Elongation factor; GTP-binding; Nucleotide-binding; Phosphoprotein; Protein biosynthesis; Reference proteome
SRR1271859_TR38030_c0_g1_i1_len=3201	EF2_BETVU	Q:3016-488,H:1-843	92.17%ID	E:0	Elongation factor 2	PF00009.24^GTP_EFTU^Elongation factor Tu GTP binding domain^17-342^E:1.5e-64`PF03144.22^GTP_EFTU_D2^Elongation factor Tu domain 2^393-468^E:3.4e-12`PF14492.3^EFG_II^Elongation Factor G, domain II^487-549^E:4.6e-12`PF03764.15^EFG_IV^Elongation factor G, domain IV^610-721^E:3.7e-33`PF00679.21^EFG_C^Elongation factor G C-terminus^724-811^E:1.3e-20	0,004	-0,702	0	2,067	0,247	-0,317	0,862	-0,058	0	1,42	EF2_BETVU	Elongation factor 2 (EF-2)		Beta vulgaris (Sugar beet)		Cytoplasm; Elongation factor; GTP-binding; Nucleotide-binding; Phosphoprotein; Protein biosynthesis
SRR342017_TR18107_c0_g2_i1_len=825	UBAX1_ARATH	Q:343-819,H:138-293	54.88%ID	E:4e-43	.	PF08059.10^SEP^SEP domain^125-181^E:2.2e-22	0,635	-0,335	0,001	3,624	0,5	-0,59	1	0,137	0	3,634	PUX5_ARATH	Plant UBX domain-containing protein 5 (PUX5)	PUX5 At4g15410 dl3750w FCAALL.290	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Reference proteome; Ubl conjugation pathway
SRR342019_TR519_c0_g1_i1_len=692	NA	NA	NA	NA	NA	.	0,084	0,546	0	1,064	0,767	0,076	0,337	0,23	0	7,129	.	.	.	.	.	.
SRR342019_TR5968_c2_g9_i3_len=682	NA	NA	NA	NA	NA	.	0,101	0,416	0	8,493	0,378	-0,23	0,281	-0,281	0	1,264	.	.	.	.	.	.
SRR342022_TR961_c4_g1_i2_len=616	AROG_SOLTU	Q:55-615,H:305-491	94.65%ID	E:6e-129	Phospho-2-dehydro-3-deoxyheptonate aldolase 2, chloroplastic	PF01474.13^DAHP_synth_2^Class-II DAHP synthetase family^1-173^E:7.8e-85	0,011	0,61	0	2,857	0,022	0,595	0,147	0,38	0	1,342	AROG_SOLTU	Phospho-2-dehydro-3-deoxyheptonate aldolase 2, chloroplastic (EC 2.5.1.54) (3-deoxy-D-arabino-heptulosonate 7-phosphate synthase 2) (DAHP synthase 2) (Phospho-2-keto-3-deoxyheptonate aldolase 2)	SHKB ARO2	Solanum tuberosum (Potato)	PATHWAY: Metabolic intermediate biosynthesis; chorismate biosynthesis; chorismate from D-erythrose 4-phosphate and phosphoenolpyruvate: step 1/7.	Amino-acid biosynthesis; Aromatic amino acid biosynthesis; Chloroplast; Complete proteome; Plastid; Reference proteome; Transferase; Transit peptide
SRR342022_TR4690_c0_g1_i4_len=2277	GLYM_SOLTU	Q:356-1909,H:1-518	90.56%ID	E:0	Serine hydroxymethyltransferase, mitochondrial	PF00464.16^SHMT^Serine hydroxymethyltransferase^58-454^E:1.2e-210	0,217	-0,322	0	9,911	0	-1,75	0	-0,886	0	1,298	GLYM_SOLTU	Serine hydroxymethyltransferase, mitochondrial (SHMT) (EC 2.1.2.1) (Glycine hydroxymethyltransferase) (Serine methylase)		Solanum tuberosum (Potato)	PATHWAY: One-carbon metabolism; tetrahydrofolate interconversion.	Complete proteome; Mitochondrion; One-carbon metabolism; Pyridoxal phosphate; Reference proteome; Transferase; Transit peptide
SRR342022_TR21447_c1_g1_i6_len=742	NA	NA	NA	NA	NA	PF00248.18^Aldo_ket_red^Aldo/keto reductase family^120-247^E:4.5e-23	0,721	-0,18	0	3,563	0,297	-0,42	0,816	0,084	0	8,409	.	.	.	.	.	.
SRR342023_TR831_c2_g6_i5_len=859	MTHR1_MAIZE	Q:113-859,H:1-249	88.76%ID	E:9e-161	Methylenetetrahydrofolate reductase 1	.	0,03	0,963	0	7,229	0,017	-1,365	0,132	-0,825	0	8,371	MTHR1_MAIZE	Methylenetetrahydrofolate reductase 1 (EC 1.5.1.20) (ZmMTHFR1)		Zea mays (Maize)	PATHWAY: One-carbon metabolism; tetrahydrofolate interconversion.	Complete proteome; FAD; Flavoprotein; NAD; Oxidoreductase; Reference proteome
SRR342023_TR23697_c2_g1_i9_len=1234	RFS2_ARATH	Q:113-1234,H:226-597	85.29%ID	E:0	Probable galactinol--sucrose galactosyltransferase 2	PF05691.9^Raffinose_syn^Raffinose synthase or seed imbibition protein Sip1^1-251^E:4.3e-141	0,56	0,895	0	3,813	0,162	0,407	0,825	-0,088	0	6,349	RFS2_ARATH	Probable galactinol--sucrose galactosyltransferase 2 (EC 2.4.1.82) (Protein SEED IMBIBITION 2) (Raffinose synthase 2)	RFS2 RS2 SIP2 At3g57520 T8H10.120	Arabidopsis thaliana (Mouse-ear cress)		Alternative splicing; Carbohydrate metabolism; Complete proteome; Glycosyltransferase; Reference proteome; Transferase
SRR342023_TR30529_c0_g9_i1_len=1364	IF4A2_NICPL	Q:212-1153,H:1-314	95.54%ID	E:0	Eukaryotic initiation factor 4A-2	PF00270.26^DEAD^DEAD/DEAH box helicase^65-226^E:2.8e-40`PF04851.12^ResIII^Type III restriction enzyme, res subunit^83-223^E:8.6e-07	0,058	-0,532	0	4,418	0,329	0,303	0,05	0,593	0	1,349	IF4A2_NICPL	Eukaryotic initiation factor 4A-2 (eIF-4A-2) (EC 3.6.4.13) (ATP-dependent RNA helicase eIF4A-2)		Nicotiana plumbaginifolia (Leadwort-leaved tobacco) (Tex-Mex tobacco)		ATP-binding; Helicase; Hydrolase; Initiation factor; Nucleotide-binding; Protein biosynthesis; RNA-binding
SRR646572_TR2358_c0_g1_i1_len=1543	NA	NA	NA	NA	NA	PF06200.11^tify^tify domain^120-151^E:1.5e-16`PF09425.7^CCT_2^Divergent CCT motif^258-271^E:1.4e-05	1	0	0	3,427	0,129	-5,085	0,129	-5,085	0	6,745	.	.	.	.	.	.
SRR646572_TR21988_c0_g1_i1_len=2298	BIP5_TOBAC	Q:237-2174,H:1-646	95.2%ID	E:0	Luminal-binding protein 5	PF00012.17^HSP70^Hsp70 protein^38-645^E:4.1e-268`PF06723.10^MreB_Mbl^MreB/Mbl protein^151-405^E:6.5e-17	0,119	-0,534	0	2,291	0,537	-0,376	0,142	-0,751	0	5,588	BIP5_TOBAC	Luminal-binding protein 5 (BiP 5) (78 kDa glucose-regulated protein homolog 5) (GRP-78-5)	BIP5	Nicotiana tabacum (Common tobacco)		ATP-binding; Endoplasmic reticulum; Glycoprotein; Nucleotide-binding; Signal
SRR646572_TR26211_c1_g3_i2_len=2581	HSP7C_PETHY	Q:2324-378,H:1-651	93.24%ID	E:0	Heat shock cognate 70 kDa protein	PF00012.17^HSP70^Hsp70 protein^9-618^E:4.7e-268`PF06723.10^MreB_Mbl^MreB/Mbl protein^142-380^E:5.5e-14	0,844	-0,049	0	1,984	0,192	0,303	0,007	0,613	0,001	0,978	HSP7C_PETHY	Heat shock cognate 70 kDa protein	HSP70	Petunia hybrida (Petunia)		ATP-binding; Nucleotide-binding; Stress response
SRR646596_TR31160_c0_g1_i5_len=5738	PP226_ARATH	Q:4997-4020,H:54-379	44.48%ID	E:1e-82	Pentatricopeptide repeat-containing protein At3g13160, mitochondrial	PF01535.17^PPR^PPR repeat^160-185^E:0.00039`PF17177.1^PPR_long^Pentacotripeptide-repeat region of PROPR^167-276^E:1.1e-07`PF13812.3^PPR_3^Pentatricopeptide repeat domain^175-233^E:2.8e-09`PF01535.17^PPR^PPR repeat^191-217^E:0.09`PF12854.4^PPR_1^PPR repeat^221-252^E:1.8e-12`PF13041.3^PPR_2^PPR repeat family^223-270^E:4.9e-16`PF01535.17^PPR^PPR repeat^226-256^E:6e-07`PF13812.3^PPR_3^Pentatricopeptide repeat domain^247-302^E:1.8e-07`PF12854.4^PPR_1^PPR repeat^255-287^E:8.9e-06`PF13041.3^PPR_2^PPR repeat family^258-305^E:8.8e-08`PF01535.17^PPR^PPR repeat^261-290^E:0.0007`PF13041.3^PPR_2^PPR repeat family^294-340^E:9.6e-11`PF01535.17^PPR^PPR repeat^297-326^E:0.0036`PF13812.3^PPR_3^Pentatricopeptide repeat domain^317-371^E:4e-11`PF13041.3^PPR_2^PPR repeat family^329-373^E:3.9e-11`PF01535.17^PPR^PPR repeat^331-361^E:1.8e-06	0,001	2,499	0	2,354	0,017	4,264	0,002	4,701	0	2,293	PP226_ARATH	Pentatricopeptide repeat-containing protein At3g13160, mitochondrial	At3g13160 MJG19.11	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Mitochondrion; Reference proteome; Repeat; Transit peptide
SRR646604_TR37414_c0_g2_i3_len=1472	GOLS2_ARATH	Q:1330-338,H:14-335	72.81%ID	E:3e-176	Galactinol synthase 2	PF01501.17^Glyco_transf_8^Glycosyl transferase family 8^28-272^E:1.8e-41	0,007	2,121	0	2,757	0,018	0,628	0,186	0,361	0	4,219	GOLS2_ARATH	Galactinol synthase 2 (AtGolS2) (GolS-2) (EC 2.4.1.123)	GOLS2 At1g56600 F25P12.95	Arabidopsis thaliana (Mouse-ear cress)		Carbohydrate metabolism; Complete proteome; Cytoplasm; Galactose metabolism; Glycosyltransferase; Manganese; Metal-binding; Reference proteome; Transferase
SRR648705_TR23795_c0_g1_i1_len=2325	YTHD2_MOUSE	Q:1266-1826,H:382-565	48.17%ID	E:7e-53	YTH domain-containing family protein 2 {ECO:0000305}	PF04146.12^YTH^YT521-B-like domain^346-487^E:2.4e-35	1	-0,02	0,001	1,232	0,064	0,672	0,01	0,886	0	3,648	YTHD2_MOUSE	YTH domain-containing family protein 2	Ythdf2	Mus musculus (Mouse)		Acetylation; Complete proteome; Cytoplasm; Phosphoprotein; RNA-binding; Reference proteome
SRR648705_TR25099_c1_g3_i4_len=1258	GEDH1_OCIBA	Q:226-936,H:11-246	57.38%ID	E:2e-71	Geraniol dehydrogenase 1	PF08240.9^ADH_N^Alcohol dehydrogenase GroES-like domain^39-152^E:4.4e-27	0,196	-0,419	0	4,309	1	-0,062	0,812	0,143	0	2,88	GEDH1_OCIBA	Geraniol dehydrogenase 1 (ObaGEDH1) (EC 1.1.1.183)	GEDH1	Ocimum basilicum (Sweet basil)		Metal-binding; NADP; Oxidoreductase; Zinc
SRR648705_TR28357_c0_g1_i2_len=2820	THIC_ARATH	Q:242-2173,H:3-643	85.74%ID	E:0	Phosphomethylpyrimidine synthase, chloroplastic	PF01964.15^ThiC_Rad_SAM^Radical SAM ThiC family^166-586^E:7.1e-198	0,397	-0,214	0	9,752	0,129	-4,919	0,129	-4,919	0	9,711	THIC_ARATH	Phosphomethylpyrimidine synthase, chloroplastic (EC 4.1.99.17) (Hydroxymethylpyrimidine phosphate synthase) (HMP-P synthase) (HMP-phosphate synthase) (HMPP synthase) (Protein PYRIMIDINE REQUIRING) (Thiamine biosynthesis protein ThiC) (Protein THIAMINE C)	THIC PY At2g29630 T27A16.27	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Cofactor biosynthesis; thiamine diphosphate biosynthesis.	3D-structure; 4Fe-4S; Chloroplast; Complete proteome; Iron; Iron-sulfur; Lyase; Metal-binding; Plastid; Reference proteome; S-adenosyl-L-methionine; Thiamine biosynthesis; Transit peptide; Zinc
SRR924147_TR14862_c0_g1_i2_len=815	UBQ11_ARATH	Q:181-813,H:1-211	100%ID	E:1e-148	Polyubiquitin 11	PF14560.3^Ubiquitin_2^Ubiquitin-like domain^59-129^E:0.00021`PF11976.5^Rad60-SLD^Ubiquitin-2 like Rad60 SUMO-like^61-131^E:7.9e-16`PF00240.20^ubiquitin^Ubiquitin family^63-134^E:1.2e-33`PF13881.3^Rad60-SLD_2^Ubiquitin-2 like Rad60 SUMO-like^70-131^E:0.1`PF11976.5^Rad60-SLD^Ubiquitin-2 like Rad60 SUMO-like^137-207^E:7.9e-16`PF00240.20^ubiquitin^Ubiquitin family^139-210^E:1.2e-33`PF14560.3^Ubiquitin_2^Ubiquitin-like domain^148-205^E:0.0005`PF13881.3^Rad60-SLD_2^Ubiquitin-2 like Rad60 SUMO-like^149-207^E:0.12`PF11976.5^Rad60-SLD^Ubiquitin-2 like Rad60 SUMO-like^213-271^E:1.3e-11`PF00240.20^ubiquitin^Ubiquitin family^215-271^E:1.2e-25`PF14560.3^Ubiquitin_2^Ubiquitin-like domain^224-258^E:0.016	0,708	0,129	0	1,903	0,909	0,049	0,778	0,095	0	1,632	UBQ11_ARATH	Polyubiquitin 11 [Cleaved into: Ubiquitin]	UBQ11 At4g05050 C17L7.6 T32N4.13	Arabidopsis thaliana (Mouse-ear cress)		Alternative splicing; Complete proteome; Cytoplasm; Isopeptide bond; Nucleus; Reference proteome; Repeat; Ubl conjugation; Ubl conjugation pathway
SRR924147_TR19409_c0_g2_i1_len=1533	ODPB3_ARATH	Q:170-1384,H:1-406	84.07%ID	E:0	Pyruvate dehydrogenase E1 component subunit beta-3, chloroplastic	PF02779.21^Transket_pyr^Transketolase, pyrimidine binding domain^89-259^E:1.2e-46`PF02780.17^Transketolase_C^Transketolase, C-terminal domain^275-396^E:1.5e-35	0,626	-0,223	0	1,765	0,129	-0,525	0,71	0,138	0,001	1,415	ODPB3_ARATH	Pyruvate dehydrogenase E1 component subunit beta-3, chloroplastic (EC 1.2.4.1)	E1-BETA-2 At2g34590 T31E10.7	Arabidopsis thaliana (Mouse-ear cress)		Chloroplast; Complete proteome; Glycolysis; Oxidoreductase; Plastid; Pyruvate; Reference proteome; Thiamine pyrophosphate; Transit peptide
SRR924148_TR26347_c0_g1_i3_len=1594	MTDH_APIGR	Q:1269-208,H:4-359	57.7%ID	E:8e-133	Mannitol dehydrogenase	PF08240.9^ADH_N^Alcohol dehydrogenase GroES-like domain^37-146^E:3.3e-23`PF02826.16^2-Hacid_dh_C^D-isomer specific 2-hydroxyacid dehydrogenase, NAD binding domain^177-227^E:3e-06`PF00107.23^ADH_zinc_N^Zinc-binding dehydrogenase^190-313^E:5.5e-14	0,013	-0,58	0	7,423	0,124	-0,455	0,468	-0,214	0	8,383	MTDH_APIGR	Mannitol dehydrogenase (EC 1.1.1.255) (NAD-dependent mannitol dehydrogenase)	MTD	Apium graveolens (Celery)		Cytoplasm; Metal-binding; NAD; Oxidoreductase; Zinc
SRR924148_TR28419_c0_g3_i7_len=1288	PIP1_SOLLC	Q:347-1114,H:1-256	86.72%ID	E:3e-160	Probable aquaporin PIP-type pTOM75	PF00230.17^MIP^Major intrinsic protein^45-256^E:5.9e-73	0,241	-0,674	0	2,936	0,22	0,487	0,562	-0,241	0	1,855	PIP1_SOLLC	Probable aquaporin PIP-type pTOM75 (Ripening-associated membrane protein) (RAMP)		Solanum lycopersicum (Tomato) (Lycopersicon esculentum)		Cell membrane; Complete proteome; Membrane; Reference proteome; Repeat; Stress response; Transmembrane; Transmembrane helix; Transport
SRR342023_TR18646_c0_g1_i1_len=508	GOLS2_ARATH	Q:198-506,H:14-116	82.52%ID	E:2e-54	Galactinol synthase 2	PF01501.17^Glyco_transf_8^Glycosyl transferase family 8^28-118^E:4.1e-09	0	6,669	0	7,825	0,496	-0,263	0,011	0,801	0	9,306	GOLS2_ARATH	Galactinol synthase 2 (AtGolS2) (GolS-2) (EC 2.4.1.123)	GOLS2 At1g56600 F25P12.95	Arabidopsis thaliana (Mouse-ear cress)		Carbohydrate metabolism; Complete proteome; Cytoplasm; Galactose metabolism; Glycosyltransferase; Manganese; Metal-binding; Reference proteome; Transferase
SRR342023_TR31063_c0_g4_i4_len=854	TRPB_CAMAC	Q:24-854,H:27-306	83.21%ID	E:2e-168	Tryptophan synthase beta chain 2, chloroplastic	PF00291.22^PALP^Pyridoxal-phosphate dependent enzyme^100-284^E:2.6e-29	0	1,355	0	9,327	0,699	-0,154	0,95	-0,04	0	1,594	TRPB_CAMAC	Tryptophan synthase beta chain 2, chloroplastic (EC 4.2.1.20)	TSB	Camptotheca acuminata (Happy tree)	PATHWAY: Amino-acid biosynthesis; L-tryptophan biosynthesis; L-tryptophan from chorismate: step 5/5.	Amino-acid biosynthesis; Aromatic amino acid biosynthesis; Chloroplast; Lyase; Plastid; Pyridoxal phosphate; Transit peptide; Tryptophan biosynthesis
SRR1144634_TR33976_c0_g2_i1_len=1286	NA	NA	NA	NA	NA	PF05627.8^AvrRpt-cleavage^Cleavage site for pathogenic type III effector avirulence factor Avr^199-235^E:2.6e-22	0	4,674	0,129	4,616	0,003	2,699	0	3,546	1	-0,586	.	.	.	.	.	.
SRR122238_TR46358_c0_g2_i1_len=1302	NA	NA	NA	NA	NA	.	0,001	1,602	0,007	1,095	0,002	1,176	0	1,61	0,76	0,608	.	.	.	.	.	.
SRR342019_TR22055_c0_g6_i8_len=2444	U89A2_ARATH	Q:1622-240,H:19-465	51.72%ID	E:9e-158	UDP-glycosyltransferase 89A2	PF00201.15^UDPGT^UDP-glucoronosyl and UDP-glucosyl transferase^263-435^E:9.1e-18	0	2,185	0,007	2,16	0,009	1,615	0	2,887	0,206	0,664	U89A2_ARATH	UDP-glycosyltransferase 89A2 (EC 2.4.1.-)	UGT89A2 At5g03490 F12E4.260	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Glycosyltransferase; Reference proteome; Transferase
SRR1144633_TR4333_c0_g2_i1_len=829	TCTP_ELAGV	Q:706-203,H:1-168	87.5%ID	E:3e-84	Translationally-controlled tumor protein homolog	PF00838.14^TCTP^Translationally controlled tumour protein^42-205^E:2.1e-58	0,882	0,122	0	3,042	0,16	1,382	0	2,58	1	0	TCTP_ELAGV	Translationally-controlled tumor protein homolog (TCTP)	TCTP	Elaeis guineensis var. tenera (Oil palm)		Calcium; Cytoplasm
SRR1144633_TR36337_c0_g1_i1_len=1588	NA	NA	NA	NA	NA	.	0,959	0,016	0	1,275	0,003	0,692	0	0,827	0,132	0,676	.	.	.	.	.	.
SRR1144634_TR8906_c0_g1_i2_len=3144	NA	NA	NA	NA	NA	PF13855.3^LRR_8^Leucine rich repeat^448-504^E:8.4e-11`PF12799.4^LRR_4^Leucine Rich repeats (2 copies)^471-507^E:3.3e-08`PF14580.3^LRR_9^Leucine-rich repeat^471-553^E:2.6e-08`PF12799.4^LRR_4^Leucine Rich repeats (2 copies)^492-533^E:1.3e-07`PF13516.3^LRR_6^Leucine Rich repeat^492-505^E:1.7`PF13855.3^LRR_8^Leucine rich repeat^493-549^E:4.5e-08`PF13516.3^LRR_6^Leucine Rich repeat^538-551^E:0.35	0,079	0,538	0	1,481	0,003	0,721	0	1,285	1	-0,038	.	.	.	.	.	.
SRR1144634_TR15551_c0_g2_i2_len=1282	GSTF_HYOMU	Q:748-251,H:48-212	68.67%ID	E:3e-79	Glutathione S-transferase	PF00043.22^GST_C^Glutathione S-transferase, C-terminal domain^9-103^E:2.9e-16`PF13410.3^GST_C_2^Glutathione S-transferase, C-terminal domain^31-97^E:4.5e-09`PF14497.3^GST_C_3^Glutathione S-transferase, C-terminal domain^37-104^E:9.6e-06	0,073	-1,985	0,001	1,75	0,003	3,262	0	3,687	1	0,198	GSTF_HYOMU	Glutathione S-transferase (EC 2.5.1.18) (25 kDa auxin-binding protein) (GST class-phi)		Hyoscyamus muticus (Egyptian henbane)		Auxin signaling pathway; Direct protein sequencing; Transferase
SRR1144634_TR23126_c3_g3_i2_len=696	PRS2_SOLTU	Q:597-130,H:1-155	38.75%ID	E:2e-25	Pathogenesis-related protein STH-2	PF00407.16^Bet_v_1^Pathogenesis-related protein Bet v I family^34-183^E:8.4e-12	1	0,059	0	2,295	0,017	0,857	0,001	1,16	0,472	0,777	PRS2_SOLTU	Pathogenesis-related protein STH-2	STH-2	Solanum tuberosum (Potato)		Complete proteome; Pathogenesis-related protein; Plant defense; Reference proteome
SRR122237_TR14951_c0_g1_i1_len=1315	GOLS2_SOLLC	Q:1251-241,H:1-337	81.23%ID	E:0	Galactinol synthase 2	PF01501.17^Glyco_transf_8^Glycosyl transferase family 8^49-292^E:4.9e-41	0,164	0,97	0	2,335	0,002	1,562	0	1,753	1	0,284	GOLS2_SOLLC	Galactinol synthase 2 (GolS-2) (SlGolS2) (EC 2.4.1.123)	GOLS2	Solanum lycopersicum (Tomato) (Lycopersicon esculentum)		Carbohydrate metabolism; Complete proteome; Cytoplasm; Galactose metabolism; Glycosyltransferase; Manganese; Metal-binding; Reference proteome; Transferase
SRR122238_TR6887_c0_g2_i1_len=1739	HST_TOBAC	Q:176-1477,H:1-435	86.01%ID	E:0	Shikimate O-hydroxycinnamoyltransferase	PF02458.12^Transferase^Transferase family^1-429^E:7.8e-109	0,281	0,564	0	3,392	0,022	0,717	0	1,271	0,196	0,807	HST_TOBAC	Shikimate O-hydroxycinnamoyltransferase (EC 2.3.1.133) (Hydroxycinnamoyl transferase) (Hydroxycinnamoyl-Coenzyme A shikimate/quinate hydroxycinnamoyltransferase)	HST HCT	Nicotiana tabacum (Common tobacco)		Acyltransferase; Direct protein sequencing; Transferase
SRR122238_TR37332_c0_g1_i1_len=1339	CSE_ARATH	Q:173-1108,H:21-330	82.37%ID	E:0	Caffeoylshikimate esterase	PF12146.5^Hydrolase_4^Serine aminopeptidase, S33^59-302^E:3.2e-52`PF12697.4^Abhydrolase_6^Alpha/beta hydrolase family^66-304^E:4e-07	0,38	0,588	0	4,278	0,066	0,709	0,001	1,17	0,077	0,916	CSE_ARATH	Caffeoylshikimate esterase (EC 3.1.1.-) (Lysophospholipase 2) (LysoPL2)	CSE At1g52760 F14G24.3	Arabidopsis thaliana (Mouse-ear cress)		Cell membrane; Complete proteome; Hydrolase; Lignin biosynthesis; Membrane; Reference proteome
SRR122238_TR61991_c0_g1_i1_len=1161	ARGI1_ARATH	Q:1098-334,H:88-342	92.16%ID	E:8e-172	Arginase 1, mitochondrial	PF00491.18^Arginase^Arginase family^4-201^E:1.7e-58	0,402	-0,902	0,001	1,949	0,005	4,237	0,001	4,711	0,848	-0,144	ARGI1_ARATH	Arginase 1, mitochondrial (EC 3.5.3.1) (Arginine amidohydrolase 1)	ARGAH1 At4g08900 T3H13.7	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Nitrogen metabolism; urea cycle; L-ornithine and urea from L-arginine: step 1/1.	Arginine metabolism; Complete proteome; Hydrolase; Manganese; Metal-binding; Mitochondrion; Reference proteome; Transit peptide
SRR122238_TR74721_c0_g1_i1_len=1411	TKPR2_ARATH	Q:82-1044,H:1-321	70.4%ID	E:3e-174	Tetraketide alpha-pyrone reductase 2	PF08659.7^KR^KR domain^30-157^E:2.2e-05`PF01370.18^Epimerase^NAD dependent epimerase/dehydratase family^32-269^E:1.1e-26`PF02719.12^Polysacc_synt_2^Polysaccharide biosynthesis protein^32-153^E:3.7e-07`PF01073.16^3Beta_HSD^3-beta hydroxysteroid dehydrogenase/isomerase family^33-266^E:3.2e-20`PF16363.2^GDP_Man_Dehyd^GDP-mannose 4,6 dehydratase^33-289^E:1e-16`PF07993.9^NAD_binding_4^Male sterility protein^33-256^E:8.1e-16`PF05368.10^NmrA^NmrA-like family^33-109^E:8.2e-08`PF13460.3^NAD_binding_10^NAD(P)H-binding^35-217^E:7.3e-15	1	3,013	0	6,893	0,002	6,369	0	6,761	1	3,562	TKPR2_ARATH	Tetraketide alpha-pyrone reductase 2 (EC 1.1.1.-) (Protein CINNAMOYL-COA REDUCTASE-LIKE 6)	TKPR2 CCRL6 At1g68540 T26J14.11	Arabidopsis thaliana (Mouse-ear cress)		Acetylation; Alternative splicing; Complete proteome; Cytoplasm; NADP; Oxidoreductase; Reference proteome
SRR122238_TR78776_c0_g1_i4_len=868	NA	NA	NA	NA	NA	PF13259.3^DUF4050^Protein of unknown function (DUF4050)^73-113^E:3.2e-11	0,095	0,504	0	2,012	0,01	0,83	0,001	1,062	1	-0,012	.	.	.	.	.	.
SRR122238_TR87584_c0_g1_i5_len=927	FER3_ARATH	Q:149-604,H:1-155	56.77%ID	E:5e-57	Ferredoxin-3, chloroplastic	PF00111.24^Fer2^2Fe-2S iron-sulfur cluster binding domain^65-138^E:2.6e-21	0,108	0,728	0	2,29	0,004	1,159	0	1,829	0	-8,72	FER3_ARATH	Ferredoxin-3, chloroplastic (AtFd3)	FD3 At2g27510 F10A12.19	Arabidopsis thaliana (Mouse-ear cress)		2Fe-2S; Acetylation; Chloroplast; Complete proteome; Electron transport; Iron; Iron-sulfur; Metal-binding; Plastid; Reference proteome; Transit peptide; Transport
SRR1271857_TR5433_c0_g2_i3_len=2219	CYSZ_CUCMA	Q:1987-596,H:12-475	88.17%ID	E:0	Citrate synthase, glyoxysomal	PF00285.18^Citrate_synt^Citrate synthase, C-terminal domain^101-469^E:2.8e-134	0,811	-0,318	0	3,073	0,044	2,337	0	3,332	1	0,871	CYSZ_CUCMA	Citrate synthase, glyoxysomal (EC 2.3.3.16) (GCS)		Cucurbita maxima (Pumpkin) (Winter squash)	PATHWAY: Carbohydrate metabolism; glyoxylate cycle; isocitrate from oxaloacetate: step 1/2.	Direct protein sequencing; Glyoxylate bypass; Glyoxysome; Peroxisome; Transferase; Transit peptide; Tricarboxylic acid cycle
SRR1271857_TR9218_c0_g4_i3_len=1163	NA	NA	NA	NA	NA	.	0,286	0,305	0	0,856	0,004	0,656	0	1,123	0,054	0,723	.	.	.	.	.	.
SRR1271857_TR9959_c0_g1_i24_len=2120	NA	NA	NA	NA	NA	PF08491.7^SE^Squalene epoxidase^78-167^E:9.5e-05	0,581	0,342	0	2,908	0,001	2,042	0	3,03	0,822	0,357	.	.	.	.	.	.
SRR1271858_TR57555_c0_g1_i4_len=965	NA	NA	NA	NA	NA	.	0,804	0,1	0	2,58	0,014	0,782	0	1,174	0,03	0,793	.	.	.	.	.	.
SRR1271858_TR57555_c0_g1_i5_len=1914	NA	NA	NA	NA	NA	.	0,32	0,273	0	0,921	0,007	0,732	0	1,046	0,065	0,534	.	.	.	.	.	.
SRR1271858_TR64995_c1_g2_i5_len=1699	E1314_ARATH	Q:546-1571,H:28-370	68.8%ID	E:9e-174	Glucan endo-1,3-beta-glucosidase 14	PF00332.15^Glyco_hydro_17^Glycosyl hydrolases family 17^28-344^E:9.2e-94	0,258	0,931	0	2,302	0,003	2,148	0	3,17	1	0,182	E1314_ARATH	Glucan endo-1,3-beta-glucosidase 14 (EC 3.2.1.39) ((1->3)-beta-glucan endohydrolase 14) ((1->3)-beta-glucanase 14) (Beta-1,3-endoglucanase 14) (Beta-1,3-glucanase 14)	At2g27500 F10A12.18	Arabidopsis thaliana (Mouse-ear cress)		Alternative splicing; Cell membrane; Cell wall; Cell wall biogenesis/degradation; Complete proteome; Cytoplasm; GPI-anchor; Glycoprotein; Glycosidase; Hydrolase; Lipoprotein; Membrane; Plant defense; Reference proteome; Secreted; Signal
SRR1271859_TR1161_c1_g1_i2_len=4252	PDR3_TOBAC	Q:4251-49,H:47-1447	74.15%ID	E:0	Pleiotropic drug resistance protein 3	PF14510.3^ABC_trans_N^ABC-transporter extracellular N-terminal^64-114^E:1.8e-07`PF00005.24^ABC_tran^ABC transporter^140-322^E:7.8e-17`PF01061.21^ABC2_membrane^ABC-2 type transporter^475-686^E:3.8e-36`PF08370.8^PDR_assoc^Plant PDR ABC transporter associated^691-750^E:1.6e-21`PF00005.24^ABC_tran^ABC transporter^831-980^E:3.4e-19`PF01061.21^ABC2_membrane^ABC-2 type transporter^1127-1340^E:2e-53	0,472	0,811	0	4,331	0,025	2,554	0	3,535	1	0,018	PDR3_TOBAC	Pleiotropic drug resistance protein 3 (NtPDR3)	PDR3	Nicotiana tabacum (Common tobacco)		ATP-binding; Membrane; Nucleotide-binding; Repeat; Transmembrane; Transmembrane helix; Transport
SRR1271859_TR10897_c0_g1_i5_len=1920	AROC2_SOLLC	Q:1612-326,H:1-426	83.45%ID	E:0	Chorismate synthase 2, chloroplastic	PF01264.18^Chorismate_synt^Chorismate synthase^60-407^E:8.6e-140	0,464	0,223	0	1,869	0,008	0,744	0,001	0,945	1	-0,063	AROC2_SOLLC	Chorismate synthase 2, chloroplastic (EC 4.2.3.5) (5-enolpyruvylshikimate-3-phosphate phospholyase 2)	CS2	Solanum lycopersicum (Tomato) (Lycopersicon esculentum)	PATHWAY: Metabolic intermediate biosynthesis; chorismate biosynthesis; chorismate from D-erythrose 4-phosphate and phosphoenolpyruvate: step 7/7.	Amino-acid biosynthesis; Aromatic amino acid biosynthesis; Chloroplast; Complete proteome; Lyase; Plastid; Reference proteome; Transit peptide
SRR1271859_TR19123_c0_g2_i1_len=1875	SPZX_ARATH	Q:222-1379,H:1-389	64.27%ID	E:4e-164	Serpin-ZX	PF00079.17^Serpin^Serpin (serine protease inhibitor)^10-386^E:3.3e-99	0,578	0,228	0	1,408	0,006	0,964	0	1,25	0,767	0,122	SPZX_ARATH	Serpin-ZX (ArathZx) (AtSerpin1) (Serpin-1)	At1g47710 F16N3.3 T2E6.22	Arabidopsis thaliana (Mouse-ear cress)		3D-structure; Apoplast; Complete proteome; Glycoprotein; Protease inhibitor; Reference proteome; Secreted; Serine protease inhibitor
SRR1271859_TR35644_c0_g1_i6_len=2224	AB13I_ARATH	Q:454-1389,H:38-345	80.63%ID	E:5e-173	.	PF00005.24^ABC_tran^ABC transporter^106-261^E:3.7e-30	0,151	0,655	0	2,729	0,001	1,542	0	1,831	0,86	0,161	TGD3_ARATH	Protein TRIGALACTOSYLDIACYLGLYCEROL 3, chloroplastic (ABC transporter I family member 13) (ABC transporter ABCI.13) (AtABCI13) (Non-intrinsic ABC protein 11) (AtNAP11)	TGD3 ABCI13 NAP11 At1g65410 T8F5.19	Arabidopsis thaliana (Mouse-ear cress)		ATP-binding; Chloroplast; Complete proteome; Lipid transport; Nucleotide-binding; Plastid; Reference proteome; Transit peptide; Transport
SRR1271859_TR38961_c0_g1_i1_len=1017	PRS2_SOLTU	Q:740-273,H:1-155	38.12%ID	E:3e-24	Pathogenesis-related protein STH-2	PF00407.16^Bet_v_1^Pathogenesis-related protein Bet v I family^1-150^E:5.3e-12	0,798	0,336	0	1,921	0,021	0,664	0,001	0,942	0,732	-0,641	PRS2_SOLTU	Pathogenesis-related protein STH-2	STH-2	Solanum tuberosum (Potato)		Complete proteome; Pathogenesis-related protein; Plant defense; Reference proteome
SRR1271859_TR45289_c0_g1_i3_len=1673	NA	NA	NA	NA	NA	.	1	0,465	0	7,062	0,003	1,416	0	2,052	0,254	3,39	.	.	.	.	.	.
SRR342017_TR18428_c3_g5_i6_len=3652	OPR11_ORYSJ	Q:2135-1071,H:9-363	78.87%ID	E:0	Putative 12-oxophytodienoate reductase 11	PF00724.17^Oxidored_FMN^NADH:flavin oxidoreductase / NADH oxidase family^20-354^E:6.5e-89	0,886	0,138	0	1,431	0,073	1,892	0	3,861	1	0,151	OPR11_ORYSJ	Putative 12-oxophytodienoate reductase 11 (EC 1.3.1.-) (OPDA-reductase 11) (OsOPR11)	OPR11 OPR3 OsJ_20711	Oryza sativa subsp. japonica (Rice)		Complete proteome; FMN; Fatty acid biosynthesis; Fatty acid metabolism; Flavoprotein; Lipid biosynthesis; Lipid metabolism; NADP; Oxidoreductase; Oxylipin biosynthesis; Reference proteome
SRR342017_TR18700_c0_g1_i1_len=1744	C74B2_ARATH	Q:1572-211,H:38-492	55.92%ID	E:0	Linolenate hydroperoxide lyase, chloroplastic {ECO:0000305|PubMed:9701595}	PF00067.19^p450^Cytochrome P450^161-502^E:3.4e-25	0,002	1,016	0	2,199	0,006	0,653	0,001	0,797	0,052	0,479	C74B2_ARATH	Linolenate hydroperoxide lyase, chloroplastic (EC 4.2.99.-) (Cytochrome P450 74B2) (Hydroperoxide lyase 1)	CYP74B2 HPL1	Arabidopsis thaliana (Mouse-ear cress)		Chloroplast; Heme; Iron; Lyase; Metal-binding; Plastid; Transit peptide
SRR342017_TR22867_c3_g6_i4_len=994	NA	NA	NA	NA	NA	PF13405.3^EF-hand_6^EF-hand domain^19-44^E:5.9e-06`PF13499.3^EF-hand_7^EF-hand domain pair^19-89^E:1.8e-09`PF13202.3^EF-hand_5^EF hand^20-43^E:4.8e-07`PF13833.3^EF-hand_8^EF-hand domain pair^20-40^E:0.02`PF13202.3^EF-hand_5^EF hand^73-89^E:0.018`PF13202.3^EF-hand_5^EF hand^113-135^E:8.9e-06`PF13405.3^EF-hand_6^EF-hand domain^113-138^E:2.1e-05`PF13833.3^EF-hand_8^EF-hand domain pair^114-138^E:0.011	0,233	0,79	0	2,456	0,008	0,745	0	1,82	0,62	-0,237	.	.	.	.	.	.
SRR342017_TR25990_c0_g1_i2_len=2253	CIGR1_ORYSJ	Q:301-2046,H:1-571	57.14%ID	E:0	Chitin-inducible gibberellin-responsive protein 1	PF03514.11^GRAS^GRAS domain family^212-581^E:8.5e-128	0,312	0,755	0	3,77	0,01	1,127	0	1,792	0,793	-0,158	CIGR1_ORYSJ	Chitin-inducible gibberellin-responsive protein 1	CIGR1 Os07g0545800 LOC_Os07g36170 P0006G05.102	Oryza sativa subsp. japonica (Rice)		Complete proteome; Nucleus; Reference proteome; Transcription; Transcription regulation
SRR342017_TR27692_c0_g1_i2_len=1548	10HGO_CATRO	Q:1448-540,H:1-303	97.36%ID	E:2e-175	8-hydroxygeraniol dehydrogenase	PF08240.9^ADH_N^Alcohol dehydrogenase GroES-like domain^38-151^E:6.2e-29`PF02826.16^2-Hacid_dh_C^D-isomer specific 2-hydroxyacid dehydrogenase, NAD binding domain^177-226^E:5.2e-06`PF01262.18^AlaDh_PNT_C^Alanine dehydrogenase/PNT, C-terminal domain^185-256^E:6.9e-06`PF00107.23^ADH_zinc_N^Zinc-binding dehydrogenase^194-295^E:8.5e-14	1	0,089	0	4,474	0,005	6,26	0	7,174	1	-1,832	10HGO_CATRO	8-hydroxygeraniol dehydrogenase (Cr10HGO) (EC 1.1.1.324)	10HGO	Catharanthus roseus (Madagascar periwinkle) (Vinca rosea)		Metal-binding; NADP; Oxidoreductase; Zinc
SRR342019_TR16612_c0_g1_i7_len=2717	ALKBH_ARATH	Q:166-1242,H:1-345	60.99%ID	E:3e-135	Alpha-ketoglutarate-dependent dioxygenase alkB	PF13532.3^2OG-FeII_Oxy_2^2OG-Fe(II) oxygenase superfamily^171-356^E:2.8e-38	0,87	0,195	0	1,932	0,004	0,903	0	1,295	1	-0,23	ALKBH_ARATH	Alpha-ketoglutarate-dependent dioxygenase alkB (EC 1.14.11.-) (Alkylated DNA repair protein alkB homolog)	At1g11780 F25C20.6	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; DNA damage; DNA repair; Dioxygenase; Iron; Metal-binding; Oxidoreductase; Reference proteome
SRR342019_TR24844_c0_g1_i1_len=1199	AX22B_VIGRR	Q:129-704,H:1-196	65.67%ID	E:2e-83	Auxin-induced protein 22B	PF02309.13^AUX_IAA^AUX/IAA family^41-189^E:3.8e-55	1	0,051	0	1,89	0,089	0,447	0,001	0,882	0,064	-0,934	AX22B_VIGRR	Auxin-induced protein 22B (Indole-3-acetic acid-induced protein ARG4)	AUX22B ARG4	Vigna radiata var. radiata (Mung bean) (Phaseolus aureus)		Auxin signaling pathway; Nucleus; Repressor; Transcription; Transcription regulation
SRR342019_TR29297_c2_g5_i1_len=1342	EXPA1_ARATH	Q:172-897,H:7-250	85.66%ID	E:4e-115	Expansin-A1	PF03330.15^DPBB_1^Lytic transglycolase^60-145^E:3.7e-22`PF01357.18^Pollen_allerg_1^Pollen allergen^156-233^E:1.2e-30	0,087	0,475	0	1,499	0,855	-0,066	0	1,466	0,175	0,41	EXPA1_ARATH	Expansin-A1 (AtEXPA1) (Alpha-expansin-1) (At-EXP1) (AtEx1) (Ath-ExpAlpha-1.2)	EXPA1 EXP1 At1g69530 F10D13_18	Arabidopsis thaliana (Mouse-ear cress)		Alternative splicing; Cell wall; Cell wall biogenesis/degradation; Complete proteome; Disulfide bond; Membrane; Reference proteome; Secreted; Signal
SRR342019_TR38071_c4_g2_i9_len=2062	ARGE_ARATH	Q:11-805,H:12-276	74.06%ID	E:5e-136	Acetylornithine deacetylase	PF01546.25^Peptidase_M20^Peptidase family M20/M25/M40^90-194^E:8.9e-20	0,007	2,004	0	3,095	0,004	4,251	0	5,04	0,095	0,744	ARGE_ARATH	Acetylornithine deacetylase (EC 3.5.1.16) (N-acetylornithinase) (AO) (Acetylornithinase) (NAO)	At4g17830 dl4945w T6K21	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Amino-acid biosynthesis; L-arginine biosynthesis; L-ornithine from N(2)-acetyl-L-ornithine (linear): step 1/1.	Alternative splicing; Amino-acid biosynthesis; Arginine biosynthesis; Cobalt; Complete proteome; Hydrolase; Metal-binding; Reference proteome; Zinc
SRR342022_TR1339_c0_g1_i1_len=988	NA	NA	NA	NA	NA	.	0,019	1,06	0	2,115	0,407	0,453	0	1,635	0,781	0,542	.	.	.	.	.	.
SRR342022_TR5402_c1_g18_i2_len=3100	THD1_ARATH	Q:990-2561,H:72-592	76.24%ID	E:0	Threonine dehydratase biosynthetic, chloroplastic	PF04576.12^Zein-binding^Zein-binding^21-111^E:6.5e-33`PF00291.22^PALP^Pyridoxal-phosphate dependent enzyme^370-656^E:2.7e-81`PF00585.15^Thr_dehydrat_C^C-terminal regulatory domain of Threonine dehydratase^669-759^E:2.9e-22`PF00585.15^Thr_dehydrat_C^C-terminal regulatory domain of Threonine dehydratase^765-850^E:6.4e-23	1	0,151	0	3,729	0,059	1,753	0,001	2,62	1	0,065	THD1_ARATH	Threonine dehydratase biosynthetic, chloroplastic (EC 4.3.1.19) (Threonine deaminase) (TD)	OMR1 At3g10050 T22K18.12	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Amino-acid biosynthesis; L-isoleucine biosynthesis; 2-oxobutanoate from L-threonine: step 1/1.	Allosteric enzyme; Amino-acid biosynthesis; Branched-chain amino acid biosynthesis; Chloroplast; Complete proteome; Isoleucine biosynthesis; Lyase; Plastid; Pyridoxal phosphate; Reference proteome; Repeat; Transit peptide
SRR342022_TR9319_c1_g5_i2_len=1841	ABAH2_ARATH	Q:286-1590,H:48-479	72.54%ID	E:0	Abscisic acid 8'-hydroxylase 2	PF00067.19^p450^Cytochrome P450^63-474^E:3.1e-74	0,428	0,372	0	1,349	0,021	0,914	0	1,877	0,683	-0,221	ABAH2_ARATH	Abscisic acid 8'-hydroxylase 2 (ABA 8'-hydroxylase 2) (EC 1.14.13.93) (Cytochrome P450 707A2)	CYP707A2 At2g29090 T9I4.17	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Plant hormone degradation; abscisic acid degradation.	Complete proteome; Heme; Iron; Membrane; Metal-binding; Monooxygenase; NADP; Oxidoreductase; Reference proteome; Stress response; Transmembrane; Transmembrane helix
SRR342022_TR13973_c1_g18_i1_len=2290	PTR30_ARATH	Q:118-1878,H:1-581	72.96%ID	E:0	Protein NRT1/ PTR FAMILY 5.1	PF00854.18^PTR2^POT family^97-525^E:4.7e-108	0,807	0,121	0	2,961	0,014	0,9	0	1,454	1	0,003	PTR30_ARATH	Protein NRT1/ PTR FAMILY 5.1 (AtNPF5.1)	NPF5.1 At2g40460 T2P4.19	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Membrane; Phosphoprotein; Reference proteome; Transmembrane; Transmembrane helix; Transport
SRR342022_TR21932_c0_g1_i2_len=2000	ISPE_SOLLC	Q:1518-460,H:31-382	83.29%ID	E:0	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase, chloroplastic/chromoplastic	PF00288.23^GHMP_kinases_N^GHMP kinases N terminal domain^182-224^E:3.5e-06`PF08544.10^GHMP_kinases_C^GHMP kinases C terminal^310-364^E:0.00022	0,208	0,343	0	1,592	0,007	0,84	0	1,186	1	-0,138	ISPE_SOLLC	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase, chloroplastic/chromoplastic (EC 2.7.1.148) (4-(cytidine-5'-diphospho)-2-C-methyl-D-erythritol kinase) (CMK) (Ripening-associated protein pTOM41) (Fragment)	ISPE	Solanum lycopersicum (Tomato) (Lycopersicon esculentum)	PATHWAY: Isoprenoid biosynthesis; isopentenyl diphosphate biosynthesis via DXP pathway; isopentenyl diphosphate from 1-deoxy-D-xylulose 5-phosphate: step 3/6.	ATP-binding; Chloroplast; Chromoplast; Complete proteome; Isoprene biosynthesis; Kinase; Nucleotide-binding; Plastid; Reference proteome; Transferase; Transit peptide
SRR342023_TR14691_c0_g2_i1_len=2457	HT1_ARATH	Q:1295-2008,H:110-341	38.52%ID	E:6e-42	Serine/threonine-protein kinase HT1	PF12796.4^Ank_2^Ankyrin repeats (3 copies)^47-135^E:5e-14`PF13637.3^Ank_4^Ankyrin repeats (many copies)^47-96^E:1.5e-07`PF00023.27^Ank^Ankyrin repeat^76-106^E:6.4e-05`PF13606.3^Ank_3^Ankyrin repeat^76-103^E:0.00035`PF07714.14^Pkinase_Tyr^Protein tyrosine kinase^175-418^E:1.6e-56`PF00069.22^Pkinase^Protein kinase domain^177-415^E:3.9e-51	0,093	0,979	0	2,666	0,004	2,082	0	3,412	0,472	-0,699	HT1_ARATH	Serine/threonine-protein kinase HT1 (EC 2.7.11.1) (High leaf temperature protein 1)	HT1 At1g62400 F24O1.13	Arabidopsis thaliana (Mouse-ear cress)		ATP-binding; Complete proteome; Kinase; Nucleotide-binding; Reference proteome; Serine/threonine-protein kinase; Transferase
SRR342023_TR24474_c0_g1_i1_len=724	SUI1_ORYSJ	Q:215-553,H:1-115	92.17%ID	E:1e-70	Protein translation factor SUI1 homolog	PF01253.19^SUI1^Translation initiation factor SUI1^28-102^E:5.4e-26	0,709	0,109	0	1,197	0,008	0,734	0	1,07	0,829	0,051	SUI1_ORYSJ	Protein translation factor SUI1 homolog (Protein GOS2) (Protein eIF1) (Translation initiation factor 1)	GOS2 Os07g0529800 LOC_Os07g34589	Oryza sativa subsp. japonica (Rice)		Complete proteome; Initiation factor; Protein biosynthesis; Reference proteome; Translation regulation
SRR342023_TR24864_c0_g3_i1_len=988	KPRS2_SPIOL	Q:494-988,H:39-206	77.98%ID	E:8e-89	Ribose-phosphate pyrophosphokinase 2, chloroplastic	PF13793.3^Pribosyltran_N^N-terminal domain of ribose phosphate pyrophosphokinase^104-220^E:9.7e-50	1	0,006	0	3,39	0,066	0,982	0,001	1,62	0,564	0,508	KPRS2_SPIOL	Ribose-phosphate pyrophosphokinase 2, chloroplastic (EC 2.7.6.1) (Phosphoribosyl pyrophosphate synthase 2)	PRS2	Spinacia oleracea (Spinach)		ATP-binding; Chloroplast; Kinase; Magnesium; Metal-binding; Nucleotide biosynthesis; Nucleotide-binding; Plastid; Transferase; Transit peptide
SRR646572_TR16312_c0_g4_i1_len=1107	NA	NA	NA	NA	NA	.	1	0,046	0	2,521	0,014	1,449	0	2,126	1	0,904	.	.	.	.	.	.
SRR646604_TR9738_c0_g2_i1_len=1683	NA	NA	NA	NA	NA	.	0,319	1,106	0	3,241	0,017	2,023	0	3,36	1	1,856	.	.	.	.	.	.
SRR646604_TR31316_c0_g2_i1_len=3589	THD1_ARATH	Q:2587-1724,H:72-357	77.24%ID	E:3e-136	Threonine dehydratase biosynthetic, chloroplastic	PF00504.18^Chloroa_b-bind^Chlorophyll A-B binding protein^84-199^E:8.2e-27`PF00291.22^PALP^Pyridoxal-phosphate dependent enzyme^375-620^E:1.5e-73	0,839	0,14	0	2,628	0,05	1,033	0	2,157	1	-0,575	THD1_ARATH	Threonine dehydratase biosynthetic, chloroplastic (EC 4.3.1.19) (Threonine deaminase) (TD)	OMR1 At3g10050 T22K18.12	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Amino-acid biosynthesis; L-isoleucine biosynthesis; 2-oxobutanoate from L-threonine: step 1/1.	Allosteric enzyme; Amino-acid biosynthesis; Branched-chain amino acid biosynthesis; Chloroplast; Complete proteome; Isoleucine biosynthesis; Lyase; Plastid; Pyridoxal phosphate; Reference proteome; Repeat; Transit peptide
SRR646604_TR37510_c1_g1_i2_len=2524	KPRS2_SPIOL	Q:1657-596,H:39-395	84.87%ID	E:0	Ribose-phosphate pyrophosphokinase 2, chloroplastic	PF13793.3^Pribosyltran_N^N-terminal domain of ribose phosphate pyrophosphokinase^2-98^E:9.5e-43`PF00156.24^Pribosyltran^Phosphoribosyl transferase domain^133-229^E:1.7e-15`PF14572.3^Pribosyl_synth^Phosphoribosyl synthetase-associated domain^184-291^E:2.1e-23	0,83	0,126	0	2,268	0,002	1,493	0	2,059	0,718	-0,177	KPRS2_SPIOL	Ribose-phosphate pyrophosphokinase 2, chloroplastic (EC 2.7.6.1) (Phosphoribosyl pyrophosphate synthase 2)	PRS2	Spinacia oleracea (Spinach)		ATP-binding; Chloroplast; Kinase; Magnesium; Metal-binding; Nucleotide biosynthesis; Nucleotide-binding; Plastid; Transferase; Transit peptide
SRR648705_TR3147_c0_g2_i1_len=2470	NA	NA	NA	NA	NA	PF07676.9^PD40^WD40-like Beta Propeller Repeat^518-547^E:0.00018`PF07676.9^PD40^WD40-like Beta Propeller Repeat^561-587^E:2.4e-07	0,865	-0,229	0	2,178	0,001	2,133	0	4,027	0,524	0,635	.	.	.	.	.	.
SRR648705_TR3706_c0_g2_i1_len=1432	NA	NA	NA	NA	NA	PF00168.27^C2^C2 domain^6-99^E:2.1e-09	0,436	0,237	0	1,575	0,014	0,79	0	1,12	0,403	0,261	.	.	.	.	.	.
SRR648705_TR12973_c0_g2_i1_len=3944	CLPD_ARATH	Q:3008-318,H:42-943	70.88%ID	E:0	Chaperone protein ClpD, chloroplastic {ECO:0000303|PubMed:11299370}	PF02861.17^Clp_N^Clp amino terminal domain, pathogenicity island component^116-164^E:2e-06`PF02861.17^Clp_N^Clp amino terminal domain, pathogenicity island component^200-248^E:8.5e-10`PF00004.26^AAA^ATPase family associated with various cellular activities (AAA)^337-439^E:6.2e-09`PF07724.11^AAA_2^AAA domain (Cdc48 subfamily)^679-854^E:2.9e-51`PF00004.26^AAA^ATPase family associated with various cellular activities (AAA)^684-792^E:2.8e-06`PF07728.11^AAA_5^AAA domain (dynein-related subfamily)^684-804^E:2e-11`PF10431.6^ClpB_D2-small^C-terminal, D2-small domain, of ClpB protein^860-939^E:1.8e-22	0,111	0,884	0	3,945	0,001	1,705	0	1,897	1	0,826	CLPD_ARATH	Chaperone protein ClpD, chloroplastic (EC 3.6.1.3) (ATP-dependent Clp protease ATP-binding subunit ClpD homolog) (Casein lytic proteinase D) (ERD1 protein) (Protein EARLY RESPONSIVE TO DEHYDRATION 1) (Protein SENESCENCE ASSOCIATED GENE 15)	CLPD ERD1 SAG15 At5g51070 K3K7.27	Arabidopsis thaliana (Mouse-ear cress)		ATP-binding; Chaperone; Chloroplast; Complete proteome; Hydrolase; Nucleotide-binding; Plastid; Reference proteome; Repeat; Stress response; Transit peptide
SRR648705_TR19380_c1_g2_i4_len=1366	NA	NA	NA	NA	NA	.	0,487	0,317	0	1,582	0,005	1,201	0	1,548	0,111	-0,886	.	.	.	.	.	.
SRR648705_TR19880_c0_g1_i2_len=1719	BEBT_TOBAC	Q:235-1251,H:3-340	76.11%ID	E:0	Benzyl alcohol O-benzoyltransferase	PF02458.12^Transferase^Transferase family^14-341^E:5.9e-66	0,195	-1,177	0	3,102	0,164	0,875	0	1,985	1	0,562	BEBT_TOBAC	Benzyl alcohol O-benzoyltransferase (EC 2.3.1.196) (Benzoyl coenzyme A:benzyl alcohol benzoyl transferase)	HSR201	Nicotiana tabacum (Common tobacco)		Acyltransferase; Transferase
SRR648705_TR21981_c0_g1_i1_len=994	ZAT8_ARATH	Q:764-324,H:12-150	46.05%ID	E:9e-31	Zinc finger protein ZAT8	PF13912.3^zf-C2H2_6^C2H2-type zinc finger^113-137^E:2.3e-10`PF13912.3^zf-C2H2_6^C2H2-type zinc finger^157-182^E:1.7e-09	1	2,397	0	5,812	0,043	3,273	0	5,337	1	0,028	ZAT8_ARATH	Zinc finger protein ZAT8	ZAT8 At3g46080 F12M12.50	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Metal-binding; Nucleus; Reference proteome; Repeat; Transcription; Transcription regulation; Zinc; Zinc-finger
SRR648705_TR23749_c0_g2_i2_len=3398	OPR11_ORYSJ	Q:338-1402,H:9-363	78.87%ID	E:0	Putative 12-oxophytodienoate reductase 11	.	0,534	-0,278	0	1,736	0,461	1,261	0	3,611	0,678	-0,149	OPR11_ORYSJ	Putative 12-oxophytodienoate reductase 11 (EC 1.3.1.-) (OPDA-reductase 11) (OsOPR11)	OPR11 OPR3 OsJ_20711	Oryza sativa subsp. japonica (Rice)		Complete proteome; FMN; Fatty acid biosynthesis; Fatty acid metabolism; Flavoprotein; Lipid biosynthesis; Lipid metabolism; NADP; Oxidoreductase; Oxylipin biosynthesis; Reference proteome
SRR648705_TR31575_c0_g1_i2_len=2132	4CL_VANPL	Q:2011-353,H:1-553	99.82%ID	E:0	4-coumarate--CoA ligase	PF00501.25^AMP-binding^AMP-binding enzyme^37-451^E:1.5e-107`PF13193.3^AMP-binding_C^AMP-binding enzyme C-terminal domain^460-535^E:3e-15	0,298	0,633	0	5,21	0,004	0,784	0	1,439	0,003	1,871	4CL_VANPL	4-coumarate--CoA ligase (4CL) (EC 6.2.1.12) (4-coumaroyl-CoA synthase)	4CL	Vanilla planifolia (Vanilla)	PATHWAY: Phytoalexin biosynthesis; 3,4',5-trihydroxystilbene biosynthesis; 3,4',5-trihydroxystilbene from trans-4-coumarate: step 1/2. PATHWAY: Amino-acid biosynthesis; L-lysine biosynthesis via DAP pathway; (S)-	ATP-binding; Ligase; Nucleotide-binding; Phenylpropanoid metabolism

SRR648705_TR42446_c0_g1_i1_len=1554	DHAS_SYNY3	Q:1240-233,H:7-334	54.17%ID	E:8e-118	Aspartate-semialdehyde dehydrogenase	PF01118.21^Semialdhyde_dh^Semialdehyde dehydrogenase, NAD binding domain^52-164^E:1.8e-32`PF02774.15^Semialdhyde_dhC^Semialdehyde dehydrogenase, dimerisation domain^192-372^E:1.1e-44	0,058	-0,889	0	1,244	0,027	1,351	0	2,216	0,356	-1,249	DHAS_SYNY3	Aspartate-semialdehyde dehydrogenase (ASA dehydrogenase) (ASADH) (EC 1.2.1.11) (Aspartate-beta-semialdehyde dehydrogenase)	asd slr0549	Synechocystis sp. (strain PCC 6803 / Kazusa)	tetrahydrodipicolinate from L-aspartate: step 2/4.; PATHWAY: Amino-acid biosynthesis; L-methionine biosynthesis via de novo pathway; L-homoserine from L-aspartate: step 2/3.; PATHWAY: Amino-acid biosynthesis; L-threonine biosynthesis; L-threonine from L-aspartate: step 2/5.	Amino-acid biosynthesis; Complete proteome; Diaminopimelate biosynthesis; Lysine biosynthesis; Methionine biosynthesis; NADP; Oxidoreductase; Reference proteome; Threonine biosynthesis
SRR648705_TR43829_c0_g1_i2_len=2224	CYSZ_CUCMA	Q:197-1708,H:12-515	86.93%ID	E:0	Citrate synthase, glyoxysomal	PF00285.18^Citrate_synt^Citrate synthase, C-terminal domain^101-469^E:3.4e-134	0,333	0,402	0	2,438	0,002	1,455	0	1,671	0,735	0,203	CYSZ_CUCMA	Citrate synthase, glyoxysomal (EC 2.3.3.16) (GCS)		Cucurbita maxima (Pumpkin) (Winter squash)	PATHWAY: Carbohydrate metabolism; glyoxylate cycle; isocitrate from oxaloacetate: step 1/2.	Direct protein sequencing; Glyoxylate bypass; Glyoxysome; Peroxisome; Transferase; Transit peptide; Tricarboxylic acid cycle
SRR648705_TR44108_c0_g1_i1_len=1039	NA	NA	NA	NA	NA	.	1	0,492	0	2,588	0,001	4,414	0	5,064	0,517	-0,824	.	.	.	.	.	.
SRR648707_TR3831_c0_g4_i1_len=3888	MMT1_WEDBI	Q:274-3525,H:1-1087	73.33%ID	E:0	Methionine S-methyltransferase	PF05175.11^MTS^Methyltransferase small domain^119-172^E:1.3e-06`PF06325.10^PrmA^Ribosomal protein L11 methyltransferase (PrmA)^119-172^E:1.1e-05`PF00155.18^Aminotran_1_2^Aminotransferase class I and II^734-1074^E:2.3e-16	0,819	0,117	0	2,637	0,003	1,463	0	2,46	0,705	0,253	MMT1_WEDBI	Methionine S-methyltransferase (EC 2.1.1.12) (AdoMet:Met S-methyltransferase)	MMT1 MMT	Wedelia biflora (Beach sunflower) (Wollastonia biflora)		Cytoplasm; Direct protein sequencing; Methyltransferase; S-adenosyl-L-methionine; Transferase
SRR648707_TR6083_c0_g1_i1_len=1103	NA	NA	NA	NA	NA	.	0,006	1,276	0	1,79	0,003	1,299	0	1,747	0,02	1,071	.	.	.	.	.	.
SRR648707_TR6922_c1_g1_i3_len=1527	DBR_TOBAC	Q:1333-302,H:1-343	82.56%ID	E:0	2-alkenal reductase (NADP(+)-dependent)	PF16884.2^ADH_N_2^N-terminal domain of oxidoreductase^8-116^E:1.6e-26`PF00107.23^ADH_zinc_N^Zinc-binding dehydrogenase^166-293^E:1.6e-24`PF13602.3^ADH_zinc_N_2^Zinc-binding dehydrogenase^200-337^E:1.7e-07	0,452	0,504	0	2,354	0,001	1,383	0	1,577	1	0,055	DBR_TOBAC	2-alkenal reductase (NADP(+)-dependent) (EC 1.3.1.102) (Alkenal double bound reductase) (Allyl-alcohol dehydrogenase) (EC 1.1.1.54) (Allylic alcohol dehydrogenase 1) (allyl-ADH1) (Flavin-free double bond reductase) (NtDBR) (Pulegone reductase) (NtRed-1)	DBR	Nicotiana tabacum (Common tobacco)		3D-structure; Direct protein sequencing; NADP; Oxidoreductase
SRR648707_TR8635_c0_g2_i1_len=1931	UGT9_GARJA	Q:271-1596,H:1-435	56.66%ID	E:1e-157	Beta-D-glucosyl crocetin beta-1,6-glucosyltransferase	PF00201.15^UDPGT^UDP-glucoronosyl and UDP-glucosyl transferase^251-421^E:3.7e-22`PF04101.13^Glyco_tran_28_C^Glycosyltransferase family 28 C-terminal domain^356-436^E:0.00025	0,692	1,257	0	5,046	0,002	3,151	0	3,956	1	0,328	UGT9_GARJA	Beta-D-glucosyl crocetin beta-1,6-glucosyltransferase (EC 2.4.1.330) (UDP-glucose glucosyltransferase 9) (GjUGT9) (UDP-glycosyltransferase 94E5)	UGT94E5 UGT9	Gardenia jasminoides (Cape jasmine) (Gardenia augusta)		Glycosyltransferase; Transferase
SRR648707_TR9966_c0_g1_i1_len=3049	RSH3C_ARATH	Q:2510-324,H:6-712	68.48%ID	E:0	Probable GTP diphosphokinase RSH3, chloroplastic	PF13328.3^HD_4^HD domain^238-390^E:9.3e-43`PF01966.19^HD^HD domain^255-359^E:2.5e-06`PF04607.14^RelA_SpoT^Region found in RelA / SpoT proteins^449-558^E:1.3e-36	0,103	1,561	0	5,064	0,003	2,231	0	2,621	1	0,507	RSH3C_ARATH	Probable GTP diphosphokinase RSH3, chloroplastic (EC 2.7.6.5) (RelA/SpoT homolog 3) (AtRSH3) (ppGpp synthetase RSH3)	RSH3 At1g54130 F15I1.23	Arabidopsis thaliana (Mouse-ear cress)		ATP-binding; Chloroplast; Complete proteome; GTP-binding; Kinase; Nucleotide-binding; Plastid; Reference proteome; Stress response; Transferase; Transit peptide
SRR648707_TR10026_c0_g2_i1_len=2229	PMGI_MESCR	Q:210-1880,H:1-557	89.05%ID	E:0	2,3-bisphosphoglycerate-independent phosphoglycerate mutase	PF01676.15^Metalloenzyme^Metalloenzyme superfamily^22-545^E:4.7e-101`PF06415.10^iPGM_N^BPG-independent PGAM N-terminus (iPGM_N)^102-322^E:6.4e-59	0,001	-2,264	0	2,743	0,006	1,921	0,001	2,244	0	-2,869	PMGI_MESCR	2,3-bisphosphoglycerate-independent phosphoglycerate mutase (BPG-independent PGAM) (Phosphoglyceromutase) (EC 5.4.2.12) (PGAM-I)	PGM1	Mesembryanthemum crystallinum (Common ice plant) (Cryophytum crystallinum)	PATHWAY: Carbohydrate degradation; glycolysis; pyruvate from D-glyceraldehyde 3-phosphate: step 3/5.	Cytoplasm; Glycolysis; Isomerase; Manganese; Metal-binding; Stress response
SRR648707_TR13267_c0_g1_i1_len=2224	HEM11_CUCSA	Q:206-1759,H:34-552	69.17%ID	E:0	Glutamyl-tRNA reductase 1, chloroplastic	PF05201.12^GlutR_N^Glutamyl-tRNAGlu reductase, N-terminal domain^98-248^E:5.3e-40`PF01488.17^Shikimate_DH^Shikimate / quinate 5-dehydrogenase^263-405^E:4.5e-45`PF02423.12^OCD_Mu_crystall^Ornithine cyclodeaminase/mu-crystallin family^277-366^E:1.6e-07`PF03807.14^F420_oxidored^NADP oxidoreductase coenzyme F420-dependent^278-347^E:3.4e-08`PF03446.12^NAD_binding_2^NAD binding domain of 6-phosphogluconate dehydrogenase^278-379^E:2e-06`PF00745.17^GlutR_dimer^Glutamyl-tRNAGlu reductase, dimerisation domain^420-523^E:9.7e-26	0,228	0,965	0	2,526	0,002	2,132	0	2,489	0,461	-0,908	HEM11_CUCSA	Glutamyl-tRNA reductase 1, chloroplastic (GluTR) (EC 1.2.1.70)	HEMA1	Cucumis sativus (Cucumber)	PATHWAY: Porphyrin-containing compound metabolism; protoporphyrin-IX biosynthesis; 5-aminolevulinate from L-glutamyl-tRNA(Glu): step 1/2.	Chlorophyll biosynthesis; Chloroplast; NADP; Oxidoreductase; Plastid; Porphyrin biosynthesis; Transit peptide
SRR648707_TR34996_c1_g1_i2_len=2295	TT12_ARATH	Q:781-2106,H:51-493	41.22%ID	E:2e-93	.	PF01554.15^MatE^MatE^40-198^E:4.2e-23`PF01554.15^MatE^MatE^260-420^E:2.6e-25	0,452	0,634	0	2,603	0,003	1,293	0	2,091	0,298	-0,714	DTX41_ARATH	Protein DETOXIFICATION 41 (AtDTX41) (Multidrug and toxic compound extrusion protein 41) (MATE protein 41) (Protein TANNIN-DEFICIENT SEED 3) (Protein TRANSPARENT TESTA 12)	DTX41 TDS3 TT12 At3g59030 F17J16_80	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Secondary metabolite biosynthesis; flavonoid biosynthesis.	Antiport; Complete proteome; Flavonoid biosynthesis; Membrane; Reference proteome; Transmembrane; Transmembrane helix; Transport; Vacuole
SRR924147_TR8076_c0_g2_i1_len=1466	ROMT_VITVI	Q:375-1394,H:14-356	57.39%ID	E:2e-123	Trans-resveratrol di-O-methyltransferase	PF08100.8^Dimerisation^Dimerisation domain^38-86^E:6.4e-18`PF00891.15^Methyltransf_2^O-methyltransferase^127-346^E:8.6e-65	0,502	2,357	0	6,108	0,034	3,97	0	5,063	1	-0,975	ROMT_VITVI	Trans-resveratrol di-O-methyltransferase (EC 2.1.1.240) (Resveratrol O-methyltransferase) (ROMT) (VvROMT)	ROMT VIT_12s0028g01880	Vitis vinifera (Grape)		Complete proteome; Methyltransferase; Reference proteome; S-adenosyl-L-methionine; Transferase
SRR924147_TR16793_c0_g1_i1_len=1821	LGT_CITUN	Q:1702-284,H:1-471	63.66%ID	E:0	Limonoid UDP-glucosyltransferase	PF00201.15^UDPGT^UDP-glucoronosyl and UDP-glucosyl transferase^262-395^E:5.6e-22	0,56	0,932	0	4,667	0,019	0,827	0,001	1,149	0,129	1,163	LGT_CITUN	Limonoid UDP-glucosyltransferase (LGTase) (Limonoid GTase) (Limonoid glucosyltransferase) (EC 2.4.1.210)		Citrus unshiu (Satsuma mandarin) (Citrus nobilis var. unshiu)		Glycosyltransferase; Transferase
SRR924147_TR20190_c0_g1_i3_len=1689	AKRC9_ARATH	Q:281-1222,H:1-315	73.33%ID	E:8e-161	Aldo-keto reductase family 4 member C9	PF00248.18^Aldo_ket_red^Aldo/keto reductase family^19-285^E:1.1e-46	0,936	0,057	0	2,284	0,003	1,734	0	2,713	1	0,05	AKRC9_ARATH	Aldo-keto reductase family 4 member C9 (EC 1.1.1.-)	AKR4C9 At2g37770 F13M22 T8P21.32	Arabidopsis thaliana (Mouse-ear cress)		3D-structure; Acetylation; Alternative splicing; Complete proteome; Detoxification; NADP; Oxidoreductase; Reference proteome; Stress response
SRR924148_TR11602_c0_g1_i9_len=2687	THIC1_ARATH	Q:2506-1376,H:2-378	83.82%ID	E:0	Acetyl-CoA acetyltransferase, cytosolic 1	PF00108.20^Thiolase_N^Thiolase, N-terminal domain^15-273^E:2e-91`PF00109.23^ketoacyl-synt^Beta-ketoacyl synthase, N-terminal domain^96-136^E:0.00022`PF02803.15^Thiolase_C^Thiolase, C-terminal domain^283-403^E:1.5e-44	0,48	0,318	0	1,74	0,005	1,571	0,001	1,82	1	0,125	THIC1_ARATH	Acetyl-CoA acetyltransferase, cytosolic 1 (EC 2.3.1.9) (Cytosolic acetoacetyl-CoA thiolase 1) (Thiolase 1) (Protein EMBRYO DEFECTIVE 1276)	AAT1 EMB1276 At5g48230 MIF21.12	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Metabolic intermediate biosynthesis; (R)-mevalonate biosynthesis; (R)-mevalonate from acetyl-CoA: step 1/3.	Acyltransferase; Alternative splicing; Complete proteome; Cytoplasm; Isoprene biosynthesis; Metal-binding; Potassium; Reference proteome; Transferase
SRR924148_TR13893_c4_g6_i5_len=2758	Y8948_DICDI	Q:312-1067,H:19-261	30.27%ID	E:2e-25	Putative methyltransferase DDB_G0268948	.	1	-0,116	0	7,375	0,001	2,572	0	2,875	1	0	Y8948_DICDI	Putative methyltransferase DDB_G0268948 (EC 2.1.1.-)	DDB_G0268948	Dictyostelium discoideum (Slime mold)		Complete proteome; Methyltransferase; Reference proteome; S-adenosyl-L-methionine; Transferase
SRR924148_TR18024_c0_g1_i1_len=636	EXPA1_ARATH	Q:489-1,H:7-171	86.06%ID	E:1e-66	Expansin-A1	PF03330.15^DPBB_1^Lytic transglycolase^103-188^E:2.6e-22	0,292	0,278	0	2,215	0,364	-0,282	0	1,45	0,018	1,148	EXPA1_ARATH	Expansin-A1 (AtEXPA1) (Alpha-expansin-1) (At-EXP1) (AtEx1) (Ath-ExpAlpha-1.2)	EXPA1 EXP1 At1g69530 F10D13_18	Arabidopsis thaliana (Mouse-ear cress)		Alternative splicing; Cell wall; Cell wall biogenesis/degradation; Complete proteome; Disulfide bond; Membrane; Reference proteome; Secreted; Signal
SRR122238_TR16898_c0_g1_i1_len=553	NA	NA	NA	NA	NA	.	0	8,597	0,688	0,124	0	1,353	0,108	0,508	0	-3,847	.	.	.	.	.	.
SRR122238_TR60344_c0_g1_i2_len=702	NA	NA	NA	NA	NA	.	0	1,183	0,821	0,095	0	2,112	0,001	1,063	0,369	0,29	.	.	.	.	.	.
SRR1271859_TR22866_c2_g2_i17_len=2668	TPSGD_VITVI	Q:1240-2517,H:134-557	54.93%ID	E:2e-161	(-)-germacrene D synthase	PF01397.18^Terpene_synth^Terpene synthase, N-terminal domain^1-66^E:4.7e-12`PF03936.13^Terpene_synth_C^Terpene synthase family, metal binding domain^97-363^E:1.7e-100	0,001	1,93	0,002	2,463	0	2,097	0,001	1,411	0,446	0,318	TPSGD_VITVI	(-)-germacrene D synthase (EC 4.2.3.22) (EC 4.2.3.75)	VIT_19s0014g04930 VIT_00014569001 VITISV_013313 VITISV_030783 Vv19s0014g04930	Vitis vinifera (Grape)	PATHWAY: Secondary metabolite biosynthesis; terpenoid biosynthesis.	Complete proteome; Cytoplasm; Lyase; Magnesium; Metal-binding; Reference proteome
SRR342019_TR36227_c0_g1_i1_len=768	VTI12_ARATH	Q:714-274,H:53-199	70.75%ID	E:2e-66	Vesicle transport v-SNARE 12	PF05008.12^V-SNARE^Vesicle transport v-SNARE protein N-terminus^19-57^E:6.3e-11`PF12352.5^V-SNARE_C^Snare region anchored in the vesicle membrane C-terminus^95-159^E:2.9e-24	0,001	6,637	0,783	0,201	0	6,948	1	0	0	-7,499	VTI12_ARATH	Vesicle transport v-SNARE 12 (AtVTI12) (Vesicle soluble NSF attachment protein receptor VTI1b) (AtVTI1b) (Vesicle transport v-SNARE protein VTI1b)	VTI12 VTI1B At1g26670 T24P13.5	Arabidopsis thaliana (Mouse-ear cress)		Acetylation; Coiled coil; Complete proteome; Golgi apparatus; Membrane; Protein transport; Reference proteome; Transmembrane; Transmembrane helix; Transport
SRR342023_TR9968_c1_g2_i1_len=1694	NA	NA	NA	NA	NA	PF05050.9^Methyltransf_21^Methyltransferase FkbM domain^293-444^E:0.00017	0	3,731	0,008	3,856	0	5,042	0,042	1,933	0,254	2,581	.	.	.	.	.	.
SRR648705_TR18574_c0_g1_i1_len=782	12KD_FRAAN	Q:64-438,H:1-109	57.6%ID	E:1e-37	Auxin-repressed 12.5 kDa protein	PF05564.9^Auxin_repressed^Dormancy/auxin associated protein^24-143^E:1.9e-56	0	7,677	0,003	1,309	0	6,786	0,129	4,955	0,629	-1,198	12KD_FRAAN	Auxin-repressed 12.5 kDa protein		Fragaria ananassa (Strawberry)		Auxin signaling pathway
SRR648707_TR6095_c0_g1_i1_len=568	SUT_SPIOL	Q:568-308,H:431-517	72.41%ID	E:4e-33	Sucrose transport protein	.	0	7,028	0	-2,224	0	7,892	1	0	1	0	SUT_SPIOL	Sucrose transport protein (Sucrose permease) (Sucrose-proton symporter)		Spinacia oleracea (Spinach)	PATHWAY: Glycan biosynthesis; sucrose metabolism.	Membrane; Sugar transport; Symport; Transmembrane; Transmembrane helix; Transport
SRR1144633_TR16170_c0_g3_i14_len=1726	ACOX4_ARATH	Q:1538-288,H:1-430	78.84%ID	E:0	Acyl-coenzyme A oxidase 4, peroxisomal	PF02771.13^Acyl-CoA_dh_N^Acyl-CoA dehydrogenase, N-terminal domain^47-152^E:1.8e-22`PF02770.16^Acyl-CoA_dh_M^Acyl-CoA dehydrogenase, middle domain^158-250^E:1.1e-22`PF00441.21^Acyl-CoA_dh_1^Acyl-CoA dehydrogenase, C-terminal domain^267-408^E:3.7e-25	0,003	1,633	0	1,867	0	1,896	0,005	1,57	1	0,022	ACOX4_ARATH	Acyl-coenzyme A oxidase 4, peroxisomal (AOX 4) (EC 1.3.3.6) (G6p) (Short-chain acyl-CoA oxidase) (AtCX4) (AtG6) (SAOX)	ACX4 G6 At3g51840 ATEM1.9	Arabidopsis thaliana (Mouse-ear cress)		3D-structure; Acetylation; Complete proteome; FAD; Fatty acid metabolism; Flavoprotein; Glyoxysome; Lipid metabolism; Oxidoreductase; Peroxisome; Reference proteome
SRR1144634_TR24946_c0_g1_i1_len=769	NA	NA	NA	NA	NA	.	0,254	3,507	0	5,211	0	2,01	0,064	0,957	1	0	.	.	.	.	.	.
SRR122236_TR3878_c0_g2_i1_len=680	NA	NA	NA	NA	NA	.	0,373	0,198	0	2,935	0	1,094	0,014	0,595	0,326	-0,3	.	.	.	.	.	.
SRR122238_TR3803_c0_g1_i1_len=948	WUN1_SOLTU	Q:281-607,H:1-105	67.89%ID	E:2e-43	Wound-induced protein 1	PF07107.8^WI12^Wound-induced protein WI12^94-202^E:2.8e-44	0,062	0,603	0	2,072	0	1,436	0,004	1,018	0	-1,487	WUN1_SOLTU	Wound-induced protein 1	WUN1	Solanum tuberosum (Potato)		Complete proteome; Reference proteome
SRR122238_TR10709_c0_g2_i2_len=1148	GST23_MAIZE	Q:229-873,H:3-218	40.09%ID	E:2e-41	Glutathione transferase GST 23	PF02798.17^GST_N^Glutathione S-transferase, N-terminal domain^4-75^E:6.5e-14`PF13417.3^GST_N_3^Glutathione S-transferase, N-terminal domain^7-78^E:6e-16`PF13409.3^GST_N_2^Glutathione S-transferase, N-terminal domain^12-76^E:3e-09`PF00043.22^GST_C^Glutathione S-transferase, C-terminal domain^107-193^E:1.7e-05`PF14497.3^GST_C_3^Glutathione S-transferase, C-terminal domain^116-198^E:2.5e-05	0,316	0,637	0,001	1,674	0,001	1,93	0,08	1,208	1	-0,107	GST23_MAIZE	Glutathione transferase GST 23 (EC 2.5.1.18) (Glutathione transferase GST 36)		Zea mays (Maize)		Complete proteome; Plant defense; Reference proteome; Transferase
SRR122238_TR32671_c0_g1_i4_len=2031	NPC2_ARATH	Q:261-1721,H:24-512	75.26%ID	E:0	Non-specific phospholipase C2	PF04185.11^Phosphoesterase^Phosphoesterase family^36-395^E:2.4e-108	0,34	0,463	0	1,782	0	1,952	0,005	1,173	0,454	0,369	NPC2_ARATH	Non-specific phospholipase C2 (EC 3.1.-.-)	NPC2 At2g26870 F12C20.9	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Hydrolase; Reference proteome; Secreted; Signal
SRR122238_TR34090_c0_g1_i1_len=728	21KD_DAUCA	Q:539-54,H:28-189	56.17%ID	E:1e-64	21 kDa protein	PF04043.12^PMEI^Plant invertase/pectin methylesterase inhibitor^63-219^E:5.7e-35	0,8	0,072	0	2,186	0	1,354	0,356	0,368	1	0,048	21KD_DAUCA	21 kDa protein (1.2 protein)		Daucus carota (Wild carrot)		Signal
SRR122238_TR34437_c0_g1_i3_len=859	NA	NA	NA	NA	NA	.	0,101	0,529	0	1,443	0,001	1,327	0,008	1,102	1	-0,023	.	.	.	.	.	.
SRR122238_TR37876_c0_g1_i2_len=802	DCTP1_RAT	Q:675-337,H:20-132	49.56%ID	E:1e-21	dCTP pyrophosphatase 1	PF03819.14^MazG^MazG nucleotide pyrophosphohydrolase domain^34-102^E:1.7e-07`PF12643.4^MazG-like^MazG-like family^45-117^E:9e-08	0,133	1,154	0	5,143	0	4,555	0,004	3,553	0,732	0,765	DCTP1_RAT	dCTP pyrophosphatase 1 (EC 3.6.1.12) (Deoxycytidine-triphosphatase 1) (dCTPase 1) (RS21-C6) (XTP3-transactivated gene A protein homolog)	Dctpp1 Rs21c6 Xtp3tpa	Rattus norvegicus (Rat)		Acetylation; Complete proteome; Cytoplasm; Hydrolase; Magnesium; Metal-binding; Phosphoprotein; Reference proteome
SRR122238_TR57082_c0_g1_i1_len=607	NA	NA	NA	NA	NA	.	0,353	0,243	0	1,984	0	1,153	0,005	0,809	0,832	0,243	.	.	.	.	.	.
SRR122238_TR60996_c0_g1_i1_len=1427	NA	NA	NA	NA	NA	PF07816.8^DUF1645^Protein of unknown function (DUF1645)^74-282^E:3.8e-43	0,01	2,068	0	3,594	0	3,549	0,016	1,997	0,62	-0,499	.	.	.	.	.	.
SRR122238_TR63763_c0_g1_i5_len=1089	SRP_VITRI	Q:935-294,H:9-241	58.55%ID	E:5e-83	Stress-related protein	PF05755.9^REF^Rubber elongation factor protein (REF)^18-212^E:1.4e-78	0,297	0,408	0	1,455	0	1,837	0,009	1,203	1	-0,672	SRP_VITRI	Stress-related protein	SRP	Vitis riparia (Frost grape) (Vitis vulpina)		Stress response
SRR122238_TR73613_c0_g1_i4_len=825	NA	NA	NA	NA	NA	.	1	0,02	0	1,818	0	1,998	1	0,126	0,732	-0,441	.	.	.	.	.	.
SRR122238_TR80906_c0_g1_i3_len=1210	RTNLA_ARATH	Q:342-959,H:70-275	71.36%ID	E:1e-100	Reticulon-like protein B1	PF02453.14^Reticulon^Reticulon^70-225^E:4e-55	0,111	0,863	0	2,371	0	1,022	0,019	0,605	0,051	0,615	RTNLA_ARATH	Reticulon-like protein B1 (AtRTNLB1) (VirB2-interacting protein 1)	RTNLB1 BTI1 At4g23630 F9D16.100	Arabidopsis thaliana (Mouse-ear cress)		Acetylation; Cell membrane; Complete proteome; Endoplasmic reticulum; Membrane; Reference proteome; Transmembrane; Transmembrane helix
SRR122238_TR82636_c0_g6_i5_len=1138	PSB4_ARATH	Q:935-198,H:1-246	73.98%ID	E:2e-138	Proteasome subunit beta type-4	PF00227.23^Proteasome^Proteasome subunit^97-280^E:2.1e-33	0,345	0,325	0	1,545	0	1,554	0,001	1,155	1	0,109	PSB4_ARATH	Proteasome subunit beta type-4 (EC 3.4.25.1) (20S proteasome beta subunit G-1) (Proteasome component H) (Proteasome subunit beta type-7)	PBG1 PRCH At1g56450 F13N6.3	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Cytoplasm; Hydrolase; Nucleus; Protease; Proteasome; Reference proteome; Threonine protease; Zymogen
SRR122238_TR85957_c0_g1_i2_len=618	NA	NA	NA	NA	NA	.	0,01	0,813	0	2,288	0	1,403	0,502	0,323	0	-0,914	.	.	.	.	.	.
SRR122238_TR88422_c0_g2_i1_len=1022	ERD2B_ARATH	Q:253-924,H:2-214	35.37%ID	E:7e-29	ER lumen protein-retaining receptor B	PF00810.15^ER_lumen_recept^ER lumen protein retaining receptor^73-215^E:1e-39	0,042	-0,896	0	1,863	0	2,195	0,011	1,472	0,559	0,381	ERD2B_ARATH	ER lumen protein-retaining receptor B	ERD2B ERD2.2 At3g25040	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; ER-Golgi transport; Endoplasmic reticulum; Golgi apparatus; Membrane; Protein transport; Receptor; Reference proteome; Transmembrane; Transmembrane helix; Transport
SRR1271857_TR7694_c0_g2_i1_len=1410	NA	NA	NA	NA	NA	.	0,14	0,479	0	1,482	0	2,31	0,004	1,78	0,341	0,391	.	.	.	.	.	.
SRR1271857_TR15103_c0_g1_i2_len=3614	IKU2_ARATH	Q:1212-3107,H:362-968	52.96%ID	E:0	Receptor-like protein kinase HAIKU2	PF00560.30^LRR_1^Leucine Rich Repeat^189-210^E:0.39`PF00069.22^Pkinase^Protein kinase domain^329-515^E:1.5e-32`PF07714.14^Pkinase_Tyr^Protein tyrosine kinase^330-504^E:3.7e-24`PF07714.14^Pkinase_Tyr^Protein tyrosine kinase^542-643^E:2.7e-08	0,356	1,137	0	4,446	0	4,922	0,005	3,957	0,635	0,344	IKU2_ARATH	Receptor-like protein kinase HAIKU2 (EC 2.7.11.1)	IKU2 At3g19700 MMB12.19	Arabidopsis thaliana (Mouse-ear cress)		ATP-binding; Complete proteome; Glycoprotein; Kinase; Leucine-rich repeat; Membrane; Nucleotide-binding; Phosphoprotein; Receptor; Reference proteome; Repeat; Serine/threonine-protein kinase; Signal; Transferase; Transmembrane; Transmembrane helix
SRR1271858_TR6827_c0_g3_i2_len=543	NA	NA	NA	NA	NA	PF14299.3^PP2^Phloem protein 2^1-108^E:4.2e-15	0,502	1,948	0	5,776	0	7,987	0,034	5,528	0,381	-2,256	.	.	.	.	.	.
SRR1271858_TR8518_c1_g1_i2_len=2379	HSBH1_SOYBN	Q:202-963,H:124-375	82.81%ID	E:1e-137	Homeobox protein SBH1	PF13202.3^EF-hand_5^EF hand^37-54^E:0.00085	0,56	0,679	0	3,756	0,001	1,406	0,232	0,599	1	1,227	HSBH1_SOYBN	Homeobox protein SBH1	H1	Glycine max (Soybean) (Glycine hispida)		Activator; Complete proteome; DNA-binding; Homeobox; Nucleus; Reference proteome; Transcription; Transcription regulation
SRR1271858_TR11242_c0_g1_i1_len=368	NA	NA	NA	NA	NA	.	0,124	1,013	0	2,808	0	4,224	0,132	2,625	0,132	1,474	.	.	.	.	.	.
SRR1271858_TR21137_c0_g1_i7_len=1352	GDL71_ARATH	Q:1107-604,H:186-352	56.55%ID	E:9e-63	GDSL esterase/lipase At5g03610	.	1	1,068	0,001	3,617	0,001	3,959	0,001	3,91	1	1,581	GDL71_ARATH	GDSL esterase/lipase At5g03610 (EC 3.1.1.-) (Extracellular lipase At5g03610)	At5g03610 F17C15.30	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Glycoprotein; Hydrolase; Lipid degradation; Lipid metabolism; Reference proteome; Secreted; Signal
SRR1271858_TR46473_c0_g1_i1_len=1193	WRK71_ARATH	Q:621-878,H:123-208	87.21%ID	E:2e-46	Probable WRKY transcription factor 71	PF03106.12^WRKY^WRKY DNA -binding domain^220-277^E:1.1e-26	0,129	5,163	0	6,904	0,001	6,639	0,254	4,446	1	-1,393	WRK71_ARATH	Probable WRKY transcription factor 71 (WRKY DNA-binding protein 71)	WRKY71 At1g29860 F1N18.10	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; DNA-binding; Nucleus; Reference proteome; Transcription; Transcription regulation
SRR1271858_TR66707_c0_g1_i6_len=1464	BCB1_ARATH	Q:315-641,H:23-130	47.71%ID	E:1e-23	Blue copper protein	PF02298.14^Cu_bind_like^Plastocyanin-like domain^45-122^E:6.9e-22`PF02298.14^Cu_bind_like^Plastocyanin-like domain^184-271^E:1.5e-20	0,009	4,397	0	7,617	0	7,739	0,009	6,101	1	-1,355	BCB1_ARATH	Blue copper protein (Blue copper-binding protein) (AtBCB) (Phytocyanin 1) (Stellacyanin)	BCB AWI 32 At5g20230 F5O24.120	Arabidopsis thaliana (Mouse-ear cress)		Cell membrane; Complete proteome; Copper; Disulfide bond; Electron transport; GPI-anchor; Glycoprotein; Lipoprotein; Membrane; Metal-binding; Reference proteome; Signal; Transport
SRR1271859_TR5282_c0_g1_i1_len=1012	NA	NA	NA	NA	NA	.	0,41	0,316	0	2,37	0	1,744	0,044	1,03	0,111	-0,495	.	.	.	.	.	.
SRR1271859_TR10638_c0_g2_i1_len=1456	NA	NA	NA	NA	NA	PF13202.3^EF-hand_5^EF hand^37-54^E:0.00085	0,255	0,61	0	2,509	0	1,274	0,079	0,532	0,117	0,959	.	.	.	.	.	.
SRR1271859_TR11478_c0_g1_i5_len=1404	XTH30_ARATH	Q:409-1161,H:63-311	72.51%ID	E:2e-137	Probable xyloglucan endotransglucosylase/hydrolase protein 30	PF00722.18^Glyco_hydro_16^Glycosyl hydrolases family 16^5-158^E:1.8e-50`PF06955.9^XET_C^Xyloglucan endo-transglycosylase (XET) C-terminus^200-237^E:5e-15	0,502	3,829	0,001	6,654	0	7,256	0,009	6,104	1	-1,511	XTH30_ARATH	Probable xyloglucan endotransglucosylase/hydrolase protein 30 (At-XTH30) (XTH-30) (EC 2.4.1.207)	XTH30 XTR4 At1g32170 F3C3.5	Arabidopsis thaliana (Mouse-ear cress)		Apoplast; Cell wall; Cell wall biogenesis/degradation; Complete proteome; Disulfide bond; Glycoprotein; Glycosidase; Hydrolase; Reference proteome; Secreted; Signal; Transferase
SRR1271859_TR13491_c0_g1_i1_len=2116	PCP_MOUSE	Q:427-1746,H:46-490	38.63%ID	E:2e-98	Lysosomal Pro-X carboxypeptidase	PF05577.9^Peptidase_S28^Serine carboxypeptidase S28^91-506^E:3.8e-76	0,356	0,355	0	1,861	0	1,298	0,043	0,701	0,09	0,634	PCP_MOUSE	Lysosomal Pro-X carboxypeptidase (EC 3.4.16.2) (Proline carboxypeptidase) (Prolylcarboxypeptidase) (PRCP)	Prcp	Mus musculus (Mouse)		Alternative splicing; Carboxypeptidase; Complete proteome; Disulfide bond; Glycoprotein; Hydrolase; Lysosome; Protease; Reference proteome; Signal; Zymogen
SRR1271859_TR34739_c0_g2_i1_len=2778	BLH1_ARATH	Q:2018-447,H:190-680	54.4%ID	E:7e-129	BEL1-like homeodomain protein 1	PF07526.8^POX^Associated with HOX^225-371^E:1.4e-48`PF05920.8^Homeobox_KN^Homeobox KN domain^445-484^E:6.9e-18`PF00046.26^Homeobox^Homeobox domain^447-484^E:1.1e-06	0,011	1,399	0	1,999	0	1,486	0,002	1,198	0,48	0,289	BLH1_ARATH	BEL1-like homeodomain protein 1 (BEL1-like protein 1) (Protein EMBRYO SAC DEVELOPMENT ARREST 29)	BLH1 EDA29 At2g35940 F11F19.15	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; DNA-binding; Homeobox; Nucleus; Reference proteome; Transcription; Transcription regulation
SRR342017_TR432_c1_g1_i1_len=1655	MY1R1_SOLTU	Q:1241-642,H:24-218	44.17%ID	E:1e-34	Transcription factor MYB1R1	PF00249.28^Myb_DNA-binding^Myb-like DNA-binding domain^104-148^E:1.1e-10	0,365	0,541	0	2,047	0,001	1,296	0,005	1,088	0,298	0,685	MY1R1_SOLTU	Transcription factor MYB1R1 (Myb-related protein R1) (StMYB1R-1)		Solanum tuberosum (Potato)		Complete proteome; Cytoplasm; DNA-binding; Nucleus; Reference proteome; Stress response; Transcription; Transcription regulation
SRR342017_TR3499_c0_g1_i1_len=1589	T5AT_TAXWC	Q:1482-190,H:8-424	30.09%ID	E:3e-51	Taxadien-5-alpha-ol O-acetyltransferase	PF02458.12^Transferase^Transferase family^4-431^E:1.6e-68	0,62	0,525	0	3,211	0	3,638	0,001	3,478	0,103	-1,895	T5AT_TAXWC	Taxadien-5-alpha-ol O-acetyltransferase (EC 2.3.1.162) (Taxa-4(20),11(12)-dien-5alpha-ol-O-acetyltransferase) (Taxadienol acetyltransferase)		Taxus wallichiana var. chinensis (Chinese yew) (Taxus chinensis)	PATHWAY: Alkaloid biosynthesis; taxol biosynthesis; 10-deacetyl-2-debenzoylbaccatin III from taxa-4(20),11-dien-5alpha-ol: step 1/3.	Acyltransferase; Taxol biosynthesis; Transferase
SRR342017_TR4055_c1_g2_i1_len=716	NA	NA	NA	NA	NA	.	0,006	1,263	0	2,585	0	2,397	0,002	1,981	0,819	0,126	.	.	.	.	.	.
SRR342017_TR21089_c0_g3_i1_len=1256	PTR21_ARATH	Q:848-3,H:49-326	56.03%ID	E:6e-97	Protein NRT1/ PTR FAMILY 2.13	PF00854.18^PTR2^POT family^137-302^E:1.3e-30	0,122	0,64	0	4,822	0	2,231	0,013	1,349	0,044	1,199	PTR21_ARATH	Protein NRT1/ PTR FAMILY 2.13 (AtNPF2.13) (Nitrate transporter 1.7)	NPF2.13 NRT1.7 At1g69870 T17F3.10	Arabidopsis thaliana (Mouse-ear cress)		Cell membrane; Complete proteome; Membrane; Nitrate assimilation; Reference proteome; Symport; Transmembrane; Transmembrane helix; Transport
SRR342017_TR24788_c2_g1_i1_len=3471	BGAL3_ARATH	Q:5-1918,H:216-853	79%ID	E:0	Beta-galactosidase 3	PF01301.16^Glyco_hydro_35^Glycosyl hydrolases family 35^2-130^E:2.8e-40`PF02140.15^Gal_Lectin^Galactose binding lectin domain^554-631^E:2.8e-22	0,01	0,955	0	2,812	0	1,349	0,002	1,084	0,165	0,517	BGAL3_ARATH	Beta-galactosidase 3 (Lactase 3) (EC 3.2.1.23)	BGAL3 At4g36360 C7A10.1000 F23E13.200	Arabidopsis thaliana (Mouse-ear cress)		Alternative splicing; Apoplast; Complete proteome; Glycoprotein; Glycosidase; Hydrolase; Reference proteome; Secreted; Signal
SRR342017_TR27304_c2_g4_i5_len=1114	NPC1_PIG	Q:91-702,H:1019-1228	45.5%ID	E:2e-51	Niemann-Pick C1 protein	PF02460.15^Patched^Patched family^17-190^E:2.1e-28	0,935	0,05	0	1,549	0	2,178	0,002	1,361	0,934	-0,065	NPC1_PIG	Niemann-Pick C1 protein	NPC1	Sus scrofa (Pig)		Cholesterol metabolism; Complete proteome; Disulfide bond; Endosome; Glycoprotein; Lipid metabolism; Lysosome; Membrane; Reference proteome; Signal; Steroid metabolism; Sterol metabolism; Transmembrane; Transmembrane helix
SRR342019_TR7514_c2_g4_i2_len=746	IPRT1_CATRO	Q:681-202,H:1-157	68.75%ID	E:1e-66	Probable intracellular pathogenesis-related protein T1	PF00407.16^Bet_v_1^Pathogenesis-related protein Bet v I family^5-157^E:1e-19	0,502	2,433	0	6,636	0	7,286	0,014	3,328	1	-0,818	IPRT1_CATRO	Probable intracellular pathogenesis-related protein T1	PCKR3	Catharanthus roseus (Madagascar periwinkle) (Vinca rosea)		Direct protein sequencing; Glycoprotein; Pathogenesis-related protein; Plant defense
SRR342019_TR18688_c0_g1_i1_len=1206	PIP23_ARATH	Q:1025-183,H:1-281	82.21%ID	E:3e-168	Aquaporin PIP2-3	PF00230.17^MIP^Major intrinsic protein^89-324^E:3.1e-84	0,158	1,515	0	4,722	0	1,297	0,01	0,875	1	0,192	PIP23_ARATH	Aquaporin PIP2-3 (Plasma membrane intrinsic protein 2-3) (AtPIP2;3) (Plasma membrane intrinsic protein 2c) (PIP2c) (RD28-PIP) (TMP2C) (Water stress-induced tonoplast intrinsic protein) (WSI-TIP) [Cleaved into: Aquaporin PIP2-3, N-terminally processed]	PIP2-3 PIP2C RD28 At2g37180 T2N18.6	Arabidopsis thaliana (Mouse-ear cress)		Acetylation; Cell membrane; Complete proteome; Membrane; Phosphoprotein; Reference proteome; Repeat; Stress response; Transmembrane; Transmembrane helix; Transport
SRR342019_TR22641_c0_g1_i1_len=1019	CPC_CUCSA	Q:308-613,H:5-105	46.08%ID	E:7e-23	Cucumber peeling cupredoxin	PF02298.14^Cu_bind_like^Plastocyanin-like domain^111-198^E:9.3e-21	0,017	5,876	0	4,627	0	3,501	1	0,721	1	-0,603	CPC_CUCSA	Cucumber peeling cupredoxin (CPC) (Stellacyanin)		Cucumis sativus (Cucumber)		3D-structure; Copper; Direct protein sequencing; Disulfide bond; Electron transport; Glycoprotein; Hydroxylation; Metal-binding; Pyrrolidone carboxylic acid; Transport
SRR342019_TR29610_c0_g2_i1_len=1674	GDL87_ARATH	Q:139-1125,H:37-374	50.29%ID	E:1e-105	GDSL esterase/lipase At5g55050	PF00657.19^Lipase_GDSL^GDSL-like Lipase/Acylhydrolase^51-354^E:5.3e-24	0,044	2,223	0	3,466	0	2,776	0,007	1,978	1	-0,291	GDL87_ARATH	GDSL esterase/lipase At5g55050 (EC 3.1.1.-) (Extracellular lipase At5g55050)	At5g55050 K13P22.5	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Glycoprotein; Hydrolase; Lipid degradation; Lipid metabolism; Reference proteome; Secreted; Signal
SRR342019_TR34700_c4_g2_i10_len=1095	GSTUA_ARATH	Q:925-104,H:2-230	36.23%ID	E:2e-42	Glutathione S-transferase U10	PF02798.17^GST_N^Glutathione S-transferase, N-terminal domain^26-96^E:6.7e-17`PF13417.3^GST_N_3^Glutathione S-transferase, N-terminal domain^28-103^E:3.6e-16`PF13409.3^GST_N_2^Glutathione S-transferase, N-terminal domain^34-97^E:4.9e-08	0,321	0,218	0	1,423	0	0,995	0,179	0,321	0,28	0,242	GSTUA_ARATH	Glutathione S-transferase U10 (AtGSTU10) (EC 2.5.1.18) (GST class-tau member 10)	GSTU10 At1g74590 F1M20.27	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Cytoplasm; Detoxification; Reference proteome; Transferase
SRR342019_TR38454_c0_g4_i1_len=2252	INT2_ARATH	Q:200-1939,H:1-578	70.5%ID	E:0	Probable inositol transporter 2	PF00083.21^Sugar_tr^Sugar (and other) transporter^30-360^E:8.7e-95`PF07690.13^MFS_1^Major Facilitator Superfamily^35-359^E:4.8e-33`PF06609.10^TRI12^Fungal trichothecene efflux pump (TRI12)^75-218^E:1.4e-07`PF00083.21^Sugar_tr^Sugar (and other) transporter^447-552^E:3.7e-29	0,151	0,71	0	2,576	0	1,533	0,044	0,739	0,004	1,716	INT2_ARATH	Probable inositol transporter 2	INT2 At1g30220 F12P21.2	Arabidopsis thaliana (Mouse-ear cress)		Cell membrane; Complete proteome; Membrane; Reference proteome; Symport; Transmembrane; Transmembrane helix; Transport
SRR342019_TR39563_c1_g1_i1_len=1751	NA	NA	NA	NA	NA	PF01277.14^Oleosin^Oleosin^22-133^E:3.5e-30	0,254	3,24	0	4,414	0	7,283	0,009	4,74	1	-0,141	.	.	.	.	.	.
SRR342022_TR539_c0_g1_i1_len=460	NA	NA	NA	NA	NA	.	0,005	6,189	0,001	6,617	0	7,744	0,034	5,593	0,502	-2,86	.	.	.	.	.	.
SRR342022_TR7941_c0_g2_i1_len=788	NA	NA	NA	NA	NA	.	0,457	0,249	0	1,492	0,001	1,033	0,002	0,983	0,787	0,126	.	.	.	.	.	.
SRR342022_TR13122_c0_g2_i3_len=1449	GPX4_SOLLC	Q:617-1123,H:1-169	82.84%ID	E:3e-100	Probable phospholipid hydroperoxide glutathione peroxidase	PF08534.7^Redoxin^Redoxin^84-236^E:2.3e-07`PF00255.16^GSHPx^Glutathione peroxidase^85-193^E:5.4e-43`PF00578.18^AhpC-TSA^AhpC/TSA family^85-148^E:1.5e-09	0,2	0,469	0	2,899	0	1,798	0,016	1,128	1	0,567	GPX4_SOLLC	Probable phospholipid hydroperoxide glutathione peroxidase (PHGPx) (EC 1.11.1.12)	GPXle-1	Solanum lycopersicum (Tomato) (Lycopersicon esculentum)		Complete proteome; Cytoplasm; Oxidoreductase; Peroxidase; Reference proteome
SRR342022_TR15877_c0_g3_i2_len=923	NA	NA	NA	NA	NA	PF04570.11^zf-FLZ^zinc-finger of the FCS-type, C2-C2^14-60^E:1.1e-23	0,023	0,633	0	1,398	0	1,051	0,113	0,443	1	1,454	.	.	.	.	.	.
SRR342022_TR29430_c1_g2_i2_len=2382	ARGE_ARATH	Q:689-1591,H:46-346	71.52%ID	E:1e-152	Acetylornithine deacetylase	PF01546.25^Peptidase_M20^Peptidase family M20/M25/M40^2-177^E:9e-19`PF07687.11^M20_dimer^Peptidase dimerisation domain^107-221^E:8.9e-13	0,003	2,085	0	3,256	0	3,809	0,008	2,956	0,76	0,573	ARGE_ARATH	Acetylornithine deacetylase (EC 3.5.1.16) (N-acetylornithinase) (AO) (Acetylornithinase) (NAO)	At4g17830 dl4945w T6K21	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Amino-acid biosynthesis; L-arginine biosynthesis; L-ornithine from N(2)-acetyl-L-ornithine (linear): step 1/1.	Alternative splicing; Amino-acid biosynthesis; Arginine biosynthesis; Cobalt; Complete proteome; Hydrolase; Metal-binding; Reference proteome; Zinc
SRR342023_TR304_c2_g4_i1_len=1349	NA	NA	NA	NA	NA	PF00257.16^Dehydrin^Dehydrin^3-81^E:1.8e-15`PF00257.16^Dehydrin^Dehydrin^103-127^E:3e-06	0,123	0,505	0	4,452	0	0,914	0,136	0,359	1	-0,104	.	.	.	.	.	.
SRR342023_TR1704_c0_g1_i1_len=1068	ERF99_ARATH	Q:183-413,H:91-167	79.22%ID	E:5e-36	Ethylene-responsive transcription factor 13	PF00847.17^AP2^AP2 domain^61-111^E:6.5e-13	0,006	1,19	0	2,346	0	1,677	0,394	0,455	0,187	1,197	ERF99_ARATH	Ethylene-responsive transcription factor 13 (AtERF13) (Ethylene-responsive element-binding factor 13) (EREBP-13)	ERF13 ERF-13 ERF099 At2g44840 T13E15.15	Arabidopsis thaliana (Mouse-ear cress)		Activator; Complete proteome; DNA-binding; Ethylene signaling pathway; Nucleus; Plant defense; Reference proteome; Transcription; Transcription regulation
SRR342023_TR9043_c0_g1_i2_len=737	Y2309_ARATH	Q:172-402,H:1-78	80.77%ID	E:8e-37	Uncharacterized protein At2g23090	.	0,271	0,286	0	0,937	0	0,805	0,006	0,633	1	0	Y2309_ARATH	Uncharacterized protein At2g23090	At2g23090 F21P24.15	Arabidopsis thaliana (Mouse-ear cress)		3D-structure; Complete proteome; Reference proteome
SRR342023_TR15478_c1_g1_i1_len=543	NA	NA	NA	NA	NA	.	0,02	0,543	0,001	0,813	0	1,229	0,241	0,341	0,485	-0,191	.	.	.	.	.	.
SRR342023_TR24096_c0_g2_i9_len=3664	IKU2_ARATH	Q:1286-420,H:675-968	62.37%ID	E:1e-102	Receptor-like protein kinase HAIKU2	PF11961.5^DUF3475^Domain of unknown function (DUF3475)^47-103^E:8.4e-26`PF05003.9^DUF668^Protein of unknown function (DUF668)^445-534^E:6.8e-31	0,255	0,647	0	2,565	0	2,413	0,012	1,68	1	-0,313	IKU2_ARATH	Receptor-like protein kinase HAIKU2 (EC 2.7.11.1)	IKU2 At3g19700 MMB12.19	Arabidopsis thaliana (Mouse-ear cress)		ATP-binding; Complete proteome; Glycoprotein; Kinase; Leucine-rich repeat; Membrane; Nucleotide-binding; Phosphoprotein; Receptor; Reference proteome; Repeat; Serine/threonine-protein kinase; Signal; Transferase; Transmembrane; Transmembrane helix
SRR342023_TR26267_c0_g1_i1_len=1198	CML36_ARATH	Q:695-946,H:124-209	59.3%ID	E:3e-36	Probable calcium-binding protein CML36	PF00036.29^EF-hand_1^EF hand^90-116^E:5e-08`PF13405.3^EF-hand_6^EF-hand domain^90-116^E:2.3e-07`PF13833.3^EF-hand_8^EF-hand domain pair^90-110^E:0.023`PF13499.3^EF-hand_7^EF-hand domain pair^91-148^E:5.8e-15`PF13202.3^EF-hand_5^EF hand^92-114^E:1.8e-08`PF13833.3^EF-hand_8^EF-hand domain pair^103-148^E:1.1e-09`PF13202.3^EF-hand_5^EF hand^133-150^E:0.0049	0,188	0,45	0	2,116	0	1,526	0,006	1,045	0,414	0,276	CML36_ARATH	Probable calcium-binding protein CML36 (Calmodulin-like protein 36)	CML36 At3g10190 F14P13.21	Arabidopsis thaliana (Mouse-ear cress)		Calcium; Complete proteome; Metal-binding; Reference proteome; Repeat
SRR342023_TR30617_c3_g3_i2_len=570	C72A1_CATRO	Q:2-394,H:394-524	95.42%ID	E:3e-85	Secologanin synthase	PF00067.19^p450^Cytochrome P450^2-104^E:6.9e-33	0,242	0,311	0	1,443	0,001	0,833	0,216	0,323	1	-0,751	C72A1_CATRO	Secologanin synthase (SLS) (EC 1.3.3.9) (CYPLXXII) (Cytochrome P450 72A1)	CYP72A1 CYP72 P450CR3	Catharanthus roseus (Madagascar periwinkle) (Vinca rosea)	PATHWAY: Alkaloid biosynthesis; secologanin biosynthesis.	Alkaloid metabolism; Heme; Iron; Membrane; Metal-binding; Monooxygenase; NADP; Oxidoreductase; Transmembrane; Transmembrane helix; Vacuole
SRR646572_TR24018_c0_g1_i1_len=866	ADF_VITVI	Q:119-541,H:3-143	85.82%ID	E:1e-76	Actin-depolymerizing factor	PF00241.17^Cofilin_ADF^Cofilin/tropomyosin-type actin-binding protein^8-129^E:1.6e-37	0,454	0,433	0	1,734	0,001	1,123	0,691	0,165	1	0,041	ADF_VITVI	Actin-depolymerizing factor (ADF)		Vitis vinifera (Grape)		Actin-binding
SRR646572_TR25614_c0_g1_i5_len=811	ARGE_ARATH	Q:811-347,H:286-438	64.52%ID	E:4e-66	Acetylornithine deacetylase	PF01546.25^Peptidase_M20^Peptidase family M20/M25/M40^61-152^E:6.2e-07	0,001	3,835	0	4,68	0	5,018	0,025	3,653	1	0,695	ARGE_ARATH	Acetylornithine deacetylase (EC 3.5.1.16) (N-acetylornithinase) (AO) (Acetylornithinase) (NAO)	At4g17830 dl4945w T6K21	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Amino-acid biosynthesis; L-arginine biosynthesis; L-ornithine from N(2)-acetyl-L-ornithine (linear): step 1/1.	Alternative splicing; Amino-acid biosynthesis; Arginine biosynthesis; Cobalt; Complete proteome; Hydrolase; Metal-binding; Reference proteome; Zinc
SRR646572_TR28058_c0_g1_i2_len=2029	SG1_RAUSE	Q:1955-321,H:1-531	71.61%ID	E:0	Strictosidine-O-beta-D-glucosidase	PF00232.15^Glyco_hydro_1^Glycosyl hydrolase family 1^49-520^E:4.2e-155	0,283	0,676	0	9,672	0	7,037	0,254	4,566	1	0,508	SG1_RAUSE	Strictosidine-O-beta-D-glucosidase (EC 3.2.1.105)	SGR1	Rauvolfia serpentina (Serpentine wood) (Ophioxylon serpentinum)		3D-structure; Alkaloid metabolism; Glycosidase; Hydrolase
SRR646596_TR2459_c0_g1_i1_len=1745	HEX6_RICCO	Q:4-1476,H:13-503	76.58%ID	E:0	Hexose carrier protein HEX6	PF00083.21^Sugar_tr^Sugar (and other) transporter^15-475^E:1.5e-114`PF07690.13^MFS_1^Major Facilitator Superfamily^65-425^E:2.5e-22	0,111	1,306	0	2,858	0	4,46	0,076	2,406	1	0,134	HEX6_RICCO	Hexose carrier protein HEX6	HEX6	Ricinus communis (Castor bean)		Membrane; Sugar transport; Symport; Transmembrane; Transmembrane helix; Transport
SRR646596_TR8627_c0_g1_i2_len=1408	WTR41_ARATH	Q:1311-448,H:71-356	46.42%ID	E:6e-70	WAT1-related protein At5g40230	PF00892.17^EamA^EamA-like transporter family^94-229^E:1.2e-09	0,015	1,862	0	1,691	0	6,876	0,002	6,383	1	0	WTR41_ARATH	WAT1-related protein At5g40230	At5g40230 MSN9.130	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Membrane; Reference proteome; Repeat; Transmembrane; Transmembrane helix
SRR646604_TR174_c3_g2_i1_len=1403	HSP7C_PETHY	Q:1204-2,H:1-401	97.01%ID	E:0	Heat shock cognate 70 kDa protein	PF00012.17^HSP70^Hsp70 protein^9-401^E:9.3e-190`PF06723.10^MreB_Mbl^MreB/Mbl protein^130-380^E:7.6e-15	0,629	1,42	0	6,325	0,001	1,111	0,002	1,031	1	0,126	HSP7C_PETHY	Heat shock cognate 70 kDa protein	HSP70	Petunia hybrida (Petunia)		ATP-binding; Nucleotide-binding; Stress response
SRR646604_TR12897_c1_g2_i4_len=781	SG1_RAUSE	Q:152-781,H:303-499	67.3%ID	E:3e-90	Strictosidine-O-beta-D-glucosidase	PF00232.15^Glyco_hydro_1^Glycosyl hydrolase family 1^7-199^E:6.5e-41	0,006	1,161	0	6,023	0	3,814	0,56	0,613	0,852	0,076	SG1_RAUSE	Strictosidine-O-beta-D-glucosidase (EC 3.2.1.105)	SGR1	Rauvolfia serpentina (Serpentine wood) (Ophioxylon serpentinum)		3D-structure; Alkaloid metabolism; Glycosidase; Hydrolase
SRR646604_TR25889_c0_g3_i1_len=1942	PTR21_ARATH	Q:1942-314,H:56-594	57.09%ID	E:0	Protein NRT1/ PTR FAMILY 2.13	PF07690.13^MFS_1^Major Facilitator Superfamily^19-480^E:2.3e-10`PF00854.18^PTR2^POT family^73-499^E:2.3e-82	0,014	0,979	0	4,344	0	7,137	0,129	5,09	0,356	-0,369	PTR21_ARATH	Protein NRT1/ PTR FAMILY 2.13 (AtNPF2.13) (Nitrate transporter 1.7)	NPF2.13 NRT1.7 At1g69870 T17F3.10	Arabidopsis thaliana (Mouse-ear cress)		Cell membrane; Complete proteome; Membrane; Nitrate assimilation; Reference proteome; Symport; Transmembrane; Transmembrane helix; Transport
SRR646604_TR34957_c0_g1_i1_len=1875	EF1A_MANES	Q:188-1492,H:1-435	98.16%ID	E:0	Elongation factor 1-alpha	PF00009.24^GTP_EFTU^Elongation factor Tu GTP binding domain^7-221^E:2.1e-52`PF03144.22^GTP_EFTU_D2^Elongation factor Tu domain 2^248-313^E:2.4e-14`PF03143.14^GTP_EFTU_D3^Elongation factor Tu C-terminal domain^322-429^E:1.3e-37	0,205	-0,351	0,001	0,896	0	1,139	0,004	0,896	0,833	0,058	EF1A_MANES	Elongation factor 1-alpha (EF-1-alpha)	EF1	Manihot esculenta (Cassava) (Jatropha manihot)		Cytoplasm; Elongation factor; GTP-binding; Nucleotide-binding; Phosphoprotein; Protein biosynthesis
SRR648705_TR21994_c0_g4_i4_len=2338	SG1_RAUSE	Q:219-1880,H:1-531	70.81%ID	E:0	Strictosidine-O-beta-D-glucosidase	PF00232.15^Glyco_hydro_1^Glycosyl hydrolase family 1^49-529^E:8.1e-153	0,048	0,673	0	4,387	0	2,924	0,748	0,279	0,053	0,522	SG1_RAUSE	Strictosidine-O-beta-D-glucosidase (EC 3.2.1.105)	SGR1	Rauvolfia serpentina (Serpentine wood) (Ophioxylon serpentinum)		3D-structure; Alkaloid metabolism; Glycosidase; Hydrolase
SRR648705_TR22083_c0_g2_i1_len=847	MY108_ARATH	Q:2-184,H:92-152	72.13%ID	E:5e-24	Transcription factor MYB108	PF00249.28^Myb_DNA-binding^Myb-like DNA-binding domain^1-26^E:9.6e-09	0,517	1,034	0	4,5	0	4,541	0,004	3,294	1	0,265	MY108_ARATH	Transcription factor MYB108 (Myb-related protein 108) (AtMYB108) (Protein BOTRYTIS-SUSCEPTIBLE 1)	MYB108 BOS1 At3g06490 F5E6.18	Arabidopsis thaliana (Mouse-ear cress)		Activator; Complete proteome; DNA-binding; Nucleus; Plant defense; Reference proteome; Repeat; Transcription; Transcription regulation; Ubl conjugation
SRR648705_TR24960_c0_g1_i1_len=1109	ADF2_PETHY	Q:378-794,H:1-139	87.77%ID	E:3e-72	Actin-depolymerizing factor 2	PF00241.17^Cofilin_ADF^Cofilin/tropomyosin-type actin-binding protein^14-135^E:2.2e-36	0,436	0,227	0	1,792	0	0,973	0,002	0,874	0,397	0,223	ADF2_PETHY	Actin-depolymerizing factor 2 (ADF-2)	ADF2	Petunia hybrida (Petunia)		Actin-binding
SRR648705_TR25311_c1_g1_i3_len=2668	LGUL_BRAOG	Q:2491-1661,H:6-281	82.31%ID	E:3e-161	Putative lactoylglutathione lyase	PF04674.9^Phi_1^Phosphate-induced protein 1 conserved region^75-337^E:2.5e-122	0,004	0,861	0	1,285	0	1,291	0,064	0,582	1	0,206	LGUL_BRAOG	Putative lactoylglutathione lyase (EC 4.4.1.5) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (Methylglyoxalase) (S-D-lactoylglutathione methylglyoxal lyase)		Brassica oleracea var. gemmifera (Brussel sprouts)	PATHWAY: Secondary metabolite metabolism; methylglyoxal degradation; (R)-lactate from methylglyoxal: step 1/2.	Lyase; Metal-binding; Repeat; Zinc
SRR648705_TR35694_c2_g7_i2_len=626	10HGO_CATRO	Q:272-3,H:2-91	73.33%ID	E:3e-40	8-hydroxygeraniol dehydrogenase	.	0,212	1,071	0	5,356	0	2,4	0,16	1,231	0,798	0,341	10HGO_CATRO	8-hydroxygeraniol dehydrogenase (Cr10HGO) (EC 1.1.1.324)	10HGO	Catharanthus roseus (Madagascar periwinkle) (Vinca rosea)		Metal-binding; NADP; Oxidoreductase; Zinc
SRR648705_TR42999_c0_g4_i1_len=913	NA	NA	NA	NA	NA	.	0,003	1,303	0	2,483	0	1,686	0,008	0,91	1	-0,029	.	.	.	.	.	.
SRR648707_TR4199_c0_g1_i3_len=5019	PDR2_ARATH	Q:1246-3840,H:135-991	80.51%ID	E:0	Probable manganese-transporting ATPase PDR2	PF00122.17^E1-E2_ATPase^E1-E2 ATPase^44-281^E:6.2e-21`PF00702.23^Hydrolase^haloacid dehalogenase-like hydrolase^291-520^E:4.1e-08`PF13246.3^Cation_ATPase^Cation transport ATPase (P-type)^347-422^E:2.5e-07	0,559	-0,326	0	3,002	0	2,358	0,214	0,794	0,173	-0,711	PDR2_ARATH	Probable manganese-transporting ATPase PDR2 (EC 3.6.3.-) (Protein MALE GAMETOGENESIS IMPAIRED ANTHERS) (Protein PHOSPHATE DEFICIENCY RESPONSE 2)	PDR2 MIA At5g23630 MQM1.11	Arabidopsis thaliana (Mouse-ear cress)		ATP-binding; Complete proteome; Endoplasmic reticulum; Hydrolase; Magnesium; Manganese; Membrane; Metal-binding; Nucleotide-binding; Reference proteome; Transmembrane; Transmembrane helix; Transport
SRR648707_TR25285_c3_g4_i4_len=4173	SG1_RAUSE	Q:4000-2339,H:1-531	69.73%ID	E:0	Strictosidine-O-beta-D-glucosidase	PF00232.15^Glyco_hydro_1^Glycosyl hydrolase family 1^49-529^E:5e-153	0,335	0,747	0	4,594	0	3,742	0,692	1,271	1	-0,011	SG1_RAUSE	Strictosidine-O-beta-D-glucosidase (EC 3.2.1.105)	SGR1	Rauvolfia serpentina (Serpentine wood) (Ophioxylon serpentinum)		3D-structure; Alkaloid metabolism; Glycosidase; Hydrolase
SRR924147_TR1813_c0_g1_i1_len=1225	WLIM1_ARATH	Q:993-475,H:3-176	72.99%ID	E:1e-87	LIM domain-containing protein WLIM1 {ECO:0000305}	PF00412.19^LIM^LIM domain^11-65^E:1.7e-10`PF00412.19^LIM^LIM domain^110-164^E:4.4e-10	1	0,069	0	2,854	0	2,03	0,094	1,124	1	0,043	WLIM1_ARATH	LIM domain-containing protein WLIM1 (Widely-expressed LIM protein 1) (AtWLIM1)	WLIM1 At1g10200 F14N23.8	Arabidopsis thaliana (Mouse-ear cress)		Acetylation; Actin-binding; Complete proteome; Cytoplasm; Cytoskeleton; LIM domain; Metal-binding; Reference proteome; Repeat; Zinc
SRR924147_TR3781_c0_g1_i1_len=2569	AL2B7_ARATH	Q:2306-795,H:30-534	81.39%ID	E:0	Aldehyde dehydrogenase family 2 member B7, mitochondrial	PF00171.19^Aldedh^Aldehyde dehydrogenase family^64-525^E:6.4e-178	0,407	0,656	0	2,806	0,001	3,014	0,517	1,227	1	-0,549	AL2B7_ARATH	Aldehyde dehydrogenase family 2 member B7, mitochondrial (ALDH2b) (EC 1.2.1.3)	ALDH2B7 ALDH3 At1g23800 F5O8.33 F5O8.35	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Mitochondrion; NAD; Oxidoreductase; Reference proteome; Transit peptide
SRR924147_TR27800_c0_g1_i2_len=1466	NLTL5_ARATH	Q:922-665,H:41-126	76.74%ID	E:6e-37	Non-specific lipid-transfer protein-like protein At5g64080	PF00234.19^Tryp_alpha_amyl^Protease inhibitor/seed storage/LTP family^2-72^E:1.5e-07`PF14368.3^LTP_2^Probable lipid transfer^4-72^E:1.2e-12	0,11	0,612	0	1,715	0	4,448	0,01	2,231	0,316	0,666	NLTL5_ARATH	Non-specific lipid-transfer protein-like protein At5g64080	At5g64080 MHJ24.6	Arabidopsis thaliana (Mouse-ear cress)		Alternative splicing; Cell membrane; Complete proteome; Disulfide bond; GPI-anchor; Glycoprotein; Lipoprotein; Membrane; Reference proteome; Signal
SRR924148_TR1761_c0_g1_i1_len=928	NLTP2_PRUAR	Q:467-670,H:1-68	72.06%ID	E:9e-26	Non-specific lipid-transfer protein 2	.	0,008	1,621	0	2,406	0	2,425	0,019	1,674	0,92	-0,08	NLTP2_PRUAR	Non-specific lipid-transfer protein 2 (LTP 2)		Prunus armeniaca (Apricot) (Armeniaca vulgaris)		Direct protein sequencing; Lipid-binding; Transport
SRR924148_TR7540_c0_g1_i1_len=1942	ANXD1_ARATH	Q:1252-368,H:22-317	68.92%ID	E:9e-147	Annexin D1	PF00191.17^Annexin^Annexin^10-75^E:2.8e-17`PF00191.17^Annexin^Annexin^94-154^E:1.9e-14`PF00191.17^Annexin^Annexin^168-233^E:1.2e-15	0,166	0,858	0	2,355	0	2,037	0,016	1,462	0,042	0,853	ANXD1_ARATH	Annexin D1 (AnnAt1) (Annexin A1)	ANN1 ANNAT1 ANX23-ATH ATOXY5 OXY5 At1g35720 F14D7.2	Arabidopsis thaliana (Mouse-ear cress)		3D-structure; Acetylation; Annexin; Calcium; Calcium/phospholipid-binding; Complete proteome; Cytoplasm; Membrane; Reference proteome; Repeat; Stress response
SRR924148_TR16752_c0_g1_i1_len=547	NA	NA	NA	NA	NA	.	1	1,71	0	6,977	0	2,705	0,001	2,277	0,811	-0,29	.	.	.	.	.	.
SRR924148_TR17782_c0_g1_i2_len=1566	HIDM_GLYEC	Q:1336-407,H:16-327	45.77%ID	E:9e-89	2-hydroxyisoflavanone dehydratase	PF00135.25^COesterase^Carboxylesterase family^59-137^E:9.9e-06`PF07859.10^Abhydrolase_3^alpha/beta hydrolase fold^74-285^E:1.3e-35	0,213	0,278	0	2,117	0	1,56	0,013	0,609	0,791	-0,063	HIDM_GLYEC	2-hydroxyisoflavanone dehydratase (EC 3.1.1.1) (EC 4.2.1.105) (Carboxylesterase HIDM)	HIDM	Glycyrrhiza echinata (Licorice)	PATHWAY: Secondary metabolite biosynthesis; flavonoid biosynthesis.	Flavonoid biosynthesis; Hydrolase; Lyase
SRR924148_TR25300_c1_g2_i3_len=1538	UXS6_ARATH	Q:169-1203,H:1-343	86.09%ID	E:0	UDP-glucuronic acid decarboxylase 6	PF04321.14^RmlD_sub_bind^RmlD substrate binding domain^33-300^E:1.1e-07`PF01370.18^Epimerase^NAD dependent epimerase/dehydratase family^35-269^E:3.9e-45`PF02719.12^Polysacc_synt_2^Polysaccharide biosynthesis protein^35-146^E:2e-08`PF16363.2^GDP_Man_Dehyd^GDP-mannose 4,6 dehydratase^36-330^E:8.5e-54`PF01073.16^3Beta_HSD^3-beta hydroxysteroid dehydrogenase/isomerase family^36-187^E:1.9e-12`PF07993.9^NAD_binding_4^Male sterility protein^87-208^E:5.2e-07	0,948	0,041	0	1,341	0,001	1,44	0,011	1,113	0,452	0,289	UXS6_ARATH	UDP-glucuronic acid decarboxylase 6 (EC 4.1.1.35) (UDP-XYL synthase 6) (UDP-glucuronate decarboxylase 6) (UGD) (UXS-6)	UXS6 At2g28760 F8N16.5	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Nucleotide-sugar biosynthesis; UDP-alpha-D-xylose biosynthesis; UDP-alpha-D-xylose from UDP-alpha-D-glucuronate: step 1/1.	Acetylation; Complete proteome; Cytoplasm; Decarboxylase; Lyase; NAD; Reference proteome
SRR924148_TR34256_c6_g1_i5_len=2115	SG1_RAUSE	Q:67-1491,H:1-454	69.33%ID	E:0	Strictosidine-O-beta-D-glucosidase	PF00232.15^Glyco_hydro_1^Glycosyl hydrolase family 1^49-475^E:1.1e-125	0,278	0,844	0	5,232	0	3,33	0,189	1,539	0,299	1,303	SG1_RAUSE	Strictosidine-O-beta-D-glucosidase (EC 3.2.1.105)	SGR1	Rauvolfia serpentina (Serpentine wood) (Ophioxylon serpentinum)		3D-structure; Alkaloid metabolism; Glycosidase; Hydrolase
SRR924148_TR34256_c6_g1_i8_len=632	SG1_RAUSE	Q:356-631,H:440-530	69.89%ID	E:2e-33	Strictosidine-O-beta-D-glucosidase	.	0,381	0,78	0	3,948	0	3,279	0,299	1,375	0,429	-0,467	SG1_RAUSE	Strictosidine-O-beta-D-glucosidase (EC 3.2.1.105)	SGR1	Rauvolfia serpentina (Serpentine wood) (Ophioxylon serpentinum)		3D-structure; Alkaloid metabolism; Glycosidase; Hydrolase
SRR122238_TR38701_c2_g1_i1_len=1273	14335_SOLTU	Q:1206-442,H:1-	93.75%ID	E:1e-171	14-3-3-like protein 16R	PF00244.17^14-3-3^14-3-3 protein^33-258^E:7.5e-105	0,332	0,226	0,037	0,528	0,002	0,751	0	0,905	0	0,954	14335_SOLTU	14-3-3-like protein 16R		Solanum tuberosum (Potato)		Complete proteome; Reference proteome

SRR122238_TR38701_c2_g1_i1_len=1273	14335_SOLTU	256	93.75%ID	E:1e-171	14-3-3-like protein 10R	PF00244.17^14-3-3^14-3-3 protein^35-236^E:7.3e-105	0,332	-0,226	0,057	0,328	0,002	0,751	0	0,903	0	0,934	14335_SOLTU	14-3-3-like protein 10R		Solanum tuberosum (Potato)		Complete proteome; Reference proteome
SRR342023_TR28516_c2_g2_i3_len=759	KIRO_ACTDE	Q:266-709,H:1-148	46.62%ID	E:2e-34	Kirola {ECO:0000303|PubMed:21309790}	PF00407.16^Bet_v_1^Pathogenesis-related protein Bet v I family^4-147^E:1.2e-32	0,686	-0,141	0,216	0,418	0,011	0,751	0	1,055	0	0,917	KIRO_ACTDE	Kirola (allergen Act d 11)		Actinidia deliciosa (Kiwi)		3D-structure; Acetylation; Allergen; Direct protein sequencing; Polymorphism
SRR122238_TR61844_c0_g3_i2_len=1160	RNLX_SOLLC	Q:953-291,H:1-220	66.67%ID	E:5e-106	Intracellular ribonuclease LX	PF00445.15^Ribonuclease_T2^Ribonuclease T2 family^52-232^E:3.2e-60	0,017	0,947	0,471	0,5	0,001	1,64	0,005	1,42	0	2,014	RNLX_SOLLC	Intracellular ribonuclease LX (RNase LX) (EC 3.1.27.1)	RNALX	Solanum lycopersicum (Tomato) (Lycopersicon esculentum)		Complete proteome; Cytoplasm; Direct protein sequencing; Disulfide bond; Endonuclease; Hydrolase; Nuclease; Reference proteome; Stress response; Zymogen
SRR342017_TR14537_c0_g1_i2_len=2077	AMYB_VIGUN	Q:177-1619,H:11-495	70.72%ID	E:0	Beta-amylase	PF01373.14^Glyco_hydro_14^Glycosyl hydrolase family 14^13-428^E:6e-119	0,087	0,534	0,275	0,448	0	1,449	0,502	0,33	0	0,917	AMYB_VIGUN	Beta-amylase (EC 3.2.1.2) (1,4-alpha-D-glucan maltohydrolase)	BMY1	Vigna unguiculata (Cowpea)		Carbohydrate metabolism; Glycosidase; Hydrolase; Polysaccharide degradation
SRR342019_TR35572_c1_g6_i1_len=1612	THCAS_CANSA	Q:140-1348,H:127-539	42.28%ID	E:7e-101	Tetrahydrocannabinolic acid synthase	PF01565.20^FAD_binding_4^FAD binding domain^15-104^E:4.9e-16`PF08031.9^BBE^Berberine and berberine like^357-415^E:5.2e-23	0,195	1,29	0,299	1,967	0,001	4,407	0,001	4,367	0	6,776	THCAS_CANSA	Tetrahydrocannabinolic acid synthase (THCAS) (EC 1.21.3.7) (Delta(1)-tetrahydrocannabinolic acid synthase) (THCA synthase)		Cannabis sativa (Hemp) (Marijuana)		3D-structure; Apoplast; Direct protein sequencing; Disulfide bond; FAD; Flavoprotein; Glycoprotein; Oxidoreductase; Secreted; Signal
SRR646572_TR33328_c0_g1_i1_len=1995	AMYB_VIGUN	Q:144-1586,H:11-495	70.52%ID	E:0	Beta-amylase	PF01373.14^Glyco_hydro_14^Glycosyl hydrolase family 14^13-428^E:3.7e-119	0,03	0,604	0,095	0,556	0	1,386	0,474	0,284	0	7,969	AMYB_VIGUN	Beta-amylase (EC 3.2.1.2) (1,4-alpha-D-glucan maltohydrolase)	BMY1	Vigna unguiculata (Cowpea)		Carbohydrate metabolism; Glycosidase; Hydrolase; Polysaccharide degradation
SRR122238_TR7054_c0_g1_i1_len=2273	P2C02_ARATH	Q:1980-1084,H:81-380	61.59%ID	E:5e-121	Probable protein phosphatase 2C 2	PF00481.18^PP2C^Protein phosphatase 2C^165-385^E:2e-56	0	3,45	0	7,19	0,001	5,561	0	6,226	1	-0,295	P2C02_ARATH	Probable protein phosphatase 2C 2 (AtPP2C02) (EC 3.1.3.16) (Protein phosphatase AP2C2)	At1g07160 F10K1.13	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Hydrolase; Magnesium; Manganese; Metal-binding; Protein phosphatase; Reference proteome
SRR122238_TR61939_c0_g1_i15_len=3514	NES1_FRAAN	Q:3212-2130,H:14-338	46.54%ID	E:9e-91	(3S,6E)-nerolidol synthase 1	PF01535.17^PPR^PPR repeat^148-173^E:0.00038`PF17177.1^PPR_long^Pentacotripeptide-repeat region of PROPR^155-264^E:1e-07`PF13812.3^PPR_3^Pentatricopeptide repeat domain^163-221^E:2.7e-09`PF01535.17^PPR^PPR repeat^179-205^E:0.087`PF12854.4^PPR_1^PPR repeat^209-240^E:1.8e-12`PF13041.3^PPR_2^PPR repeat family^211-258^E:4.6e-16`PF01535.17^PPR^PPR repeat^214-244^E:5.8e-07`PF13812.3^PPR_3^Pentatricopeptide repeat domain^235-290^E:1.7e-07`PF12854.4^PPR_1^PPR repeat^243-275^E:8.6e-06`PF13041.3^PPR_2^PPR repeat family^246-293^E:8.4e-08`PF01535.17^PPR^PPR repeat^249-278^E:0.00068`PF13041.3^PPR_2^PPR repeat family^282-328^E:9.3e-11`PF01535.17^PPR^PPR repeat^285-314^E:0.0034`PF13812.3^PPR_3^Pentatricopeptide repeat domain^305-359^E:3.9e-11`PF13041.3^PPR_2^PPR repeat family^317-361^E:3.7e-11`PF01535.17^PPR^PPR repeat^319-349^E:1.7e-06	0	2,186	0	1,953	0,004	3,608	0	4,468	0,025	2,511	NES1_FRAAN	(3S,6E)-nerolidol synthase 1 (FaNES1) (EC 4.2.3.48)		Fragaria ananassa (Strawberry)	PATHWAY: Secondary metabolite biosynthesis; terpenoid biosynthesis.	Cytoplasm; Lyase; Magnesium; Manganese; Metal-binding
SRR342022_TR23185_c0_g3_i11_len=1836	MYRS_QUEIL	Q:1564-425,H:38-414	57.63%ID	E:4e-141	Myrcene synthase, chloroplastic	PF01397.18^Terpene_synth^Terpene synthase, N-terminal domain^67-243^E:3e-44`PF03936.13^Terpene_synth_C^Terpene synthase family, metal binding domain^275-418^E:1.3e-56	0	4,216	0	6,568	1	-3,468	0	4,595	1	0	MYRS_QUEIL	Myrcene synthase, chloroplastic (EC 4.2.3.15)		Quercus ilex (Holly oak)		Chloroplast; Lyase; Magnesium; Manganese; Metal-binding; Plastid; Transit peptide
SRR648707_TR4925_c0_g1_i2_len=2058	P2C30_ARATH	Q:949-1638,H:156-389	67.09%ID	E:1e-99	Probable protein phosphatase 2C 30	PF00481.18^PP2C^Protein phosphatase 2C^6-220^E:9.5e-56	0	6,029	0	8,845	0,002	5,327	0	5,822	0	-2,226	P2C30_ARATH	Probable protein phosphatase 2C 30 (AtPP2C30) (EC 3.1.3.16) (AthPP2C5)	PP2C5 At2g40180 T7M7.17	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Hydrolase; Magnesium; Manganese; Metal-binding; Protein phosphatase; Reference proteome
SRR1144634_TR11657_c0_g2_i1_len=1291	PIP22_ORYSJ	Q:81-827,H:1-252	80.56%ID	E:1e-141	Probable aquaporin PIP2-2	PF00230.17^MIP^Major intrinsic protein^31-250^E:2.8e-73	0	1,932	0	4,172	0	1,188	0,023	0,48	0,007	1,374	PIP22_ORYSJ	Probable aquaporin PIP2-2 (OsPIP2;2) (Plasma membrane intrinsic protein 2-2)	PIP2-2 Os02g0629200 LOC_Os02g41860 B1469H02.22-1	Oryza sativa subsp. japonica (Rice)		Cell membrane; Complete proteome; Membrane; Reference proteome; Repeat; Transmembrane; Transmembrane helix; Transport
SRR1144634_TR14318_c0_g1_i1_len=972	SERA2_ARATH	Q:61-732,H:401-624	81.25%ID	E:1e-120	D-3-phosphoglycerate dehydrogenase 2, chloroplastic	PF01842.22^ACT^ACT domain^101-161^E:5.2e-11	0	1,585	0	2,934	0	1,887	0,009	0,783	0,23	0,291	SERA2_ARATH	D-3-phosphoglycerate dehydrogenase 2, chloroplastic (PGDH) (EC 1.1.1.95)	PGDH2 3-PGDH PGDH At1g17745 F11A6.8	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Amino-acid biosynthesis; L-serine biosynthesis; L-serine from 3-phospho-D-glycerate: step 1/3.	Alternative splicing; Amino-acid biosynthesis; Chloroplast; Complete proteome; NAD; Oxidoreductase; Phosphoprotein; Plastid; Reference proteome; Serine biosynthesis; Transit peptide
SRR1144634_TR22915_c0_g1_i1_len=571	CVIF1_ARATH	Q:163-501,H:26-138	41.59%ID	E:2e-22	Cell wall / vacuolar inhibitor of fructosidase 1	PF04043.12^PMEI^Plant invertase/pectin methylesterase inhibitor^54-187^E:1e-13	0	1,217	0	1,991	0	1,233	0,932	-0,046	0	-7,8	CVIF1_ARATH	Cell wall / vacuolar inhibitor of fructosidase 1 (AtC/VIF1)	C/VIF1 CIF1 VIF1 At1g47960 T2J15.13	Arabidopsis thaliana (Mouse-ear cress)		Alternative splicing; Complete proteome; Disulfide bond; Glycoprotein; Reference proteome; Signal; Vacuole
SRR1144634_TR34616_c0_g1_i1_len=653	ML423_ARATH	Q:125-583,H:7-153	36.6%ID	E:6e-29	MLP-like protein 423	PF00407.16^Bet_v_1^Pathogenesis-related protein Bet v I family^3-153^E:4.4e-28	0	1,425	0	2,785	0,001	1,46	0,281	0,548	1	0	ML423_ARATH	MLP-like protein 423	MLP423 At1g24020 T23E23.17 T23E23_22	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Reference proteome
SRR122238_TR7709_c0_g1_i3_len=827	NA	NA	NA	NA	NA	PF14299.3^PP2^Phloem protein 2^27-186^E:7.8e-28	0	4,79	0	6,692	0	5,058	0,381	2,186	0,381	0,823	.	.	.	.	.	.
SRR122238_TR20261_c1_g1_i1_len=928	NA	NA	NA	NA	NA	PF00847.17^AP2^AP2 domain^75-124^E:2.5e-14	0	5,162	0	5,968	0	6,112	0,129	3,83	1	-0,64	.	.	.	.	.	.
SRR122238_TR42251_c0_g1_i1_len=827	DR206_PEA	Q:741-175,H:1-184	57.67%ID	E:2e-73	Disease resistance response protein 206	PF03018.11^Dirigent^Dirigent-like protein^36-181^E:1.4e-38	0,001	1,329	0	2,071	0	1,72	0,009	1,344	0,254	-4,433	DR206_PEA	Disease resistance response protein 206 (Dirigent protein PI206)	PI206	Pisum sativum (Garden pea)		3D-structure; Apoplast; Disulfide bond; Glycoprotein; Pathogenesis-related protein; Plant defense; Secreted; Signal
SRR122238_TR44565_c0_g2_i1_len=1611	C81F1_ARATH	Q:65-1396,H:39-499	44.73%ID	E:5e-125	Cytochrome P450 81F1 {ECO:0000305}	PF00067.19^p450^Cytochrome P450^12-449^E:6.7e-90	0	1,507	0	3,237	0	1,654	0,02	0,866	1	0,47	C81F1_ARATH	Cytochrome P450 81F1 (EC 1.14.-.-)	CYP81F1 CYP91A2 At4g37430 F6G17.80	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Heme; Iron; Membrane; Metal-binding; Monooxygenase; Oxidoreductase; Reference proteome; Transmembrane; Transmembrane helix
SRR122238_TR54493_c1_g2_i1_len=1095	NA	NA	NA	NA	NA	.	0	1,124	0	2,135	0	1,124	0,001	0,878	0,886	0,186	.	.	.	.	.	.
SRR1271858_TR25211_c0_g2_i1_len=675	NA	NA	NA	NA	NA	.	0	1,292	0	6,744	0	8,539	0,129	4,207	0	-2,021	.	.	.	.	.	.
SRR1271858_TR59441_c0_g1_i2_len=1968	NA	NA	NA	NA	NA	PF11891.5^DUF3411^Domain of unknown function (DUF3411)^203-381^E:1.3e-64	0	1,519	0	2,425	0,001	2,103	0,006	1,848	0,739	0,28	.	.	.	.	.	.
SRR1271859_TR27501_c0_g1_i1_len=893	CVIF1_ARATH	Q:257-691,H:26-162	37.24%ID	E:2e-22	Cell wall / vacuolar inhibitor of fructosidase 1	PF04043.12^PMEI^Plant invertase/pectin methylesterase inhibitor^28-172^E:2e-14	0	1,257	0	1,298	0	2,143	0,58	0,243	0,073	-2,39	CVIF1_ARATH	Cell wall / vacuolar inhibitor of fructosidase 1 (AtC/VIF1)	C/VIF1 CIF1 VIF1 At1g47960 T2J15.13	Arabidopsis thaliana (Mouse-ear cress)		Alternative splicing; Complete proteome; Disulfide bond; Glycoprotein; Reference proteome; Signal; Vacuole
SRR1271859_TR33815_c0_g2_i4_len=2647	LDOX_MALDO	Q:1392-2384,H:10-341	38.84%ID	E:3e-75	Leucoanthocyanidin dioxygenase	PF14226.3^DIOX_N^non-haem dioxygenase in morphine synthesis N-terminal^56-167^E:1e-32`PF03171.17^2OG-FeII_Oxy^2OG-Fe(II) oxygenase superfamily^216-314^E:7e-27	0	4,739	0	7,48	0	3,467	0,014	2,776	1	0,759	LDOX_MALDO	Leucoanthocyanidin dioxygenase (LDOX) (Leucocyanidin oxygenase) (EC 1.14.11.19) (Anthocyanidin synthase) (Leucoanthocyanidin hydroxylase)	ANS	Malus domestica (Apple) (Pyrus malus)	PATHWAY: Pigment biosynthesis; anthocyanin biosynthesis.	Dioxygenase; Flavonoid biosynthesis; Iron; Metal-binding; Oxidoreductase; Vitamin C
SRR1271859_TR38596_c0_g1_i7_len=1181	DCE_SOLLC	Q:1062-46,H:165-502	76.99%ID	E:0	Glutamate decarboxylase	PF00282.16^Pyridoxal_deC^Pyridoxal-dependent decarboxylase conserved domain^10-228^E:1.2e-66	0	1,444	0	1,848	0	2,084	0,002	1,274	0,43	0,637	DCE_SOLLC	Glutamate decarboxylase (GAD) (EC 4.1.1.15) (ERT D1)		Solanum lycopersicum (Tomato) (Lycopersicon esculentum)		Calmodulin-binding; Complete proteome; Decarboxylase; Lyase; Pyridoxal phosphate; Reference proteome
SRR342019_TR2813_c0_g5_i1_len=1177	NA	NA	NA	NA	NA	.	0	2,226	0	3,523	0	2,776	0,003	2,063	1	-0,108	.	.	.	.	.	.
SRR342019_TR34225_c0_g1_i1_len=617	PRS1_SOLTU	Q:85-528,H:1-155	35.9%ID	E:5e-21	Pathogenesis-related protein STH-21	PF00407.16^Bet_v_1^Pathogenesis-related protein Bet v I family^4-143^E:1.3e-12	0	1,02	0	1,571	0,001	0,715	0,002	0,653	1	-0,255	PRS1_SOLTU	Pathogenesis-related protein STH-21	STH-21	Solanum tuberosum (Potato)		Complete proteome; Pathogenesis-related protein; Plant defense; Reference proteome
SRR342019_TR36227_c6_g7_i2_len=893	C7BL3_CICIN	Q:838-245,H:290-486	42.93%ID	E:1e-57	Costunolide synthase	PF00067.19^p450^Cytochrome P450^3-185^E:2.1e-49	0	1,586	0	1,968	0,001	0,852	0,001	-0,994	0,16	1,341	C7BL3_CICIN	Costunolide synthase (CiCOS) (EC 1.14.13.120) (Cytochrome P450 71BL3)	CYP71BL3 COS	Cichorium intybus (Chicory)		Heme; Iron; Membrane; Metal-binding; Monooxygenase; NADP; Oxidoreductase; Transmembrane; Transmembrane helix
SRR342023_TR3935_c3_g7_i1_len=2430	SERA2_ARATH	Q:1973-336,H:79-624	84.62%ID	E:0	D-3-phosphoglycerate dehydrogenase 2, chloroplastic	PF00389.27^2-Hacid_dh^D-isomer specific 2-hydroxyacid dehydrogenase, catalytic domain^98-407^E:3.7e-35`PF02826.16^2-Hacid_dh_C^D-isomer specific 2-hydroxyacid dehydrogenase, NAD binding domain^200-375^E:5.3e-63`PF00670.18^AdoHcyase_NAD^S-adenosyl-L-homocysteine hydrolase, NAD binding domain^230-325^E:8.4e-05`PF07991.9^IlvN^Acetohydroxy acid isomeroreductase, NADPH-binding domain^232-391^E:8e-06`PF01842.22^ACT^ACT domain^567-627^E:4.6e-10	0	1,635	0	4,331	0	1,436	0,004	0,78	0,003	1,02	SERA2_ARATH	D-3-phosphoglycerate dehydrogenase 2, chloroplastic (PGDH) (EC 1.1.1.95)	PGDH2 3-PGDH PGDH At1g17745 F11A6.8	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Amino-acid biosynthesis; L-serine biosynthesis; L-serine from 3-phospho-D-glycerate: step 1/3.	Alternative splicing; Amino-acid biosynthesis; Chloroplast; Complete proteome; NAD; Oxidoreductase; Phosphoprotein; Plastid; Reference proteome; Serine biosynthesis; Transit peptide
SRR342023_TR15323_c0_g2_i2_len=2096	SG1_RAUSE	Q:2001-340,H:1-531	70.45%ID	E:0	Strictosidine-O-beta-D-glucosidase	PF00232.15^Glyco_hydro_1^Glycosyl hydrolase family 1^49-529^E:2.6e-152	0	0,922	0	4,449	0	3,101	0,875	0,068	0,468	0,307	SG1_RAUSE	Strictosidine-O-beta-D-glucosidase (EC 3.2.1.105)	SGR1	Rauvolfia serpentina (Serpentine wood) (Ophioxylon serpentinum)		3D-structure; Alkaloid metabolism; Glycosidase; Hydrolase
SRR342023_TR17313_c0_g2_i1_len=529	NA	NA	NA	NA	NA	.	0	2,974	0,001	1,015	0	1,788	0,314	0,428	0,811	-0,314	.	.	.	.	.	.
SRR646596_TR9280_c1_g1_i2_len=521	NA	NA	NA	NA	NA	.	0	1,171	0	7,188	0	3,838	1	0,605	0	-1,602	.	.	.	.	.	.
SRR646604_TR1357_c0_g1_i1_len=1551	PIP25_ARATH	Q:1277-429,H:1-281	80.57%ID	E:1e-161	Probable aquaporin PIP2-5	PF00230.17^MIP^Major intrinsic protein^31-267^E:7.9e-84	0	1,842	0	3,817	0	1,338	0,006	0,604	0,028	0,611	PIP25_ARATH	Probable aquaporin PIP2-5 (Plasma membrane intrinsic protein 2-5) (AtPIP2;5) (Plasma membrane intrinsic protein 2d) (PIP2d) [Cleaved into: Probable aquaporin PIP2-5, N-terminally processed]	PIP2-5 PIP2D At3g54820 F28P10.200	Arabidopsis thaliana (Mouse-ear cress)		Acetylation; Cell membrane; Complete proteome; Membrane; Methylation; Phosphoprotein; Reference proteome; Repeat; Transmembrane; Transmembrane helix; Transport
SRR648705_TR12352_c0_g1_i6_len=1079	GSTUA_ARATH	Q:264-953,H:1-230	43.72%ID	E:5e-51	Glutathione S-transferase U10	PF02798.17^GST_N^Glutathione S-transferase, N-terminal domain^25-96^E:1.8e-16`PF13417.3^GST_N_3^Glutathione S-transferase, N-terminal domain^28-103^E:1.4e-15`PF13409.3^GST_N_2^Glutathione S-transferase, N-terminal domain^34-97^E:1.8e-07	0	1,492	0	3,21	0	3,28	1	0,129	0,967	-0,028	GSTUA_ARATH	Glutathione S-transferase U10 (AtGSTU10) (EC 2.5.1.18) (GST class-tau member 10)	GSTU10 At1g74590 F1M20.27	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Cytoplasm; Detoxification; Reference proteome; Transferase
SRR648705_TR37787_c0_g1_i3_len=844	NA	NA	NA	NA	NA	.	0,001	5,133	0	8,865	0	4,866	0,629	2,101	1	-0,425	.	.	.	.	.	.
SRR648707_TR1151_c0_g3_i1_len=1633	MT878_ARATH	Q:253-1323,H:1-361	44.26%ID	E:1e-83	Probable S-adenosylmethionine-dependent methyltransferase At5g38780	PF03492.12^Methyltransf_7^SAM dependent carboxyl methyltransferase^69-368^E:4e-102	0	1,65	0	4,011	0	1,589	0,071	0,403	0,005	0,647	MT878_ARATH	Probable S-adenosylmethionine-dependent methyltransferase At5g38780 (EC 2.1.1.-)	At5g38780 MKD10.80	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Methyltransferase; Reference proteome; S-adenosyl-L-methionine; Transferase
SRR648707_TR26086_c0_g1_i11_len=1848	TRPD_ARATH	Q:534-1208,H:110-334	84%ID	E:1e-141	Anthranilate phosphoribosyltransferase, chloroplastic	PF02885.14^Glycos_trans_3N^Glycosyl transferase family, helical bundle domain^66-124^E:2.7e-12`PF00591.18^Glycos_transf_3^Glycosyl transferase family, a/b domain^133-290^E:2.1e-71	0	1,476	0	2,824	0,001	1,135	0,004	0,976	0,081	0,622	TRPD_ARATH	Anthranilate phosphoribosyltransferase, chloroplastic (EC 2.4.2.18)	PAT1 At5g17990 MCM23.6	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Amino-acid biosynthesis; L-tryptophan biosynthesis; L-tryptophan from chorismate: step 2/5.	Amino-acid biosynthesis; Aromatic amino acid biosynthesis; Chloroplast; Complete proteome; Glycosyltransferase; Plastid; Reference proteome; Transferase; Transit peptide; Tryptophan biosynthesis
SRR648707_TR35839_c0_g1_i2_len=1717	ILL6_ARATH	Q:1344-142,H:67-462	68.58%ID	E:0	IAA-amino acid hydrolase ILR1-like 6	PF01546.25^Peptidase_M20^Peptidase family M20/M25/M40^167-482^E:9.5e-36`PF07687.11^M20_dimer^Peptidase dimerisation domain^280-373^E:1.6e-06	0,001	3,714	0	6,88	0,001	6,555	0,034	5,502	1	1,043	ILL6_ARATH	IAA-amino acid hydrolase ILR1-like 6 (EC 3.5.1.-) (Protein gr1)	ILL6 GR1 At1g44350 T18F15.9	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Hydrolase; Reference proteome; Signal
SRR924147_TR27644_c0_g1_i2_len=1043	NA	NA	NA	NA	NA	.	0	1,003	0	1,807	0	0,888	0,002	0,762	0,591	0,141	.	.	.	.	.	.
SRR1144634_TR14237_c0_g1_i4_len=622	NA	NA	NA	NA	NA	.	0,111	0,387	0	1,044	0,012	0,542	0	1,09	0	0,812	.	.	.	.	.	.
SRR342019_TR38071_c4_g2_i4_len=1544	ARGE_ARATH	Q:260-1432,H:1-394	67.09%ID	E:0	Acetylornithine deacetylase	PF01546.25^Peptidase_M20^Peptidase family M20/M25/M40^95-379^E:3.1e-23`PF07687.11^M20_dimer^Peptidase dimerisation domain^203-317^E:5.5e-13	0,052	1,666	0	3,036	0,002	4,402	0	4,843	0	1,741	ARGE_ARATH	Acetylornithine deacetylase (EC 3.5.1.16) (N-acetylornithinase) (AO) (Acetylornithinase) (NAO)	At4g17830 dl4945w T6K21	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Amino-acid biosynthesis; L-arginine biosynthesis; L-ornithine from N(2)-acetyl-L-ornithine (linear): step 1/1.	Alternative splicing; Amino-acid biosynthesis; Arginine biosynthesis; Cobalt; Complete proteome; Hydrolase; Metal-binding; Reference proteome; Zinc
SRR646596_TR9632_c0_g1_i1_len=1847	TAR4_ARATH	Q:1665-346,H:6-449	52.8%ID	E:4e-159	Tryptophan aminotransferase-related protein 4	PF04863.10^EGF_alliinase^Alliinase EGF-like domain^40-94^E:2.4e-27`PF04864.10^Alliinase_C^Allinase^96-451^E:9.5e-143`PF00155.18^Aminotran_1_2^Aminotransferase class I and II^137-432^E:1.3e-06	0	2,345	0,004	2,429	0	3,048	0,006	2,377	0	3,116	TAR4_ARATH	Tryptophan aminotransferase-related protein 4 (EC 2.6.1.-)	TAR4 At1g34060 F12G12.12 F12G12.150	Arabidopsis thaliana (Mouse-ear cress)		Aminotransferase; Complete proteome; Membrane; Pyridoxal phosphate; Reference proteome; Transferase; Transmembrane; Transmembrane helix
SRR122238_TR29423_c1_g1_i7_len=1817	RFS2_ARATH	Q:1450-206,H:359-773	78.37%ID	E:0	Probable galactinol–sucrose galactosyltransferase 2	PF05691.9^Raffinose_syn^Raffinose synthase or seed imbibition protein Sip1^2-123^E:1.5e-51`PF05691.9^Raffinose_syn^Raffinose synthase or seed imbibition protein Sip1^123-521^E:7.7e-183	0,025	1,249	0	1,711	0	1,237	0,391	0,23	0	1,783	RFS2_ARATH	Probable galactinol–sucrose galactosyltransferase 2 (EC 2.4.1.82) (Protein SEED IMBIBITION 2) (Raffinose synthase 2)	RFS2 RS2 SIP2 At3g57520 T8H10.120	Arabidopsis thaliana (Mouse-ear cress)		Alternative splicing; Carbohydrate metabolism; Complete proteome; Glycosyltransferase; Reference proteome; Transferase
SRR122238_TR51320_c0_g2_i2_len=1710	BCAT5_ARATH	Q:130-1314,H:13-414	70.44%ID	E:0	Branched-chain-amino-acid aminotransferase 5, chloroplastic	PF01063.16^Aminotran_4^Amino-transferase class IV^156-394^E:1.4e-41	0,009	-5,939	0	7,09	0	6,711	0,129	4,989	0	7,39	BCAT5_ARATH	Branched-chain-amino-acid aminotransferase 5, chloroplastic (Atbcat-5) (EC 2.6.1.42)	BCAT5 At5g65780 F6H11.110 MPA24.13	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Amino-acid biosynthesis; L-isoleucine biosynthesis; L-isoleucine from 2-oxobutanoate: step 4/4.; PATHWAY: Amino-acid biosynthesis; L-leucine biosynthesis; L-leucine from 3-methyl-2-oxobutanoate: step 4/4.; PATHWAY: Amino-acid biosynthesis; L-valine biosynthesis; L-valine from pyruvate: step 4/4.	Alternative splicing; Amino-acid biosynthesis; Aminotransferase; Branched-chain amino acid biosynthesis; Chloroplast; Complete proteome; Plastid; Pyridoxal phosphate; Reference proteome; Transferase; Transit peptide
SRR1271857_TR3142_c0_g1_i3_len=2155	PIP1_SOLLC	Q:1865-1236,H:1-210	87.62%ID	E:2e-127	Probable aquaporin PIP-type pTOM75	PF00230.17^MIP^Major intrinsic protein^45-210^E:5.8e-57	0,484	0,426	0	3,43	0	1,631	0,005	1,145	0	4,571	PIP1_SOLLC	Probable aquaporin PIP-type pTOM75 (Ripening-associated membrane protein) (RAMP)		Solanum lycopersicum (Tomato) (Lycopersicon esculentum)		Cell membrane; Complete proteome; Membrane; Reference proteome; Repeat; Stress response; Transmembrane; Transmembrane helix; Transport
SRR1271858_TR7347_c0_g2_i10_len=1896	DCE_SOLLC	Q:346-1851,H:2-502	79.28%ID	E:0	Glutamate decarboxylase	PF00282.16^Pyridoxal_deC^Pyridoxal-dependent decarboxylase conserved domain^33-381^E:3.8e-106	0,006	0,983	0	2,867	0	1,612	0,038	0,981	0	1,629	DCE_SOLLC	Glutamate decarboxylase (GAD) (EC 4.1.1.15) (ERT D1)		Solanum lycopersicum (Tomato) (Lycopersicon esculentum)		Calmodulin-binding; Complete proteome; Decarboxylase; Lyase; Pyridoxal phosphate; Reference proteome
SRR1271858_TR43612_c0_g1_i4_len=1111	NA	NA	NA	NA	NA	PF14364.3^DUF4408^Domain of unknown function (DUF4408)^80-104^E:4.4e-08	0,01	1,838	0	3,116	0	2,419	0,001	2,194	0	1,628	.	.	.	.	.	.
SRR342019_TR17274_c0_g1_i1_len=514	14337_ARATH	Q:1-459,H:7-159	88.89%ID	E:4e-95	14-3-3-like protein GF14 nu	PF00244.17^14-3-3^14-3-3 protein^5-154^E:9.2e-60	0,516	0,244	0	1,754	0,001	1,378	0,077	0,75	0	1,334	14337_ARATH	14-3-3-like protein GF14 nu (General regulatory factor 7)	GRF7 At3g02520 F16B3.15	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Reference proteome
SRR342022_TR33543_c0_g1_i3_len=1830	GCAL1_ARATH	Q:800-231,H:60-249	88.95%ID	E:2e-116	Gamma carbonic anhydrase-like 1, mitochondrial	PF00257.16^Dehydrin^Dehydrin^47-174^E:2e-23`PF00257.16^Dehydrin^Dehydrin^196-220^E:9.4e-06	0,181	0,409	0	2,438	0	1,145	0,102	0,424	0	2,332	GCAL1_ARATH	Gamma carbonic anhydrase-like 1, mitochondrial (AtCAL1) (GAMMA CAL1)	GAMMACAL1 At5g63510 MLE2.14	Arabidopsis thaliana (Mouse-ear cress)		Alternative splicing; Complete proteome; Direct protein sequencing; Membrane; Metal-binding; Mitochondrion; Reference proteome; Transit peptide; Zinc
SRR648705_TR12352_c0_g1_i3_len=1005	GSTUA_ARATH	Q:196-879,H:2-230	43.04%ID	E:3e-51	Glutathione S-transferase U10	PF02798.17^GST_N^Glutathione S-transferase, N-terminal domain^26-96^E:2.6e-16`PF13417.3^GST_N_3^Glutathione S-transferase, N-terminal domain^28-103^E:1.4e-15`PF13409.3^GST_N_2^Glutathione S-transferase, N-terminal domain^34-97^E:1.8e-07	0,185	0,337	0	1,921	0	1,873	0,002	1,197	0	1,089	GSTUA_ARATH	Glutathione S-transferase U10 (AtGSTU10) (EC 2.5.1.18) (GST class-tau member 10)	GSTU10 At1g74590 F1M20.27	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Cytoplasm; Detoxification; Reference proteome; Transferase
SRR648707_TR17303_c0_g2_i4_len=1601	NA	NA	NA	NA	NA	PF13456.3^RVT_3^Reverse transcriptase-like^145-266^E:3.8e-26`PF00075.21^RNase_H^RNase H^145-239^E:1.1e-08	0,183	-0,653	0	6,667	0	6,919	1	0	0	7,023	.	.	.	.	.	.
SRR648707_TR33835_c0_g6_i3_len=788	GSTUA_ARATH	Q:216-650,H:1-146	52.05%ID	E:2e-45	Glutathione S-transferase U10	PF02798.17^GST_N^Glutathione S-transferase, N-terminal domain^25-96^E:1.3e-16`PF13417.3^GST_N_3^Glutathione S-transferase, N-terminal domain^28-103^E:1e-15`PF13409.3^GST_N_2^Glutathione S-transferase, N-terminal domain^34-97^E:1.3e-07	0,172	0,318	0	3,664	0	1,807	0,512	0,229	0	0,893	GSTUA_ARATH	Glutathione S-transferase U10 (AtGSTU10) (EC 2.5.1.18) (GST class-tau member 10)	GSTU10 At1g74590 F1M20.27	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Cytoplasm; Detoxification; Reference proteome; Transferase
SRR122238_TR61811_c0_g2_i1_len=517	PIP27_MAIZE	Q:325-2,H:1-109	75.23%ID	E:1e-51	Aquaporin PIP2-7	PF00230.17^MIP^Major intrinsic protein^95-172^E:3.8e-19	0	1,785	0	4,515	0	0,897	0,014	0,552	0	1,403	PIP27_MAIZE	Aquaporin PIP2-7 (Plasma membrane intrinsic protein 2-7) (ZmPIP2-7) (ZmPIP2;7)	PIP2-7	Zea mays (Maize)		Cell membrane; Complete proteome; Membrane; Reference proteome; Repeat; Transmembrane; Transmembrane helix; Transport
SRR342017_TR18257_c0_g1_i1_len=761	PIP21_ORYSJ	Q:12-635,H:80-287	86.54%ID	E:5e-130	Probable aquaporin PIP2-1	PF00230.17^MIP^Major intrinsic protein^7-195^E:1.2e-72	0	2,126	0	4,388	0	1,473	0,337	0,253	0	0,968	PIP21_ORYSJ	Probable aquaporin PIP2-1 (OsPIP2;1) (Plasma membrane intrinsic protein 2-1) (Plasma membrane intrinsic protein 2a) (PIP2a)	PIP2-1 PIP2a Os07g0448800 LOC_Os07g26690 OJ1047_A06.117 OsJ_023145	Oryza sativa subsp. japonica (Rice)		Cell membrane; Complete proteome; Membrane; Reference proteome; Repeat; Transmembrane; Transmembrane helix; Transport
SRR648707_TR34961_c0_g1_i1_len=1876	C7BL3_CICIN	Q:291-1673,H:33-486	38.53%ID	E:2e-116	Costunolide synthase	PF00067.19^p450^Cytochrome P450^34-480^E:5.1e-86	0	1,218	0	3,356	0,001	0,79	0,057	-0,476	0	1,255	C7BL3_CICIN	Costunolide synthase (CiCOS) (EC 1.14.13.120) (Cytochrome P450 71BL3)	CYP71BL3 COS	Cichorium intybus (Chicory)		Heme; Iron; Membrane; Metal-binding; Monooxygenase; NADP; Oxidoreductase; Transmembrane; Transmembrane helix
SRR924148_TR37769_c0_g1_i3_len=2445	AGT23_ARATH	Q:228-1616,H:20-481	75.59%ID	E:0	Alanine–glyoxylate aminotransferase 2 homolog 3, mitochondrial	PF00202.18^Aminotran_3^Aminotransferase class-III^89-483^E:5.3e-98	0	2,683	0	4,769	0	3,523	0,002	2,8	0	3,307	AGT23_ARATH	Alanine–glyoxylate aminotransferase 2 homolog 3, mitochondrial (EC 2.6.1.44) (Beta-alanine-pyruvate aminotransferase 3)	At3g08860 T16O11.21	Arabidopsis thaliana (Mouse-ear cress)		Aminotransferase; Complete proteome; Mitochondrion; Photorespiration; Pyridoxal phosphate; Reference proteome; Transferase; Transit peptide
SRR122238_TR57645_c0_g1_i2_len=874	C7BL3_CICIN	Q:75-668,H:290-486	42.93%ID	E:1e-57	Costunolide synthase	PF00067.19^p450^Cytochrome P450^2-166^E:3e-46	0	8,473	0,075	0,469	0	10,114	0	7,254	0,009	-0,589	C7BL3_CICIN	Costunolide synthase (CiCOS) (EC 1.14.13.120) (Cytochrome P450 71BL3)	CYP71BL3 COS	Cichorium intybus (Chicory)		Heme; Iron; Membrane; Metal-binding; Monooxygenase; NADP; Oxidoreductase; Transmembrane; Transmembrane helix
SRR342017_TR30366_c0_g3_i1_len=657	NA	NA	NA	NA	NA	.	0	1,195	0,01	0,62	0	2,599	0	1,351	0,142	0,397	.	.	.	.	.	.
SRR342022_TR17097_c2_g5_i1_len=2501	TPSGD_VITVI	Q:2424-784,H:19-557	53.75%ID	E:0	(-)-germacrene D synthase	PF01397.18^Terpene_synth^Terpene synthase, N-terminal domain^38-218^E:2.9e-51`PF03936.13^Terpene_synth_C^Terpene synthase family, metal binding domain^249-515^E:3.8e-100	0	5,384	1	2,398	0	9,941	0	9,442	1	0,924	TPSGD_VITVI	(-)-germacrene D synthase (EC 4.2.3.22) (EC 4.2.3.75)	VIT_19s0014g04930 VIT_00014569001 VITISV_013313 VITISV_030783 Vv19s0014g04930	Vitis vinifera (Grape)	PATHWAY: Secondary metabolite biosynthesis; terpenoid biosynthesis.	Complete proteome; Cytoplasm; Lyase; Magnesium; Metal-binding; Reference proteome
SRR342023_TR14526_c0_g1_i2_len=1978	ATP4_IPOBA	Q:131-736,H:1-200	76.73%ID	E:2e-95	ATP synthase subunit delta', mitochondrial	PF02823.13^ATP-synt_DE_N^ATP synthase, Delta/Epsilon chain, beta-sandwich domain^115-186^E:2.8e-17	0,001	1,898	0,014	1,313	0	2,869	0	2,928	0,204	-0,54	ATP4_IPOBA	ATP synthase subunit delta', mitochondrial (F-ATPase delta' subunit)		Ipomoea batatas (Sweet potato) (Convolvulus batatas)		ATP synthesis; CF(1); Direct protein sequencing; Hydrogen ion transport; Ion transport; Membrane; Mitochondrion; Mitochondrion inner membrane; Transit peptide; Transport
SRR646572_TR15307_c0_g4_i1_len=832	NA	NA	NA	NA	NA	PF07172.8^GRP^Glycine rich protein family^1-100^E:4.6e-10	0	1,133	0,535	0,19	0	4,972	0	3,743	0	-1,645	.	.	.	.	.	.
SRR646596_TR19953_c0_g1_i1_len=664	NA	NA	NA	NA	NA	.	0	7,426	1	3,463	0	8,327	0	8,986	0,502	3,751	.	.	.	.	.	.
SRR648705_TR2780_c0_g3_i1_len=850	SUMO2_ARATH	Q:649-383,H:6-93	89.89%ID	E:9e-49	Small ubiquitin-related modifier 2	PF11976.5^Rad60-SLD^Ubiquitin-2 like Rad60 SUMO-like^26-96^E:1.4e-25`PF00240.20^ubiquitin^Ubiquitin family^28-98^E:2.5e-14	0	1,302	0,756	0,109	0	1,062	0	0,994	0,836	-0,15	SUMO2_ARATH	Small ubiquitin-related modifier 2 (AtSUMO2)	SUMO2 SUM2 At5g55160 MCO15.11	Arabidopsis thaliana (Mouse-ear cress)		Alternative splicing; Complete proteome; Cytoplasm; Isopeptide bond; Nucleus; Reference proteome; Ubl conjugation pathway
SRR924147_TR732_c0_g1_i1_len=811	NA	NA	NA	NA	NA	.	0	7,034	0,001	6,489	0	9,833	0	7,074	1	0,939	.	.	.	.	.	.
SRR1144633_TR1165_c0_g1_i1_len=957	NA	NA	NA	NA	NA	PF02519.11^Auxin_inducible^Auxin responsive protein^51-149^E:2.2e-15	0,278	-0,831	0	4,367	0	4,284	0	5,291	0,282	-1,174	.	.	.	.	.	.
SRR1144633_TR1309_c1_g1_i1_len=811	NA	NA	NA	NA	NA	.	0,09	1,022	0	2,102	0	1,968	0	2,405	0,694	0,439	.	.	.	.	.	.
SRR1144633_TR2352_c0_g2_i1_len=2310	PLT5_ARATH	Q:2071-608,H:35-525	68.7%ID	E:0	Polyol transporter 5	PF00083.21^Sugar_tr^Sugar (and other) transporter^67-525^E:1.4e-109`PF07690.13^MFS_1^Major Facilitator Superfamily^73-465^E:4.1e-28	0,004	2,063	0	3,769	0	2,267	0	1,968	0,094	-1,199	PLT5_ARATH	Polyol transporter 5 (Protein POLYOL TRANSPORTER 5) (AtPLT5) (Sugar-proton symporter PLT5)	PLT5 At3g18830 MVE11.10 MVE11.22	Arabidopsis thaliana (Mouse-ear cress)		Cell membrane; Complete proteome; Membrane; Reference proteome; Sugar transport; Symport; Transmembrane; Transmembrane helix; Transport
SRR1144633_TR6816_c0_g1_i1_len=1331	GUAD_BACSU	Q:588-875,H:6-101	56.25%ID	E:2e-28	Guanine deaminase	PF00383.20^dCMP_cyt_deam_1^Cytidine and deoxycytidylate deaminase zinc-binding region^31-130^E:2.7e-24`PF14437.3^MafB19-deam^MafB19-like deaminase^32-146^E:4.8e-22	0,123	0,718	0	2,159	0	1,147	0	1,155	0,597	0,226	GUAD_BACSU	Guanine deaminase (GDEase) (Guanase) (Guanine aminase) (EC 3.5.4.3) (Guanine aminohydrolase) (GAH)	guaD gde BSU13170	Bacillus subtilis (strain 168)	PATHWAY: Purine metabolism; guanine degradation; xanthine from guanine: step 1/1.	3D-structure; Complete proteome; Hydrolase; Metal-binding; Purine metabolism; Reference proteome; Zinc
SRR1144633_TR7186_c0_g1_i1_len=1308	ATHB7_ARATH	Q:1059-739,H:34-140	67.29%ID	E:1e-39	Homeobox-leucine zipper protein ATHB-7	PF00046.26^Homeobox^Homeobox domain^31-85^E:1.1e-16`PF02183.15^HALZ^Homeobox associated leucine zipper^87-127^E:2.7e-13	0,044	2,169	0	4,445	0	2,8	0	1,977	1	1,415	ATHB7_ARATH	Homeobox-leucine zipper protein ATHB-7 (HD-ZIP protein ATHB-7) (Homeodomain transcription factor ATHB-7)	ATHB-7 At2g46680 T3A4.6	Arabidopsis thaliana (Mouse-ear cress)		Alternative splicing; Complete proteome; DNA-binding; Homeobox; Nucleus; Reference proteome; Stress response; Transcription; Transcription regulation
SRR1144633_TR10881_c0_g1_i1_len=1161	ERF08_ARATH	Q:731-360,H:28-166	59.71%ID	E:2e-43	Ethylene-responsive transcription factor ERF008	PF00847.17^AP2^AP2 domain^28-77^E:1.7e-10	0,679	0,375	0	2,789	0	1,678	0,001	1,495	1	-0,7	ERF08_ARATH	Ethylene-responsive transcription factor ERF008	ERF008 At2g23340 T20D16.3	Arabidopsis thaliana (Mouse-ear cress)		Activator; Complete proteome; DNA-binding; Ethylene signaling pathway; Nucleus; Reference proteome; Transcription; Transcription regulation
SRR1144633_TR22909_c1_g1_i1_len=934	CSPLB_RICCO	Q:735-136,H:3-202	77%ID	E:3e-97	CASP-like protein 2B1	PF04535.9^DUF588^Domain of unknown function (DUF588)^28-176^E:1.4e-43	0,03	0,638	0	1,736	0	1,802	0,001	1,049	0,781	-0,435	CSPLB_RICCO	CASP-like protein 2B1 (RcCASPL2B1)	RCOM_0864260	Ricinus communis (Castor bean)		Cell membrane; Complete proteome; Membrane; Reference proteome; Transmembrane; Transmembrane helix
SRR1144633_TR24313_c0_g2_i2_len=1720	STR12_ARATH	Q:913-221,H:70-299	55.84%ID	E:1e-84	Rhodanese-like/PpiC domain-containing protein 12, chloroplastic	PF13616.3^Rotamase_3^PPIC-type PPIASE domain^298-383^E:2.5e-15`PF00639.18^Rotamase^PPIC-type PPIASE domain^307-382^E:4.3e-14`PF00581.17^Rhodanese^Rhodanese-like domain^407-490^E:5.2e-06	0,226	1,812	0	7,652	0	4,231	0	4,294	1	1,679	STR12_ARATH	Rhodanese-like/PpiC domain-containing protein 12, chloroplastic (Sulfurtransferase 12) (AtStr12)	At5g19370 F7K24.120	Arabidopsis thaliana (Mouse-ear cress)		Acetylation; Chloroplast; Complete proteome; Plastid; Reference proteome; Transit peptide
SRR1144633_TR36724_c1_g1_i2_len=1424	PIP1_SOLLC	Q:234-1082,H:1-283	86.57%ID	E:2e-179	Probable aquaporin PIP-type pTOM75	PF00230.17^MIP^Major intrinsic protein^45-274^E:3.2e-84	0,245	0,266	0	1,287	0	1,511	0	0,915	1	0,298	PIP1_SOLLC	Probable aquaporin PIP-type pTOM75 (Ripening-associated membrane protein) (RAMP)		Solanum lycopersicum (Tomato) (Lycopersicon esculentum)		Cell membrane; Complete proteome; Membrane; Reference proteome; Repeat; Stress response; Transmembrane; Transmembrane helix; Transport
SRR1144633_TR37810_c0_g2_i2_len=1025	NA	NA	NA	NA	NA	.	0,083	0,75	0	1,674	0	1,715	0	1,641	1	0,626	.	.	.	.	.	.
SRR1144633_TR37810_c0_g2_i3_len=942	NA	NA	NA	NA	NA	.	0,003	1,259	0	1,183	0	1,653	0,001	1,557	1	0	.	.	.	.	.	.
SRR1144634_TR8901_c0_g1_i1_len=668	NA	NA	NA	NA	NA	PF14009.3^DUF4228^Domain of unknown function (DUF4228)^48-217^E:2.2e-26	1	0	0	7,899	0	1,932	0	2,329	1	-2,355	.	.	.	.	.	.
SRR1144634_TR9562_c0_g1_i4_len=3140	B2_DAUCA	Q:794-1249,H:55-206	91.45%ID	E:2e-93	B2 protein	PF10539.6^Dev_Cell_Death^Development and cell death domain^199-326^E:2.2e-41	0,108	0,763	0	2,127	0	1,647	0	1,883	0,629	2,203	B2_DAUCA	B2 protein		Daucus carota (Wild carrot)		
SRR1144634_TR10749_c0_g1_i2_len=1593	10HGO_CATRO	Q:1458-379,H:1-360	100%ID	E:0	8-hydroxygeraniol dehydrogenase	PF08240.9^ADH_N^Alcohol dehydrogenase GroES-like domain^38-151^E:8.9e-29`PF02826.16^2-Hacid_dh_C^D-isomer specific 2-hydroxyacid dehydrogenase, NAD binding domain^177-226^E:6.8e-06`PF01262.18^AlaDh_PNT_C^Alanine dehydrogenase/PNT, C-terminal domain^185-256^E:9.3e-06`PF00107.23^ADH_zinc_N^Zinc-binding dehydrogenase^194-317^E:1.2e-18	0,041	0,835	0	3,082	0	2,41	0	2,799	0,646	-0,328	10HGO_CATRO	8-hydroxygeraniol dehydrogenase (Cr10HGO) (EC 1.1.1.324)	10HGO	Catharanthus roseus (Madagascar periwinkle) (Vinca rosea)		Metal-binding; NADP; Oxidoreductase; Zinc
SRR1144634_TR11003_c0_g2_i7_len=772	GPX4_MESCR	Q:251-727,H:1-160	83.75%ID	E:5e-98	Probable phospholipid hydroperoxide glutathione peroxidase	PF08534.7^Redoxin^Redoxin^10-154^E:1.7e-07`PF00255.16^GSHPx^Glutathione peroxidase^11-119^E:2.2e-43`PF00578.18^AhpC-TSA^AhpC/TSA family^11-75^E:5.5e-10	0,271	0,34	0	3,976	0	1,874	0	1,615	1	1,985	GPX4_MESCR	Probable phospholipid hydroperoxide glutathione peroxidase (PHGPx) (EC 1.11.1.12)	GPXMC1	Mesembryanthemum crystallinum (Common ice plant) (Cryophytum crystallinum)		Cytoplasm; Oxidoreductase; Peroxidase
SRR1144634_TR11418_c1_g2_i1_len=1627	Y3158_ARATH	Q:1369-902,H:3-143	65.38%ID	E:7e-50	B3 domain-containing protein At3g11580	PF02362.18^B3^B3 DNA binding domain^116-241^E:3.1e-28	0,002	1,501	0	3,303	0	4,739	0	4,342	0,299	-1,38	Y3158_ARATH	B3 domain-containing protein At3g11580 (Protein AUXIN RESPONSE FACTOR 32)	ARF32 At3g11580 F24K9.25	Arabidopsis thaliana (Mouse-ear cress)		Alternative splicing; Complete proteome; DNA-binding; Nucleus; Reference proteome; Transcription; Transcription regulation
SRR1144634_TR13333_c0_g1_i1_len=842	NA	NA	NA	NA	NA	.	0,043	0,984	0	2,059	0	3,905	0	1,983	1	-0,813	.	.	.	.	.	.
SRR1144634_TR14795_c0_g4_i1_len=1925	SCGT_TOBAC	Q:961-1668,H:242-473	67.37%ID	E:1e-171	Scopoletin glucosyltransferase	.	0,312	0,608	0	4,441	0	3,327	0	4,818	0,258	-1,014	SCGT_TOBAC	Scopoletin glucosyltransferase (EC 2.4.1.128) (Phenylpropanoid:glucosyltransferase 1)	TOGT1	Nicotiana tabacum (Common tobacco)		Glycosyltransferase; Transferase
SRR1144634_TR23126_c3_g4_i2_len=688	PRS2_SOLTU	Q:589-134,H:1-155	35.03%ID	E:2e-23	Pathogenesis-related protein STH-2	PF00407.16^Bet_v_1^Pathogenesis-related protein Bet v I family^34-180^E:4.1e-12	0,019	0,54	0	2,568	0	1,44	0	1,492	0,381	1,41	PRS2_SOLTU	Pathogenesis-related protein STH-2	STH-2	Solanum tuberosum (Potato)		Complete proteome; Pathogenesis-related protein; Plant defense; Reference proteome
SRR1144634_TR27142_c0_g1_i4_len=2112	CSE_ARATH	Q:412-1278,H:36-323	35.86%ID	E:4e-52	Caffeoylshikimate esterase	PF12146.5^Hydrolase_4^Serine aminopeptidase, S33^137-379^E:5.8e-65`PF00561.17^Abhydrolase_1^alpha/beta hydrolase fold^139-375^E:1.9e-15`PF12697.4^Abhydrolase_6^Alpha/beta hydrolase family^143-381^E:9.9e-13	0,004	1,469	0	4,393	0	2,347	0	2,578	0,352	0,858	CSE_ARATH	Caffeoylshikimate esterase (EC 3.1.1.-) (Lysophospholipase 2) (LysoPL2)	CSE At1g52760 F14G24.3	Arabidopsis thaliana (Mouse-ear cress)		Cell membrane; Complete proteome; Hydrolase; Lignin biosynthesis; Membrane; Reference proteome
SRR1144634_TR28149_c0_g1_i1_len=645	PRS1_SOLTU	Q:567-124,H:1-155	36.54%ID	E:4e-22	Pathogenesis-related protein STH-21	PF00407.16^Bet_v_1^Pathogenesis-related protein Bet v I family^4-143^E:1e-12	0,082	0,933	0	0,939	0	0,955	0	0,955	1	-1,144	PRS1_SOLTU	Pathogenesis-related protein STH-21	STH-21	Solanum tuberosum (Potato)		Complete proteome; Pathogenesis-related protein; Plant defense; Reference proteome
SRR1144634_TR29160_c0_g1_i5_len=1010	UBC2_WHEAT	Q:744-289,H:1-152	96.05%ID	E:8e-106	Ubiquitin-conjugating enzyme E2 2	PF00179.23^UQ_con^Ubiquitin-conjugating enzyme^8-144^E:1.9e-52	0,484	-0,389	0	2,498	0	7,996	0	7,267	0,461	-1,351	UBC2_WHEAT	Ubiquitin-conjugating enzyme E2 2 (EC 2.3.2.23) (E2 ubiquitin-conjugating enzyme 2) (Ubiquitin carrier protein 2) (Ubiquitin-conjugating enzyme E2-16 kDa) (Ubiquitin-protein ligase 2)	UBC2 UBC1	Triticum aestivum (Wheat)	PATHWAY: Protein modification; protein ubiquitination. {ECO:0000255|PROSITE-ProRule:PRU00388}.	ATP-binding; Complete proteome; Nucleotide-binding; Reference proteome; Transferase; Ubl conjugation pathway
SRR1144634_TR33949_c0_g1_i2_len=1018	APX1_ARATH	Q:86-835,H:1-250	85.6%ID	E:4e-147	L-ascorbate peroxidase 1, cytosolic	PF00141.20^peroxidase^Peroxidase^22-227^E:4.7e-49	0,42	-0,182	0	1,665	0,001	0,789	0,001	0,777	0,7	-0,092	APX1_ARATH	L-ascorbate peroxidase 1, cytosolic (AP) (AtAPx01) (EC 1.11.1.11)	APX1 At1g07890 F24B9.2	Arabidopsis thaliana (Mouse-ear cress)		Alternative splicing; Calcium; Complete proteome; Cytoplasm; Direct protein sequencing; Heme; Hydrogen peroxide; Iron; Metal-binding; Oxidoreductase; Peroxidase; Phosphoprotein; Potassium; Reference proteome
SRR1144634_TR37303_c0_g2_i6_len=4832	LOX31_SOLTU	Q:2366-4831,H:1-826	79.21%ID	E:0	Linoleate 13S-lipoxygenase 3-1, chloroplastic	PF12146.5^Hydrolase_4^Serine aminopeptidase, S33^68-184^E:1e-08`PF01477.20^PLAT^PLAT/LH2 domain^592-676^E:1.4e-12`PF00305.16^Lipoxygenase^Lipoxygenase^689-1285^E:9.5e-273	0,05	1,004	0	3,803	0	2,61	0	3,358	1	0,694	LOX31_SOLTU	Linoleate 13S-lipoxygenase 3-1, chloroplastic (EC 1.13.11.12)	LOX3.1 LOX-H3	Solanum tuberosum (Potato)	PATHWAY: Lipid metabolism; oxylipin biosynthesis. {ECO:0000255|PROSITE-ProRule:PRU00726}.	Chloroplast; Complete proteome; Dioxygenase; Fatty acid biosynthesis; Fatty acid metabolism; Iron; Lipid biosynthesis; Lipid metabolism; Metal-binding; Oxidoreductase; Oxylipin biosynthesis; Plastid; Reference proteome; Thylakoid; Transit peptide
SRR122236_TR298_c0_g1_i1_len=791	GASAE_ARATH	Q:400-594,H:211-275	76.92%ID	E:2e-26	Gibberellin-regulated protein 14	PF02704.11^GASA^Gibberellin regulated protein^138-198^E:7.6e-19	0,023	1,827	0	4,891	0	8,66	0	9,195	0,266	-0,533	GASAE_ARATH	Gibberellin-regulated protein 14 (GAST1 protein homolog 14)	GASA14 At5g14920 F2G14.40	Arabidopsis thaliana (Mouse-ear cress)		Alternative splicing; Complete proteome; Disulfide bond; Gibberellin signaling pathway; Reference proteome; Secreted; Signal
SRR122237_TR5686_c0_g2_i1_len=1769	FAD3E_TOBAC	Q:1666-572,H:12-374	76.16%ID	E:0	Omega-3 fatty acid desaturase, endoplasmic reticulum	PF11960.5^DUF3474^Domain of unknown function (DUF3474)^6-62^E:7.5e-26`PF00487.21^FA_desaturase^Fatty acid desaturase^77-328^E:4.4e-33	0,29	0,358	0	2,32	0	2,532	0	3,026	0,004	-0,676	FAD3E_TOBAC	Omega-3 fatty acid desaturase, endoplasmic reticulum (EC 1.14.19.-)	FAD3	Nicotiana tabacum (Common tobacco)	PATHWAY: Lipid metabolism; polyunsaturated fatty acid biosynthesis.	Endoplasmic reticulum; Fatty acid biosynthesis; Fatty acid metabolism; Lipid biosynthesis; Lipid metabolism; Membrane; Oxidoreductase; Transmembrane; Transmembrane helix
SRR122237_TR18628_c0_g2_i1_len=534	NA	NA	NA	NA	NA	.	0,286	0,85	0	3,296	0	6,432	0	6,944	0,132	-1,567	.	.	.	.	.	.
SRR122237_TR28134_c0_g1_i1_len=746	PRS2_SOLTU	Q:110-565,H:1-155	36.94%ID	E:1e-24	Pathogenesis-related protein STH-2	PF00407.16^Bet_v_1^Pathogenesis-related protein Bet v I family^37-183^E:3.4e-13	0,029	1,132	0	1,737	0	1,691	0	1,658	0,019	0,492	PRS2_SOLTU	Pathogenesis-related protein STH-2	STH-2	Solanum tuberosum (Potato)		Complete proteome; Pathogenesis-related protein; Plant defense; Reference proteome
SRR122238_TR814_c0_g1_i2_len=757	IPRT1_CATRO	Q:100-579,H:1-157	68.75%ID	E:1e-66	Probable intracellular pathogenesis-related protein T1	PF00407.16^Bet_v_1^Pathogenesis-related protein Bet v I family^38-190^E:4.4e-19	0,76	0,71	0	6,45	0	7,666	0	3,568	0,381	-2,222	IPRT1_CATRO	Probable intracellular pathogenesis-related protein T1	PCKR3	Catharanthus roseus (Madagascar periwinkle) (Vinca rosea)		Direct protein sequencing; Glycoprotein; Pathogenesis-related protein; Plant defense
SRR122238_TR6367_c0_g1_i2_len=3126	LAL5_ARATH	Q:2989-1592,H:8-464	59.87%ID	E:6e-164	.	PF01554.15^MatE^MatE^57-216^E:1.4e-29`PF01554.15^MatE^MatE^278-439^E:1.1e-25	0,002	1,289	0	2,917	0	2,075	0	2,067	0,854	-0,18	DTX18_ARATH	Protein DETOXIFICATION 18 (AtDTX18) (Multidrug and toxic compound extrusion protein 18) (MATE protein 18) (Protein LIKE ALF5)	DTX18 LAL5 At3g23550 MDB19.3	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Membrane; Reference proteome; Transmembrane; Transmembrane helix; Transport
SRR122238_TR7833_c0_g1_i1_len=1316	BI1L_ARATH	Q:894-196,H:24-256	52.97%ID	E:6e-69	BI1-like protein	PF01027.17^Bax1-I^Inhibitor of apoptosis-promoting Bax1^31-237^E:1.5e-47	0,729	0,262	0	2,297	0,001	1,866	0,001	1,896	1	-0,194	BI1L_ARATH	BI1-like protein	At4g15470 dl3775w FCAALL.58	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Membrane; Reference proteome; Transmembrane; Transmembrane helix
SRR122238_TR8264_c1_g1_i3_len=1114	UBC4_WHEAT	Q:278-721,H:1-148	82.43%ID	E:6e-86	Ubiquitin-conjugating enzyme E2-23 kDa	PF00179.23^UQ_con^Ubiquitin-conjugating enzyme^12-142^E:1.5e-40	0,611	0,401	0	1,876	0	3	0	3,836	0,611	-0,318	UBC4_WHEAT	Ubiquitin-conjugating enzyme E2-23 kDa (EC 2.3.2.23) (E2 ubiquitin-conjugating enzyme) (Ubiquitin carrier protein) (Ubiquitin-protein ligase)	UBC4	Triticum aestivum (Wheat)	PATHWAY: Protein modification; protein ubiquitination. {ECO:0000255|PROSITE-ProRule:PRU00388}.	ATP-binding; Complete proteome; Nucleotide-binding; Reference proteome; Transferase; Ubl conjugation pathway
SRR122238_TR17655_c0_g1_i2_len=618	PRS2_SOLTU	Q:10-438,H:12-153	38.78%ID	E:6e-22	Pathogenesis-related protein STH-2	PF00407.16^Bet_v_1^Pathogenesis-related protein Bet v I family^4-142^E:1.5e-10	0,226	0,716	0	2,061	0	1,103	0	1,107	0,1	0,887	PRS2_SOLTU	Pathogenesis-related protein STH-2	STH-2	Solanum tuberosum (Potato)		Complete proteome; Pathogenesis-related protein; Plant defense; Reference proteome
SRR122238_TR20762_c0_g1_i2_len=771	NA	NA	NA	NA	NA	.	1	0,098	0	6,97	0	4,028	0	5,133	1	-0,174	.	.	.	.	.	.
SRR122238_TR21292_c1_g1_i1_len=1399	COMT1_CATRO	Q:79-1158,H:1-360	100%ID	E:0	Caffeic acid 3-O-methyltransferase	PF08100.8^Dimerisation^Dimerisation domain^34-85^E:1e-22`PF00891.15^Methyltransf_2^O-methyltransferase^129-345^E:7.8e-90	0,096	0,539	0	2,176	0	1,621	0	1,391	0,927	-0,042	COMT1_CATRO	Caffeic acid 3-O-methyltransferase (CAOMT) (COMT) (EC 2.1.1.68) (S-adenosysl-L-methionine:caffeic acid 3-O-methyltransferase)	COMT1	Catharanthus roseus (Madagascar periwinkle) (Vinca rosea)	PATHWAY: Aromatic compound metabolism; phenylpropanoid biosynthesis.	Lignin biosynthesis; Methyltransferase; S-adenosyl-L-methionine; Transferase
SRR122238_TR21630_c0_g1_i2_len=2241	NA	NA	NA	NA	NA	PF06200.11^tify^tify domain^98-128^E:7.1e-18	0,017	4,016	0	5,4	0	5,453	0	5,21	1	0,235	.	.	.	.	.	.
SRR122238_TR32710_c0_g1_i1_len=1131	NA	NA	NA	NA	NA	.	0,002	1,07	0	2,671	0	2,01	0	2,224	0,729	0,219	.	.	.	.	.	.
SRR122238_TR34712_c0_g1_i1_len=841	12KD_FRAAN	Q:65-439,H:1-109	57.6%ID	E:1e-37	Auxin-repressed 12.5 kDa protein	PF05564.9^Auxin_repressed^Dormancy/auxin associated protein^28-147^E:2.1e-56	0,005	0,643	0	1,069	0	2,604	0	2,24	0,18	0,378	12KD_FRAAN	Auxin-repressed 12.5 kDa protein		Fragaria ananassa (Strawberry)		Auxin signaling pathway
SRR122238_TR38504_c0_g1_i2_len=1384	BUP1_DICDI	Q:181-1251,H:5-390	59.33%ID	E:5e-154	Beta-ureidopropionase	PF00795.19^CN_hydrolase^Carbon-nitrogen hydrolase^134-381^E:6.5e-51	0,129	0,918	0	1,718	0	1,827	0	2,012	1	0,075	BUP1_DICDI	Beta-ureidopropionase (EC 3.5.1.6) (Beta-alanine synthase) (N-carbamoyl-beta-alanine amidohydrolase)	pyd3 bup1 upb1 DDB_G0274123	Dictyostelium discoideum (Slime mold)	PATHWAY: Amino-acid biosynthesis; beta-alanine biosynthesis.	Acetylation; Complete proteome; Direct protein sequencing; Hydrolase; Reference proteome
SRR122238_TR39267_c0_g2_i3_len=2340	PPH_ARATH	Q:471-1886,H:3-472	59.37%ID	E:0	Pheophytinase, chloroplastic	PF00561.17^Abhydrolase_1^alpha/beta hydrolase fold^157-439^E:1.7e-13`PF12697.4^Abhydrolase_6^Alpha/beta hydrolase family^159-445^E:4.6e-18	0,002	2,095	0	5,778	0	3,13	0	3,552	0,079	1,017	PPH_ARATH	Pheophytinase, chloroplastic (EC 3.1.1.-) (Pheophytin pheophorbide hydrolase) (Protein CO-REGULATED WITH NYE1)	PPH CRN1 At5g13800 MAC12.25	Arabidopsis thaliana (Mouse-ear cress)		Chlorophyll catabolism; Chloroplast; Complete proteome; Hydrolase; Membrane; Plastid; Reference proteome; Thylakoid; Transit peptide
SRR122238_TR40662_c1_g2_i7_len=2549	INVE_ARATH	Q:304-2142,H:1-617	72.34%ID	E:0	Alkaline/neutral invertase E, chloroplastic {ECO:0000305}	PF12899.4^Glyco_hydro_100^Alkaline and neutral invertase^131-572^E:4.9e-215	0,419	0,474	0,001	1,471	0	1,687	0	2,076	0,748	0,26	INVE_ARATH	Alkaline/neutral invertase E, chloroplastic (A/N-INVE) (EC 3.2.1.26)	INVE At5g22510 MQJ16.5	Arabidopsis thaliana (Mouse-ear cress)		Carbohydrate metabolism; Chloroplast; Complete proteome; Glycosidase; Hydrolase; Phosphoprotein; Plastid; Reference proteome; Transit peptide
SRR122238_TR42430_c0_g1_i1_len=615	NA	NA	NA	NA	NA	.	0,029	0,777	0	2,509	0	1,251	0	1,142	0,304	-0,42	.	.	.	.	.	.
SRR122238_TR42512_c0_g1_i16_len=1198	LGUL_CICAR	Q:953-396,H:1-186	80.65%ID	E:6e-110	Lactoylglutathione lyase	PF00903.22^Glyoxalase^Glyoxalase/Bleomycin resistance protein/Dioxygenase superfamily^29-171^E:5.6e-23`PF13669.3^Glyoxalase_4^Glyoxalase/Bleomycin resistance protein/Dioxygenase superfamily^30-153^E:3.9e-06	1	0	0	6,875	0	7,377	0	7,239	0,066	5,397	LGUL_CICAR	Lactoylglutathione lyase (EC 4.4.1.5) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (Methylglyoxalase) (S-D-lactoylglutathione methylglyoxal lyase)		Cicer arietinum (Chickpea) (Garbanzo)	PATHWAY: Secondary metabolite metabolism; methylglyoxal degradation; (R)-lactate from methylglyoxal: step 1/2.	Lyase; Metal-binding; Zinc
SRR122238_TR43316_c0_g1_i3_len=1378	NA	NA	NA	NA	NA	.	0,059	1,55	0	3,449	0	2,898	0	3,719	0,407	0,781	.	.	.	.	.	.
SRR122238_TR44242_c1_g1_i2_len=2780	ANXD2_ARATH	Q:290-1234,H:1-316	73.42%ID	E:5e-166	Annexin D2	PF00191.17^Annexin^Annexin^16-79^E:1.1e-21`PF00191.17^Annexin^Annexin^88-152^E:5.2e-17`PF00191.17^Annexin^Annexin^171-233^E:2.1e-12`PF00191.17^Annexin^Annexin^248-310^E:1e-17	0,493	-0,229	0	1,387	0	4,188	0	4,562	0,029	-0,779	ANXD2_ARATH	Annexin D2 (AnnAt2)	ANN2 ANNAT2 At5g65020 MXK3.27	Arabidopsis thaliana (Mouse-ear cress)		Acetylation; Alternative splicing; Annexin; Calcium; Calcium/phospholipid-binding; Complete proteome; Cytoplasm; Membrane; Reference proteome; Repeat
SRR122238_TR45975_c1_g1_i3_len=3347	LOX31_SOLTU	Q:619-3030,H:114-914	83.23%ID	E:0	Linoleate 13S-lipoxygenase 3-1, chloroplastic	PF00305.16^Lipoxygenase^Lipoxygenase^1-585^E:2.8e-266	0,023	1,736	0	3,909	0	3,68	0	4,294	1	3,41	LOX31_SOLTU	Linoleate 13S-lipoxygenase 3-1, chloroplastic (EC 1.13.11.12)	LOX3.1 LOX-H3	Solanum tuberosum (Potato)	PATHWAY: Lipid metabolism; oxylipin biosynthesis. {ECO:0000255|PROSITE-ProRule:PRU00726}.	Chloroplast; Complete proteome; Dioxygenase; Fatty acid biosynthesis; Fatty acid metabolism; Iron; Lipid biosynthesis; Lipid metabolism; Metal-binding; Oxidoreductase; Oxylipin biosynthesis; Plastid; Reference proteome; Thylakoid; Transit peptide

SRR122238_TR47659_c1_g2_i4_len=1025	NA	NA	NA	NA	NA	.	0,065	1,405	0	2,151	0	1,907	0,001	1,437	1	0,238	.	.	.	.	.	.
SRR122238_TR49802_c0_g1_i3_len=1065	SRG1_ARATH	Q:1033-218,H:83-356	51.46%ID	E:6e-103	Protein SRG1	PF14226.3^DIOX_N^non-haem dioxygenase in morphine synthesis N-terminal^12-78^E:6.2e-13`PF03171.17^2OG-FeII_Oxy^2OG-Fe(II) oxygenase superfamily^139-235^E:2.2e-25	0,129	2,924	0	7,444	0	6,787	0	6,095	1	0	SRG1_ARATH	Protein SRG1 (AtSRG1) (Protein SENESCENCE-RELATED GENE 1)	SRG1 At1g17020 F20D23.28 F6I1.30	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Iron; Metal-binding; Oxidoreductase; Reference proteome
SRR122238_TR53155_c1_g1_i1_len=887	NA	NA	NA	NA	NA	.	0,629	1,092	0	4,796	0	4,536	0	4,896	1	2,191	.	.	.	.	.	.
SRR122238_TR58674_c0_g1_i2_len=1920	WTR41_ARATH	Q:1627-587,H:13-356	46.31%ID	E:8e-88	WAT1-related protein At5g40230	PF00892.17^EamA^EamA-like transporter family^17-156^E:2.9e-13`PF00892.17^EamA^EamA-like transporter family^187-322^E:2.4e-09	0,017	0,817	0	2,578	0	1,977	0	1,736	0,004	2,914	WTR41_ARATH	WAT1-related protein At5g40230	At5g40230 MSN9.130	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Membrane; Reference proteome; Repeat; Transmembrane; Transmembrane helix
SRR122238_TR60351_c0_g1_i3_len=1058	OP24B_ARATH	Q:194-829,H:3-213	67.92%ID	E:4e-101	Outer envelope pore protein 24B, chloroplastic	.	0,088	0,512	0	1,529	0	1,995	0	2,32	0,352	-0,294	OP24B_ARATH	Outer envelope pore protein 24B, chloroplastic (Chloroplastic outer envelope pore protein of 24 kDa B)	OEP24B At5g42960 MBD2.16	Arabidopsis thaliana (Mouse-ear cress)		Chloroplast; Complete proteome; Ion transport; Membrane; Plastid; Plastid outer membrane; Porin; Reference proteome; Transmembrane; Transmembrane beta strand; Transport
SRR122238_TR62791_c2_g1_i6_len=2165	PTR21_ARATH	Q:1982-279,H:31-594	55.28%ID	E:0	Protein NRT1/ PTR FAMILY 2.13	PF00854.18^PTR2^POT family^155-585^E:1.9e-85	0,08	1,259	0	7,27	0	2,658	0	1,714	0,017	5,744	PTR21_ARATH	Protein NRT1/ PTR FAMILY 2.13 (AtNPF2.13) (Nitrate transporter 1.7)	NPF2.13 NRT1.7 At1g69870 T17F3.10	Arabidopsis thaliana (Mouse-ear cress)		Cell membrane; Complete proteome; Membrane; Nitrate assimilation; Reference proteome; Symport; Transmembrane; Transmembrane helix; Transport
SRR122238_TR62903_c2_g1_i4_len=1839	C81E8_MEDTR	Q:1611-265,H:43-494	45.26%ID	E:2e-131	Cytochrome P450 81E8 {ECO:0000303|PubMed:14617078}	PF00067.19^p450^Cytochrome P450^39-483^E:9.3e-88	1	-0,252	0,001	3,25	0	4,198	0	5,47	1	-0,984	C81E8_MEDTR	Cytochrome P450 81E8 (EC 1.14.13.-)	CYP81E8	Medicago truncatula (Barrel medic) (Medicago tribuloides)		Heme; Iron; Membrane; Metal-binding; Monooxygenase; NADP; Oxidoreductase; Transmembrane; Transmembrane helix
SRR122238_TR66612_c0_g1_i2_len=1471	MY108_ARATH	Q:1330-899,H:10-151	69.44%ID	E:2e-60	Transcription factor MYB108	PF00249.28^Myb_DNA-binding^Myb-like DNA-binding domain^61-108^E:1.1e-16`PF13921.3^Myb_DNA-bind_6^Myb-like DNA-binding domain^64-122^E:1.1e-13`PF00249.28^Myb_DNA-binding^Myb-like DNA-binding domain^114-157^E:1.3e-15`PF13921.3^Myb_DNA-bind_6^Myb-like DNA-binding domain^118-161^E:4.9e-06	0,356	1,29	0	3,119	0	5,501	0	5,805	0,56	-0,723	MY108_ARATH	Transcription factor MYB108 (Myb-related protein 108) (AtMYB108) (Protein BOTRYTIS-SUSCEPTIBLE 1)	MYB108 BOS1 At3g06490 F5E6.18	Arabidopsis thaliana (Mouse-ear cress)		Activator; Complete proteome; DNA-binding; Nucleus; Plant defense; Reference proteome; Repeat; Transcription; Transcription regulation; Ubl conjugation
SRR122238_TR67350_c0_g1_i1_len=1628	U74E2_ARATH	Q:53-1420,H:6-450	44.86%ID	E:3e-136	UDP-glycosyltransferase 74E2	PF00201.15^UDPGT^UDP-glucoronosyl and UDP-glucosyl transferase^292-449^E:4.4e-30	0,87	0,225	0	2,485	0	1,825	0	1,467	0,013	1,211	U74E2_ARATH	UDP-glycosyltransferase 74E2 (EC 2.4.1.-)	UGT74E2 At1g05680 F3F20.13	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Glycosyltransferase; Reference proteome; Stress response; Transferase
SRR122238_TR68934_c0_g2_i3_len=1541	NA	NA	NA	NA	NA	.	0,438	0,314	0	1,946	0	1,23	0,001	1,209	0,781	0,396	.	.	.	.	.	.
SRR122238_TR76492_c0_g1_i2_len=1199	NA	NA	NA	NA	NA	.	0,006	1,124	0	1,993	0	2,211	0	1,733	0,355	-0,419	.	.	.	.	.	.
SRR122238_TR84651_c0_g1_i2_len=944	NDADA_ARATH	Q:737-309,H:1-143	87.41%ID	E:8e-87	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13-A	PF06212.9^GRIM-19^GRIM-19 protein^20-138^E:2.2e-42	0,657	-0,194	0	8,565	0	8,785	0	8,29	0,196	-0,541	NDADA_ARATH	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13-A (Protein MATERNAL EFFECT EMBRYO ARREST 4)	MEE4 At1g04630 T1G11.12	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Electron transport; Membrane; Mitochondrion; Mitochondrion inner membrane; Reference proteome; Respiratory chain; Transmembrane; Transmembrane helix; Transport
SRR122238_TR86615_c1_g1_i2_len=1397	XTH30_ARATH	Q:1265-342,H:9-311	64.61%ID	E:2e-148	Probable xyloglucan endotransglucosylase/hydrolase protein 30	PF00722.18^Glyco_hydro_16^Glycosyl hydrolases family 16^45-226^E:2.7e-54`PF06955.9^XET_C^Xyloglucan endo-transglycosylase (XET) C-terminus^268-305^E:6.8e-15	1	2,324	0	5,927	0	4,567	0	4,035	1	0,355	XTH30_ARATH	Probable xyloglucan endotransglucosylase/hydrolase protein 30 (At-XTH30) (XTH-30) (EC 2.4.1.207)	XTH30 XTR4 At1g32170 F3C3.5	Arabidopsis thaliana (Mouse-ear cress)		Apoplast; Cell wall; Cell wall biogenesis/degradation; Complete proteome; Disulfide bond; Glycoprotein; Glycosidase; Hydrolase; Reference proteome; Secreted; Signal; Transferase
SRR122238_TR87584_c0_g1_i2_len=1109	FER3_ARATH	Q:331-786,H:1-155	56.77%ID	E:3e-56	Ferredoxin-3, chloroplastic	PF00111.24^Fer2^2Fe-2S iron-sulfur cluster binding domain^65-138^E:2.6e-21	0,184	0,347	0	3,73	0	1,45	0	1,825	0,443	-0,213	FER3_ARATH	Ferredoxin-3, chloroplastic (AtFd3)	FD3 At2g27510 F10A12.19	Arabidopsis thaliana (Mouse-ear cress)		2Fe-2S; Acetylation; Chloroplast; Complete proteome; Electron transport; Iron; Iron-sulfur; Metal-binding; Plastid; Reference proteome; Transit peptide; Transport
SRR1271857_TR5151_c0_g1_i1_len=696	EP1G_DAUCA	Q:547-74,H:26-183	67.09%ID	E:1e-71	Epidermis-specific secreted glycoprotein EP1	PF01453.21^B_lectin^D-mannose binding lectin^87-172^E:1.1e-26	0,007	-0,998	0	9,106	0	4,411	0	2,312	0	-1,524	EP1G_DAUCA	Epidermis-specific secreted glycoprotein EP1 (52/54 kDa medium protein)	EP1	Daucus carota (Wild carrot)		Direct protein sequencing; Glycoprotein; Lectin; Secreted; Signal
SRR1271857_TR6476_c0_g1_i2_len=887	PIP27_MAIZE	Q:864-1,H:1-287	81.66%ID	E:2e-152	Aquaporin PIP2-7	PF00230.17^MIP^Major intrinsic protein^41-276^E:3.5e-83	0,502	2,562	0	5,866	0	3,847	0	2,899	1	0,232	PIP27_MAIZE	Aquaporin PIP2-7 (Plasma membrane intrinsic protein 2-7) (ZmPIP2-7) (ZmPIP2;7)	PIP2-7	Zea mays (Maize)		Cell membrane; Complete proteome; Membrane; Reference proteome; Repeat; Transmembrane; Transmembrane helix; Transport
SRR1271857_TR10912_c0_g1_i3_len=1661	AOC4_ARATH	Q:1020-1412,H:117-248	68.18%ID	E:1e-49	Allene oxide cyclase 4, chloroplastic	.	0,004	1,818	0	4,532	0	2,994	0	3,249	0,398	0,342	AOC4_ARATH	Allene oxide cyclase 4, chloroplastic (EC 5.3.99.6)	AOC4 At1g13280 T6J4.4 T6J4_23	Arabidopsis thaliana (Mouse-ear cress)		Chloroplast; Complete proteome; Isomerase; Plastid; Reference proteome; Transit peptide
SRR1271857_TR11128_c0_g1_i2_len=1627	AOC4_ARATH	Q:743-1444,H:22-254	63.14%ID	E:3e-88	Allene oxide cyclase 4, chloroplastic	PF06351.8^Allene_ox_cyc^Allene oxide cyclase^80-252^E:1.2e-93	0,004	1,957	0	5,905	0	3,774	0	4,753	0,593	0,662	AOC4_ARATH	Allene oxide cyclase 4, chloroplastic (EC 5.3.99.6)	AOC4 At1g13280 T6J4.4 T6J4_23	Arabidopsis thaliana (Mouse-ear cress)		Chloroplast; Complete proteome; Isomerase; Plastid; Reference proteome; Transit peptide
SRR1271857_TR17545_c0_g1_i3_len=880	NA	NA	NA	NA	NA	.	1	0,707	0	3,76	0	4,687	0	4,882	0,076	3,277	.	.	.	.	.	.
SRR1271857_TR21990_c0_g1_i1_len=649	DCTP1_MOUSE	Q:217-519,H:30-130	48.51%ID	E:2e-28	dCTP pyrophosphatase 1	PF03819.14^MazG^MazG nucleotide pyrophosphohydrolase domain^76-149^E:2e-07`PF12643.4^MazG-like^MazG-like family^87-156^E:1.8e-07	0,01	2,514	0	1,939	0	2,083	0	2,881	0,299	-1,53	DCTP1_MOUSE	dCTP pyrophosphatase 1 (EC 3.6.1.12) (Deoxycytidine-triphosphatase 1) (dCTPase 1) (RS21-C6) (XTP3-transactivated gene A protein homolog)	Dctpp1 Tdrg-TL1	Mus musculus (Mouse)		3D-structure; Acetylation; Complete proteome; Cytoplasm; Hydrolase; Magnesium; Metal-binding; Nucleotide-binding; Phosphoprotein; Reference proteome
SRR1271857_TR27295_c0_g2_i1_len=1107	PX24B_DICDI	Q:153-737,H:1-182	31.28%ID	E:3e-25	PXMP2/4 family protein 2	PF04117.9^Mpv17_PMP22^Mpv17 / PMP22 family^129-189^E:1.2e-15	1	0,004	0	3,551	0	3,517	0,001	3,243	0,076	-2,445	PX24B_DICDI	PXMP2/4 family protein 2	DDB_G0278529	Dictyostelium discoideum (Slime mold)		Complete proteome; Membrane; Reference proteome; Transmembrane; Transmembrane helix
SRR1271857_TR32991_c0_g2_i1_len=825	NA	NA	NA	NA	NA	PF00582.23^Usp^Universal stress protein family^45-190^E:2.8e-26	1	3,408	0	4,301	0	3,459	0	2,459	1	0	.	.	.	.	.	.
SRR1271857_TR34670_c0_g1_i1_len=957	NA	NA	NA	NA	NA	PF06813.10^Nodulin-like^Nodulin-like^69-314^E:9.6e-95	0,461	1,168	0	3,986	0	5,317	0	6,32	1	-1,155	.	.	.	.	.	.
SRR1271857_TR37691_c0_g1_i1_len=1014	NA	NA	NA	NA	NA	PF06232.8^ATS3^Embryo-specific protein 3, (ATS3)^30-132^E:2.4e-08`PF01477.20^PLAT^PLAT/LH2 domain^36-153^E:2.8e-13	0,005	1,595	0	5,677	0	4,542	0	4,919	0,079	1,056	.	.	.	.	.	.
SRR1271858_TR1997_c0_g3_i1_len=1635	NA	NA	NA	NA	NA	.	0,195	1,381	0	3,585	0	2,445	0	2,263	1	0,559	.	.	.	.	.	.
SRR1271858_TR2946_c0_g1_i4_len=4181	PAO2_ARATH	Q:2382-2840,H:244-396	79.74%ID	E:1e-80	Probable polyamine oxidase 2	PF01593.21^Amino_oxidase^Flavin containing amine oxidoreductase^5-147^E:1.6e-30	0,003	1,799	0	4,457	0	3,995	0	4,631	0,854	0,263	PAO2_ARATH	Probable polyamine oxidase 2 (AtPAO2) (EC 1.5.3.-) (Amine oxidase 1)	PAO2 At2g43020 MFL8.12	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; FAD; Flavoprotein; Oxidoreductase; Peroxisome; Reference proteome
SRR1271858_TR5114_c0_g1_i8_len=3929	THD1_ARATH	Q:3108-2584,H:188-355	77.71%ID	E:2e-115	Threonine dehydratase biosynthetic, chloroplastic	PF00291.22^PALP^Pyridoxal-phosphate dependent enzyme^143-231^E:6.3e-27	0,357	0,662	0	3,029	0	2,897	0	3,746	0,034	-4,996	THD1_ARATH	Threonine dehydratase biosynthetic, chloroplastic (EC 4.3.1.19) (Threonine deaminase) (TD)	OMR1 At3g10050 T22K18.12	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Amino-acid biosynthesis; L-isoleucine biosynthesis; 2-oxobutanoate from L-threonine: step 1/1.	Allosteric enzyme; Amino-acid biosynthesis; Branched-chain amino acid biosynthesis; Chloroplast; Complete proteome; Isoleucine biosynthesis; Lyase; Plastid; Pyridoxal phosphate; Reference proteome; Repeat; Transit peptide
SRR1271858_TR6554_c0_g1_i1_len=1057	NA	NA	NA	NA	NA	PF00561.17^Abhydrolase_1^alpha/beta hydrolase fold^53-157^E:2e-15`PF12697.4^Abhydrolase_6^Alpha/beta hydrolase family^54-271^E:1.1e-14	0,025	2,834	0	9,553	0	5,825	0	6,134	1	-0,307	.	.	.	.	.	.
SRR1271858_TR10263_c0_g2_i3_len=1017	NA	NA	NA	NA	NA	.	0,132	2,282	0	7,691	0	9,602	0	10,128	1	-0,092	.	.	.	.	.	.
SRR1271858_TR14849_c0_g1_i3_len=1333	NA	NA	NA	NA	NA	.	1	0,191	0	3,353	0	4,839	0	5,385	0,694	-0,318	.	.	.	.	.	.
SRR1271858_TR15848_c0_g1_i3_len=1769	CCR1_ARATH	Q:337-1287,H:11-322	50.16%ID	E:2e-86	Cinnamoyl-CoA reductase 1	PF01370.18^Epimerase^NAD dependent epimerase/dehydratase family^4-241^E:9.1e-24`PF05368.10^NmrA^NmrA-like family^4-100^E:1e-07`PF01073.16^3Beta_HSD^3-beta hydroxysteroid dehydrogenase/isomerase family^6-238^E:1.1e-20`PF07993.9^NAD_binding_4^Male sterility protein^6-236^E:9.1e-11`PF16363.2^GDP_Man_Dehyd^GDP-mannose 4,6 dehydratase^6-245^E:3.1e-10`PF13460.3^NAD_binding_10^NAD(P)H-binding^8-190^E:3e-13	0,659	0,146	0	1,484	0	2,344	0	2,104	0,76	0,113	CCR1_ARATH	Cinnamoyl-CoA reductase 1 (AtCCR1) (EC 1.2.1.44) (Protein IRREGULAR XYLEM 4)	CCR1 IRX4 At1g15950 T24D18.5	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Aromatic compound metabolism; phenylpropanoid biosynthesis.	Alternative splicing; Complete proteome; Lignin biosynthesis; NADP; Oxidoreductase; Phosphoprotein; Reference proteome
SRR1271858_TR20404_c0_g2_i5_len=3343	CRSP_ARATH	Q:1692-2909,H:355-762	55.31%ID	E:6e-143	CO(2)-response secreted protease {ECO:0000303|PubMed:25043023}	PF05922.13^Inhibitor_I9^Peptidase inhibitor I9^7-69^E:5.2e-14`PF00082.19^Peptidase_S8^Subtilase family^97-284^E:3.5e-23	0,239	1,641	0	3,541	0	3,636	0	3,231	1	-0,202	CRSP_ARATH	CO(2)-response secreted protease (Subtilisin-like serine protease) (AtSBT5.2) (Tripeptidyl-peptidase II) (EC 3.4.14.10)	CRSP SBT5.2 At1g20160 T20H2.6	Arabidopsis thaliana (Mouse-ear cress)		Alternative splicing; Cell wall; Complete proteome; Hydrolase; Protease; Reference proteome; Secreted; Serine protease; Signal
SRR1271858_TR20619_c0_g1_i1_len=910	NA	NA	NA	NA	NA	.	0,461	0,905	0	4,669	0	2,472	0,001	1,732	0,025	1,997	.	.	.	.	.	.
SRR1271858_TR20656_c0_g1_i1_len=2019	NA	NA	NA	NA	NA	.	0,132	1,55	0	4,574	0	4,648	0	5,459	1	0,223	.	.	.	.	.	.
SRR1271858_TR21130_c1_g1_i5_len=1339	PIP27_MAIZE	Q:1241-378,H:1-287	82.7%ID	E:7e-151	Aquaporin PIP2-7	PF00230.17^MIP^Major intrinsic protein^34-269^E:4e-83	0,502	3,601	0	8,446	0	5,285	0	3,511	1	0	PIP27_MAIZE	Aquaporin PIP2-7 (Plasma membrane intrinsic protein 2-7) (ZmPIP2-7) (ZmPIP2;7)	PIP2-7	Zea mays (Maize)		Cell membrane; Complete proteome; Membrane; Reference proteome; Repeat; Transmembrane; Transmembrane helix; Transport
SRR1271858_TR28290_c0_g1_i1_len=1275	NA	NA	NA	NA	NA	.	0,003	1,459	0	2,105	0	2,007	0	1,622	0,255	-0,616	.	.	.	.	.	.
SRR1271858_TR28350_c0_g1_i3_len=1607	TLP1_PRUPE	Q:1265-558,H:16-246	53.59%ID	E:3e-73	Thaumatin-like protein 1	PF00314.14^Thaumatin^Thaumatin family^33-253^E:2.4e-84	0,257	0,856	0	3,831	0	1,873	0	2,082	0,118	-1,751	TLP1_PRUPE	Thaumatin-like protein 1 (PpAZ44)		Prunus persica (Peach) (Amygdalus persica)		Disulfide bond; Plant defense; Secreted; Signal
SRR1271858_TR32754_c0_g2_i1_len=840	NA	NA	NA	NA	NA	.	0,62	0,732	0	3,277	0	3,166	0,001	2,819	0	-2,698	.	.	.	.	.	.
SRR1271858_TR36359_c0_g2_i3_len=1956	NA	NA	NA	NA	NA	PF03619.13^Solute_trans_a^Organic solute transporter Ostalpha^9-84^E:2.5e-16	0,051	1,087	0	3,414	0	2,789	0	3,167	0,524	0,585	.	.	.	.	.	.
SRR1271858_TR37116_c0_g1_i1_len=1461	FABG_THEMA	Q:965-165,H:2-246	32.96%ID	E:6e-28	3-oxoacyl-[acyl-carrier-protein] reductase FabG	PF00106.22^adh_short^short chain dehydrogenase^17-226^E:9.2e-48`PF08659.7^KR^KR domain^18-196^E:9e-07`PF13561.3^adh_short_C2^Enoyl-(Acyl carrier protein) reductase^23-278^E:3.9e-45	0,56	0,819	0	6,408	0	6,36	0	7,049	1	0,454	FABG_THEMA	3-oxoacyl-[acyl-carrier-protein] reductase FabG (EC 1.1.1.100) (3-ketoacyl-acyl carrier protein reductase) (Beta-Ketoacyl-acyl carrier protein reductase) (Beta-ketoacyl-ACP reductase)	fabG TM_1724	Thermotoga maritima (strain ATCC 43589 / MSB8 / DSM 3109 / JCM 10099)	PATHWAY: Lipid metabolism; fatty acid biosynthesis.	Complete proteome; Fatty acid biosynthesis; Fatty acid metabolism; Lipid biosynthesis; Lipid metabolism; NADP; Oxidoreductase; Reference proteome
SRR1271858_TR37267_c0_g1_i1_len=930	NA	NA	NA	NA	NA	PF15697.2^DUF4666^Domain of unknown function (DUF4666)^60-99^E:5.1e-12`PF15697.2^DUF4666^Domain of unknown function (DUF4666)^107-141^E:7.5e-08	0,129	1,066	0,001	2,083	0	1,982	0	1,889	0,564	-0,423	.	.	.	.	.	.
SRR1271858_TR38460_c0_g1_i2_len=1583	NA	NA	NA	NA	NA	.	0,254	2,447	0	5,581	0	5,623	0	6,949	0,629	-1,167	.	.	.	.	.	.
SRR1271858_TR45931_c0_g1_i2_len=1180	NA	NA	NA	NA	NA	.	0,068	0,861	0	2,287	0	1,648	0	1,803	0,735	0,211	.	.	.	.	.	.
SRR1271858_TR46225_c0_g1_i1_len=2111	GATP1_SOLLC	Q:1905-391,H:4-515	82.81%ID	E:0	Gamma aminobutyrate transaminase 1, mitochondrial	PF00202.18^Aminotran_3^Aminotransferase class-III^77-495^E:3.5e-98	0,287	0,357	0	1,58	0	1,741	0	1,725	1	-0,364	GATP1_SOLLC	Gamma aminobutyrate transaminase 1, mitochondrial (Gamma-aminobutyrate transaminase isozyme 1) (LeGABA-TP1) (SlGABA-T1) (EC 2.6.1.96)	GABA-TP1 GABA-T1	Solanum lycopersicum (Tomato) (Lycopersicon esculentum)		Aminotransferase; Complete proteome; Mitochondrion; Pyridoxal phosphate; Reference proteome; Transferase; Transit peptide
SRR1271858_TR46904_c0_g1_i3_len=1857	C72A1_CATRO	Q:1148-309,H:245-524	97.14%ID	E:0	Secologanin synthase	PF00067.19^p450^Cytochrome P450^1-236^E:1.7e-63	0,002	1,094	0	3,233	0	3,116	0	2,619	0,38	0,535	C72A1_CATRO	Secologanin synthase (SLS) (EC 1.3.3.9) (CYPLXXII) (Cytochrome P450 72A1)	CYP72A1 CYP72 P450CR3	Catharanthus roseus (Madagascar periwinkle) (Vinca rosea)	PATHWAY: Alkaloid biosynthesis; secologanin biosynthesis.	Alkaloid metabolism; Heme; Iron; Membrane; Metal-binding; Monooxygenase; NADP; Oxidoreductase; Transmembrane; Transmembrane helix; Vacuole
SRR1271858_TR56764_c0_g1_i11_len=2126	IAA26_ARATH	Q:1278-1898,H:60-267	56.62%ID	E:1e-61	Auxin-responsive protein IAA26	PF02309.13^AUX_IAA^AUX/IAA family^43-342^E:2e-68	0,252	0,555	0	3,461	0	3,964	0	4,739	0,763	0,245	IAA26_ARATH	Auxin-responsive protein IAA26 (Indoleacetic acid-induced protein 26) (Phytochrome-associated protein 1)	IAA26 PAP1 At3g16500 MDC8.13	Arabidopsis thaliana (Mouse-ear cress)		Auxin signaling pathway; Complete proteome; Nucleus; Reference proteome; Repressor; Transcription; Transcription regulation
SRR1271858_TR57115_c0_g1_i3_len=1069	NA	NA	NA	NA	NA	PF06232.8^ATS3^Embryo-specific protein 3, (ATS3)^30-132^E:2.4e-08`PF01477.20^PLAT^PLAT/LH2 domain^36-153^E:3.4e-13	0,001	0,805	0	3,109	0	4,579	0	4,177	0,24	0,434	.	.	.	.	.	.
SRR1271858_TR60403_c2_g1_i3_len=3073	NA	NA	NA	NA	NA	.	0,001	4,178	0	4,244	0	3,412	0	2,97	1	-0,417	.	.	.	.	.	.
SRR1271858_TR60616_c0_g1_i3_len=617	NA	NA	NA	NA	NA	.	0,129	3,059	0	6,779	0	7,82	0,001	6,542	1	2,528	.	.	.	.	.	.
SRR1271858_TR61038_c0_g3_i2_len=925	10HGO_CATRO	Q:141-866,H:1-242	100%ID	E:6e-140	8-hydroxygeraniol dehydrogenase	PF08240.9^ADH_N^Alcohol dehydrogenase GroES-like domain^38-151^E:4.4e-29`PF02826.16^2-Hacid_dh_C^D-isomer specific 2-hydroxyacid dehydrogenase, NAD binding domain^177-225^E:4.3e-06`PF00107.23^ADH_zinc_N^Zinc-binding dehydrogenase^194-239^E:2.1e-07	0,35	0,575	0	5,058	0	2,07	0	2,876	0,142	0,587	10HGO_CATRO	8-hydroxygeraniol dehydrogenase (Cr10HGO) (EC 1.1.1.324)	10HGO	Catharanthus roseus (Madagascar periwinkle) (Vinca rosea)		Metal-binding; NADP; Oxidoreductase; Zinc
SRR1271858_TR61149_c0_g1_i1_len=1715	GATL9_ARATH	Q:1368-442,H:51-363	81.79%ID	E:0	Probable galacturonosyltransferase-like 9	PF01501.17^Glyco_transf_8^Glycosyl transferase family 8^77-337^E:1.4e-52	0,886	-0,167	0	2,014	0	2,652	0	3,179	0,004	-1,36	GATL9_ARATH	Probable galacturonosyltransferase-like 9 (EC 2.4.1.-) (Like glycosyl transferase 8)	GATL9 LGT8 At1g70090 F20P5.18	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Glycan metabolism; pectin biosynthesis.	Cell wall biogenesis/degradation; Complete proteome; Glycoprotein; Glycosyltransferase; Golgi apparatus; Membrane; Reference proteome; Signal-anchor; Transferase; Transmembrane; Transmembrane helix
SRR1271858_TR63842_c0_g1_i1_len=1678	PLA11_ARATH	Q:303-1394,H:84-447	62.43%ID	E:3e-162	Phospholipase A(1) DAD1, chloroplastic	PF01764.22^Lipase_3^Lipase (class 3)^190-340^E:3e-37	0,629	1,588	0	5,787	0	5,909	0	6,989	1	0	PLA11_ARATH	Phospholipase A(1) DAD1, chloroplastic (EC 3.1.1.32) (Phospholipase A1-Ibeta1) (Protein DEFECTIVE IN ANTHER DEHISCENCE 1) (AtDAD1)	DAD1 At2g44810 T13E15.18	Arabidopsis thaliana (Mouse-ear cress)		Chloroplast; Complete proteome; Hydrolase; Lipid degradation; Lipid metabolism; Plastid; Reference proteome; Transit peptide
SRR1271858_TR64491_c0_g2_i1_len=1521	YODA_ARATH	Q:155-946,H:400-656	40.29%ID	E:2e-45	Mitogen-activated protein kinase kinase kinase YODA	PF00069.22^Pkinase^Protein kinase domain^5-266^E:2.2e-53`PF07714.14^Pkinase_Tyr^Protein tyrosine kinase^6-261^E:2.3e-33	0,005	6,218	0	3,904	0	6,256	0	6,425	1	-0,476	YODA_ARATH	Mitogen-activated protein kinase kinase kinase YODA (EC 2.7.11.25) (YODA MAPKK kinase)	YDA At1g63700 F24D7.11	Arabidopsis thaliana (Mouse-ear cress)		ATP-binding; Complete proteome; Developmental protein; Growth regulation; Kinase; Nucleotide-binding; Reference proteome; Transferase
SRR1271858_TR65581_c0_g1_i4_len=2815	LIP_STAHY	Q:662-1381,H:309-542	29.46%ID	E:1e-23	Lipase	.	0,003	2,057	0	3,278	0	2,55	0	2,495	1	-0,214	LIP_STAHY	Lipase (EC 3.1.1.3) (EC 3.1.1.32) (Phospholipase A1) (Triacylglycerol lipase) [Cleaved into: Lipase 86 kDa form; Lipase 46 kDa form]	lip	Staphylococcus hyicus		3D-structure; Calcium; Direct protein sequencing; Hydrolase; Lipid degradation; Lipid metabolism; Metal-binding; Secreted; Signal
SRR1271858_TR65593_c1_g3_i1_len=865	NA	NA	NA	NA	NA	.	0,692	1,043	0	3,246	0	2,435	0	2,423	1	-0,725	.	.	.	.	.	.
SRR1271858_TR68287_c3_g2_i11_len=4091	RBOHC_SOLTU	Q:3788-1779,H:16-687	81.43%ID	E:0	Respiratory burst oxidase homolog protein C	PF08414.7^NADPH_Ox^Respiratory burst NADPH oxidase^149-250^E:3.9e-40`PF13202.3^EF-hand_5^EF hand^252-274^E:0.004`PF01794.16^Ferric_reduct^Ferric reductase like transmembrane component^410-566^E:4e-23`PF08022.9^FAD_binding_8^FAD-binding domain^609-688^E:5e-28	0,16	1,14	0	3,215	0	6,675	0	8,093	0,502	1,559	RBOHC_SOLTU	Respiratory burst oxidase homolog protein C (EC 1.11.1.-) (EC 1.6.3.-) (NADPH oxidase RBOHC) (StRBOHC)	RBOHC	Solanum tuberosum (Potato)		Calcium; Coiled coil; Complete proteome; FAD; Flavoprotein; Membrane; Metal-binding; NADP; Oxidoreductase; Peroxidase; Phosphoprotein; Reference proteome; Repeat; Transmembrane; Transmembrane helix
SRR1271859_TR897_c0_g1_i1_len=3560	IKU2_ARATH	Q:3307-509,H:24-968	54.1%ID	E:0	Receptor-like protein kinase HAIKU2	PF08263.9^LRRNT_2^Leucine rich repeat N-terminal domain^40-78^E:1e-09`PF08263.9^LRRNT_2^Leucine rich repeat N-terminal domain^342-348^E:7000`PF00560.30^LRR_1^Leucine Rich Repeat^542-563^E:0.62`PF08263.9^LRRNT_2^Leucine rich repeat N-terminal domain^649-658^E:9600`PF00069.22^Pkinase^Protein kinase domain^682-965^E:3.1e-44`PF07714.14^Pkinase_Tyr^Protein tyrosine kinase^683-967^E:1.4e-39	0,111	1,33	0	5,575	0	4,328	0	3,706	1	0,309	IKU2_ARATH	Receptor-like protein kinase HAIKU2 (EC 2.7.11.1)	IKU2 At3g19700 MMB12.19	Arabidopsis thaliana (Mouse-ear cress)		ATP-binding; Complete proteome; Glycoprotein; Kinase; Leucine-rich repeat; Membrane; Nucleotide-binding; Phosphoprotein; Receptor; Reference proteome; Repeat; Serine/threonine-protein kinase; Signal; Transferase; Transmembrane; Transmembrane helix
SRR1271859_TR6380_c0_g1_i1_len=6125	NA	NA	NA	NA	NA	PF07765.9^KIP1^KIP1-like protein^14-87^E:3.5e-38	0,026	0,943	0	3,609	0	1,437	0	1,751	0,109	1,052	.	.	.	.	.	.
SRR1271859_TR7412_c1_g2_i1_len=2743	SPL6_ARATH	Q:989-1627,H:83-262	48.13%ID	E:4e-49	Squamosa promoter-binding-like protein 6	PF03110.11^SBP^SBP domain^174-247^E:8e-32	0,026	1,089	0	3,762	0	2,692	0	2,977	0,663	0,535	SPL6_ARATH	Squamosa promoter-binding-like protein 6	SPL6 At1g69170 F23O10.24 F4N2.13	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; DNA-binding; Metal-binding; Nucleus; Reference proteome; Transcription; Transcription regulation; Zinc; Zinc-finger
SRR1271859_TR8465_c1_g1_i1_len=2849	RAP24_ARATH	Q:907-1719,H:54-329	51.53%ID	E:1e-58	Ethylene-responsive transcription factor RAP2-4	PF00847.17^AP2^AP2 domain^203-251^E:3.9e-14	0,031	0,863	0	3,156	0	1,928	0	1,805	0,104	-0,492	RAP24_ARATH	Ethylene-responsive transcription factor RAP2-4 (Ethylene-responsive transcription factor ERF059) (Protein RELATED TO APETALA2 4)	RAP2-4 ERF059 At1g78080 F28K19.29 T11I11.1	Arabidopsis thaliana (Mouse-ear cress)		Activator; Complete proteome; DNA-binding; Ethylene signaling pathway; Nucleus; Reference proteome; Transcription; Transcription regulation
SRR1271859_TR10808_c0_g1_i10_len=2365	PPH_ARATH	Q:2002-791,H:3-402	62.47%ID	E:5e-172	Pheophytinase, chloroplastic	PF00561.17^Abhydrolase_1^alpha/beta hydrolase fold^157-439^E:1.1e-13`PF12697.4^Abhydrolase_6^Alpha/beta hydrolase family^159-443^E:7.4e-18	0,502	2,452	0	8,648	0	5,716	0	6,627	1	-0,813	PPH_ARATH	Pheophytinase, chloroplastic (EC 3.1.1.-) (Pheophytin pheophorbide hydrolase) (Protein CO-REGULATED WITH NYE1)	PPH CRN1 At5g13800 MAC12.25	Arabidopsis thaliana (Mouse-ear cress)		Chlorophyll catabolism; Chloroplast; Complete proteome; Hydrolase; Membrane; Plastid; Reference proteome; Thylakoid; Transit peptide
SRR1271859_TR11304_c0_g1_i1_len=2270	CIPK5_ORYSJ	Q:1791-430,H:1-442	70.02%ID	E:0	CBL-interacting protein kinase 5	PF00069.22^Pkinase^Protein kinase domain^18-272^E:1.9e-73`PF07714.14^Pkinase_Tyr^Protein tyrosine kinase^19-268^E:5.7e-40`PF14531.3^Kinase-like^Kinase-like^111-260^E:3.5e-09`PF03822.11^NAF^NAF domain^329-388^E:5.5e-22	0,409	0,43	0	2,447	0	1,423	0	1,792	0,423	0,381	CIPK5_ORYSJ	CBL-interacting protein kinase 5 (EC 2.7.11.1) (OsCIPK05)	CIPK5 Os01g0206700 LOC_Os01g10890 OsJ_000797 OSJNBa0016I09.5 P0451C06.36	Oryza sativa subsp. japonica (Rice)		ATP-binding; Complete proteome; Kinase; Manganese; Nucleotide-binding; Reference proteome; Serine/threonine-protein kinase; Transferase
SRR1271859_TR12174_c0_g1_i2_len=1710	WRK18_ARATH	Q:440-568,H:174-216	88.37%ID	E:2e-33	WRKY transcription factor 18	.	0,044	2,607	0	4,819	0	3,19	0	3,819	0,08	-1,292	WRK18_ARATH	WRKY transcription factor 18 (WRKY DNA-binding protein 18) (AtWRKY18)	WRKY18 At4g31800 F28M20.10	Arabidopsis thaliana (Mouse-ear cress)		Alternative splicing; Complete proteome; DNA-binding; Nucleus; Reference proteome; Transcription; Transcription regulation
SRR1271859_TR12356_c0_g2_i1_len=584	MIRA_SYNDU	Q:44-379,H:103-216	59.13%ID	E:6e-37	Miraculin	PF00197.15^Kunitz_legume^Trypsin and protease inhibitor^2-108^E:1.3e-26	0,003	0,755	0	1,59	0	2,085	0	1,819	0	-1,733	MIRA_SYNDU	Miraculin (MIR)		Synsepalum dulcificum (Miracle fruit) (Richadella dulcifica)		Direct protein sequencing; Disulfide bond; Glycoprotein; Signal; Taste-modifying protein
SRR1271859_TR16070_c0_g1_i2_len=2864	BH013_ARATH	Q:363-2156,H:1-584	52.15%ID	E:0	Transcription factor bHLH13	PF14215.3^bHLH-MYC_N^bHLH-MYC and R2R3-MYB transcription factors N-terminal^52-240^E:1e-54`PF00010.23^HLH^Helix-loop-helix DNA-binding domain^437-483^E:3.4e-10	0,798	0,304	0	2,687	0	4,737	0	5,218	1	0,001	BH013_ARATH	Transcription factor bHLH13 (Basic helix-loop-helix protein 13) (AtbHLH13) (bHLH 13) (Transcription factor EN 39) (bHLH transcription factor bHLH013)	BHLH13 EN39 At1g01260 F6F3.7	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; DNA-binding; Nucleus; Reference proteome; Transcription; Transcription regulation
SRR1271859_TR17852_c0_g2_i1_len=1088	BH035_ARATH	Q:133-846,H:5-240	53.47%ID	E:5e-69	Transcription factor bHLH35	PF00010.23^HLH^Helix-loop-helix DNA-binding domain^95-137^E:1.1e-11	0,044	1,03	0	3,66	0	3,557	0	3,518	0,748	0,297	BH035_ARATH	Transcription factor bHLH35 (Basic helix-loop-helix protein 35) (AtbHLH35) (bHLH 35) (Transcription factor EN 41) (bHLH transcription factor bHLH035)	BHLH35 EN41 At5g57150 MUL3.10	Arabidopsis thaliana (Mouse-ear cress)		Alternative splicing; Complete proteome; DNA-binding; Nucleus; Reference proteome; Transcription; Transcription regulation
SRR1271859_TR19051_c0_g2_i1_len=938	NA	NA	NA	NA	NA	PF06200.11^tify^tify domain^77-107^E:6.3e-15`PF09425.7^CCT_2^Divergent CCT motif^143-162^E:2.3e-08	0,158	1,613	0	5,176	0	6,89	0	7,416	1	-1,531	.	.	.	.	.	.
SRR1271859_TR21346_c0_g1_i1_len=1347	ASPGB_ARATH	Q:1190-222,H:3-324	83.28%ID	E:0	Probable isoaspartyl peptidase/L-asparaginase 2	PF01112.15^Asparaginase_2^Asparaginase^5-326^E:7.2e-108	0,489	-0,503	0	5,637	0	5,856	0	7,562	0,025	-1,924	ASPGB_ARATH	Probable isoaspartyl peptidase/L-asparaginase 2 (EC 3.4.19.5) (L-asparagine amidohydrolase 2) [Cleaved into: Isoaspartyl peptidase/L-asparaginase 2 subunit alpha; Isoaspartyl peptidase/L-asparaginase 2 subunit beta]	At3g16150 MSL1.19	Arabidopsis thaliana (Mouse-ear cress)		Alternative splicing; Autocatalytic cleavage; Complete proteome; Hydrolase; Protease; Reference proteome
SRR1271859_TR27908_c1_g1_i1_len=945	HSP7C_PETHY	Q:944-168,H:360-618	95.37%ID	E:3e-152	Heat shock cognate 70 kDa protein	PF00012.17^HSP70^Hsp70 protein^2-259^E:1.2e-91	1	1,578	0	4,071	0	2,44	0	1,629	1	1,067	HSP7C_PETHY	Heat shock cognate 70 kDa protein	HSP70	Petunia hybrida (Petunia)		ATP-binding; Nucleotide-binding; Stress response
SRR1271859_TR28170_c0_g1_i1_len=965	NA	NA	NA	NA	NA	.	0,195	1,325	0	3,868	0	4,121	0	4,383	0,239	1,548	.	.	.	.	.	.
SRR1271859_TR28775_c1_g4_i1_len=1553	Y1500_ARATH	Q:394-840,H:53-201	64.67%ID	E:1e-62	Probable tyrosine-protein phosphatase At1g05000	PF03162.10^Y_phosphatase2^Tyrosine phosphatase family^15-169^E:2.2e-56`PF13350.3^Y_phosphatase3^Tyrosine phosphatase family^90-142^E:1.5e-06	0,719	-0,284	0	2,687	0	3,212	0	4,362	1	0,124	Y1500_ARATH	Probable tyrosine-protein phosphatase At1g05000 (EC 3.1.3.48)	At1g05000 T7A14.14	Arabidopsis thaliana (Mouse-ear cress)		3D-structure; Alternative splicing; Complete proteome; Hydrolase; Protein phosphatase; Reference proteome
SRR1271859_TR29245_c0_g2_i1_len=1178	GSTF_HYOMU	Q:187-900,H:2-212	61.34%ID	E:2e-98	Glutathione S-transferase	PF00043.22^GST_C^Glutathione S-transferase, C-terminal domain^48-141^E:7e-16`PF13410.3^GST_C_2^Glutathione S-transferase, C-terminal domain^69-135^E:9.3e-09`PF14497.3^GST_C_3^Glutathione S-transferase, C-terminal domain^75-142^E:2.1e-05	0,588	0,213	0	2,336	0	2,425	0	2,214	0,006	0,648	GSTF_HYOMU	Glutathione S-transferase (EC 2.5.1.18) (25 kDa auxin-binding protein) (GST class-phi)		Hyoscyamus muticus (Egyptian henbane)		Auxin signaling pathway; Direct protein sequencing; Transferase
SRR1271859_TR31061_c2_g2_i2_len=1457	NAC72_ARATH	Q:1455-853,H:84-242	53.92%ID	E:8e-54	NAC domain-containing protein 72	.	0,226	2,179	0	7,041	0	7,453	0	7,341	1	0,874	NAC72_ARATH	NAC domain-containing protein 72 (ANAC072) (Protein RESPONSIVE TO DESICCATION 26)	NAC072 RD26 At4g27410 F27G19.10	Arabidopsis thaliana (Mouse-ear cress)		Alternative splicing; Complete proteome; DNA-binding; Nucleus; Reference proteome; Transcription; Transcription regulation
SRR1271859_TR32557_c0_g1_i1_len=1232	IF4E1_MAIZE	Q:233-802,H:30-217	78.42%ID	E:9e-107	Eukaryotic translation initiation factor 4E-1	PF01652.15^IF4E^Eukaryotic initiation factor 4E^50-205^E:3.9e-53	0,959	0,033	0	1,408	0	1,585	0	1,611	0,323	0,296	IF4E1_MAIZE	Eukaryotic translation initiation factor 4E-1 (eIF-4E-1) (eIF4E-1) (eIF-4F 25 kDa subunit) (eIF-4F p26 subunit) (mRNA cap-binding protein)		Zea mays (Maize)		Complete proteome; Disulfide bond; Initiation factor; Protein biosynthesis; RNA-binding; Reference proteome; Translation regulation
SRR1271859_TR34460_c0_g1_i2_len=1465	SABP2_TOBAC	Q:399-893,H:5-169	47.13%ID	E:4e-38	Salicylic acid-binding protein 2	PF00561.17^Abhydrolase_1^alpha/beta hydrolase fold^105-213^E:2.1e-14`PF12146.5^Hydrolase_4^Serine aminopeptidase, S33^106-211^E:3.1e-12`PF12697.4^Abhydrolase_6^Alpha/beta hydrolase family^106-210^E:2.1e-10	1	-0,181	0	3,512	0	4,153	0	4,652	1	1,178	SABP2_TOBAC	Salicylic acid-binding protein 2 (NtSABP2) (EC 3.1.1.-) (Methyl salicylate esterase)	SABP2	Nicotiana tabacum (Common tobacco)		3D-structure; Hydrolase; Immunity; Innate immunity; Plant defense
SRR1271859_TR34460_c0_g1_i4_len=1440	MES9_ARATH	Q:399-1169,H:2-255	43.19%ID	E:2e-63	Methylesterase 9	PF00561.17^Abhydrolase_1^alpha/beta hydrolase fold^105-344^E:6.5e-15`PF12697.4^Abhydrolase_6^Alpha/beta hydrolase family^106-349^E:1.4e-16`PF12146.5^Hydrolase_4^Serine aminopeptidase, S33^106-215^E:2.4e-12	0,062	0,928	0	6,473	0	5,181	0	6,001	0,196	0,748	MES9_ARATH	Methylesterase 9 (AtMES9) (EC 3.1.1.-)	MES9 At4g37150 AP22.78 C7A10.210	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Hydrolase; Immunity; Innate immunity; Plant defense; Reference proteome
SRR1271859_TR37173_c0_g1_i6_len=1610	JMT_ARATH	Q:286-1422,H:2-387	47.46%ID	E:3e-104	Jasmonate O-methyltransferase	PF03492.12^Methyltransf_7^SAM dependent carboxyl methyltransferase^43-256^E:9.8e-86	0,01	2,04	0	5,42	0	4,594	0	5,229	1	0,14	JMT_ARATH	Jasmonate O-methyltransferase (EC 2.1.1.141) (S-adenosyl-L-methionine:jasmonic acid carboxyl methyltransferase)	JMT At1g19640 F14P1.3	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Lipid metabolism; oxylipin biosynthesis.	Complete proteome; Cytoplasm; Fatty acid biosynthesis; Fatty acid metabolism; Lipid biosynthesis; Lipid metabolism; Methyltransferase; Nucleus; Oxylipin biosynthesis; Reference proteome; S-adenosyl-L-methionine; Transferase
SRR1271859_TR38142_c0_g1_i3_len=2406	CIPKC_ARATH	Q:2081-735,H:5-459	81.54%ID	E:0	CBL-interacting serine/threonine-protein kinase 12	PF00069.22^Pkinase^Protein kinase domain^53-307^E:8.3e-77`PF07714.14^Pkinase_Tyr^Protein tyrosine kinase^54-303^E:2.3e-40`PF14531.3^Kinase-like^Kinase-like^147-295^E:1.6e-09`PF03822.11^NAF^NAF domain^359-415^E:6e-24	0,429	0,524	0	2,666	0	1,834	0	2,241	0,623	0,432	CIPKC_ARATH	CBL-interacting serine/threonine-protein kinase 12 (EC 2.7.11.1) (SNF1-related kinase 3.9) (SOS2-like protein kinase PKS8)	CIPK12 PKS8 SnRK3.9 At4g18700 F28A21.110	Arabidopsis thaliana (Mouse-ear cress)		ATP-binding; Complete proteome; Kinase; Manganese; Nucleotide-binding; Phosphoprotein; Reference proteome; Serine/threonine-protein kinase; Transferase
SRR1271859_TR39144_c0_g1_i5_len=1581	NAGK_DICDI	Q:1124-159,H:3-316	33.13%ID	E:3e-50	N-acetyl-D-glucosamine kinase	PF01869.17^BcrAD_BadFG^BadF/BadG/BcrA/BcrD ATPase family^30-345^E:3.5e-51	0,593	0,553	0	2,395	0	2,765	0	3,08	1	-0,458	NAGK_DICDI	N-acetyl-D-glucosamine kinase (N-acetylglucosamine kinase) (EC 2.7.1.59) (GlcNAc kinase)	nagk DDB_G0284433	Dictyostelium discoideum (Slime mold)		ATP-binding; Complete proteome; Kinase; Nucleotide-binding; Reference proteome; Transferase
SRR1271859_TR39719_c1_g1_i1_len=1323	HYES_RAT	Q:179-1096,H:245-542	33.44%ID	E:4e-49	Bifunctional epoxide hydrolase 2	PF07224.8^Chlorophyllase^Chlorophyllase^19-116^E:9.8e-05`PF12740.4^Chlorophyllase2^Chlorophyllase enzyme^20-129^E:2.2e-07`PF00561.17^Abhydrolase_1^alpha/beta hydrolase fold^25-158^E:1.6e-17`PF12146.5^Hydrolase_4^Serine aminopeptidase, S33^26-143^E:1.1e-11`PF12697.4^Abhydrolase_6^Alpha/beta hydrolase family^27-311^E:9.9e-21	0,16	0,612	0	2,866	0	1,584	0	1,232	0,679	0,223	HYES_RAT	Bifunctional epoxide hydrolase 2 [Includes: Cytosolic epoxide hydrolase 2 (CEH) (EC 3.3.2.10) (Epoxide hydratase) (Soluble epoxide hydrolase) (SEH); Lipid-phosphate phosphatase (EC 3.1.3.76)]	Ephx2	Rattus norvegicus (Rat)		Acetylation; Aromatic hydrocarbons catabolism; Complete proteome; Cytoplasm; Detoxification; Direct protein sequencing; Hydrolase; Lipid metabolism; Lipoprotein; Magnesium; Metal-binding; Multifunctional enzyme; Peroxisome; Phosphoprotein; Reference proteome
SRR1271859_TR41321_c0_g1_i1_len=1998	C94C1_ARATH	Q:1754-378,H:31-494	60%ID	E:0	Cytochrome P450 94C1	PF00067.19^p450^Cytochrome P450^121-522^E:6.9e-58	0,001	1,713	0	3,425	0	4,029	0	4,1	0,352	-0,978	C94C1_ARATH	Cytochrome P450 94C1 (EC 1.14.-.-)	CYP94C1 At2g27690 F15K20.21	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Heme; Iron; Jasmonic acid signaling pathway; Membrane; Metal-binding; Monooxygenase; Oxidoreductase; Reference proteome; Transmembrane; Transmembrane helix
SRR1271859_TR41420_c0_g1_i1_len=2164	LIP_STAHY	Q:1435-602,H:309-570	30.41%ID	E:3e-26	Lipase	.	0,002	1,836	0	3,943	0	2,254	0	2,352	0,62	-0,547	LIP_STAHY	Lipase (EC 3.1.1.3) (EC 3.1.1.32) (Phospholipase A1) (Triacylglycerol lipase) [Cleaved into: Lipase 86 kDa form; Lipase 46 kDa form]	lip	Staphylococcus hyicus		3D-structure; Calcium; Direct protein sequencing; Hydrolase; Lipid degradation; Lipid metabolism; Metal-binding; Secreted; Signal
SRR1271859_TR41710_c0_g1_i3_len=1393	SGRW_PEA	Q:230-952,H:1-236	70.66%ID	E:6e-116	Protein STAY-GREEN, chloroplastic	PF12638.4^Staygreen^Staygreen protein^54-205^E:3.3e-58	0,189	2,074	0	4,901	0	5,451	0	5,636	1	1,198	SGRW_PEA	Protein STAY-GREEN, chloroplastic (Protein STAYGREEN)	SGR	Pisum sativum (Garden pea)		Chloroplast; Plastid; Transit peptide
SRR1271859_TR43882_c0_g2_i1_len=2471	PTR8_ARATH	Q:1249-2139,H:288-581	53.36%ID	E:7e-107	Protein NRT1/ PTR FAMILY 2.9	PF00854.18^PTR2^POT family^128-326^E:2.1e-34	0,003	1,186	0	3,09	0	1,838	0	1,399	0,675	0,31	PTR8_ARATH	Protein NRT1/ PTR FAMILY 2.9 (AtNPF2.9) (Nitrate transporter 1.9)	NPF2.9 NRT1.9 At1g18880 F6A14.2	Arabidopsis thaliana (Mouse-ear cress)		Cell membrane; Complete proteome; Membrane; Reference proteome; Transmembrane; Transmembrane helix; Transport
SRR1271859_TR44464_c0_g1_i1_len=3383	SUS2_PEA	Q:2961-541,H:1-807	82.4%ID	E:0	Sucrose synthase 2	PF00862.16^Sucrose_synth^Sucrose synthase^10-556^E:1.1e-292`PF00534.17^Glycos_transf_1^Glycosyl transferases group 1^561-744^E:1.7e-32`PF13692.3^Glyco_trans_1_4^Glycosyl transferases group 1^574-727^E:2.1e-10	0,537	0,291	0	2,164	0	2,021	0	1,661	0,152	0,863	SUS2_PEA	Sucrose synthase 2 (EC 2.4.1.13) (Sucrose-UDP glucosyltransferase 2)	SUS2	Pisum sativum (Garden pea)		Glycosyltransferase; Transferase
SRR1271859_TR46848_c0_g2_i4_len=2239	NA	NA	NA	NA	NA	PF04199.10^Cyclase^Putative cyclase^60-213^E:1.4e-19	0,306	0,565	0	1,937	0	3,894	0	2,763	0,798	0,376	.	.	.	.	.	.
SRR1271859_TR46937_c0_g1_i3_len=1732	WRKY6_ARATH	Q:400-1233,H:204-498	60.93%ID	E:1e-81	WRKY transcription factor 6	PF03106.12^WRKY^WRKY DNA -binding domain^158-215^E:6.1e-27	0,118	1,762	0	6,914	0	4,02	0	4,521	0,732	-0,455	WRKY6_ARATH	WRKY transcription factor 6 (WRKY DNA-binding protein 6) (AtWRKY6)	WRKY6 At1g62300 F19K23.22	Arabidopsis thaliana (Mouse-ear cress)		Activator; Complete proteome; DNA-binding; Ethylene signaling pathway; Nucleus; Reference proteome; Repressor; Transcription; Transcription regulation
SRR342017_TR2816_c0_g1_i1_len=1302	PPCK1_ARATH	Q:1163-360,H:13-279	57.41%ID	E:1e-106	Phosphoenolpyruvate carboxylase kinase 1	PF00069.22^Pkinase^Protein kinase domain^10-268^E:5.6e-70`PF07714.14^Pkinase_Tyr^Protein tyrosine kinase^10-263^E:9e-29`PF14531.3^Kinase-like^Kinase-like^44-217^E:9.2e-10	0,077	0,662	0	2,033	0	2,702	0	2,988	0,204	0,552	PPCK1_ARATH	Phosphoenolpyruvate carboxylase kinase 1 (AtPPCK1) (EC 2.7.11.1)	PPCK1 At1g08650 F22O13.13	Arabidopsis thaliana (Mouse-ear cress)		ATP-binding; Alternative splicing; Complete proteome; Kinase; Nucleotide-binding; Pyruvate; Reference proteome; Serine/threonine-protein kinase; Transferase
SRR342017_TR3714_c0_g1_i2_len=2246	IAA26_ARATH	Q:1052-1657,H:60-261	51.63%ID	E:7e-52	Auxin-responsive protein IAA26	PF02309.13^AUX_IAA^AUX/IAA family^43-322^E:5.1e-56	0,832	0,311	0	3,89	0	3,87	0	4,569	0,299	1,209	IAA26_ARATH	Auxin-responsive protein IAA26 (Indoleacetic acid-induced protein 26) (Phytochrome-associated protein 1)	IAA26 PAP1 At3g16500 MDC8.13	Arabidopsis thaliana (Mouse-ear cress)		Auxin signaling pathway; Complete proteome; Nucleus; Reference proteome; Repressor; Transcription; Transcription regulation
SRR342017_TR5017_c0_g2_i5_len=1434	MIRA_SYNDU	Q:143-682,H:31-216	50.53%ID	E:3e-46	Miraculin	PF00197.15^Kunitz_legume^Trypsin and protease inhibitor^53-227^E:6.9e-42	0,001	0,84	0	2,057	0	2,022	0	1,92	0,005	-1,158	MIRA_SYNDU	Miraculin (MIR)		Synsepalum dulcificum (Miracle fruit) (Richadella dulcifica)		Direct protein sequencing; Disulfide bond; Glycoprotein; Signal; Taste-modifying protein
SRR342017_TR8814_c0_g1_i1_len=4768	ALDO4_ARATH	Q:496-4563,H:2-1333	58.24%ID	E:0	Benzaldehyde dehydrogenase (NAD(+))	PF00111.24^Fer2^2Fe-2S iron-sulfur cluster binding domain^23-90^E:2.6e-07`PF01799.17^Fer2_2^[2Fe-2S] binding domain^101-187^E:2.7e-22`PF00941.18^FAD_binding_5^FAD binding domain in molybdopterin dehydrogenase^244-423^E:3.8e-39`PF03450.14^CO_deh_flav_C^CO dehydrogenase flavoprotein C-terminal domain^444-546^E:1.3e-21`PF01315.19^Ald_Xan_dh_C^Aldehyde oxidase and xanthine dehydrogenase, a/b hammerhead domain^620-726^E:1.4e-24`PF02738.15^Ald_Xan_dh_C2^Molybdopterin-binding domain of aldehyde dehydrogenase^756-1277^E:5.8e-158	0,115	0,536	0	1,647	0	1,515	0,001	1,488	0,37	0,417	ALDO4_ARATH	Benzaldehyde dehydrogenase (NAD(+)) (EC 1.2.1.28) (Aldehyde oxidase 4) (AO-4) (AtAO-4) (AtAO2) (Indole-3-acetaldehyde oxidase) (IAA oxidase) (EC 1.2.3.7)	AAO4 AO2 At1g04580 T1G11.17	Arabidopsis thaliana (Mouse-ear cress)		2Fe-2S; Abscisic acid biosynthesis; Auxin biosynthesis; Complete proteome; Cytoplasm; FAD; Flavoprotein; Iron; Iron-sulfur; Metal-binding; Molybdenum; NAD; Oxidoreductase; Reference proteome
SRR342017_TR19436_c1_g5_i2_len=967	GILT_HUMAN	Q:584-36,H:62-243	37.23%ID	E:1e-29	Gamma-interferon-inducible lysosomal thiol reductase	PF03227.13^GILT^Gamma interferon inducible lysosomal thiol reductase (GILT)^41-143^E:3e-29	0,105	-1	0	7,226	0	8,307	0	7,927	1	0	GILT_HUMAN	Gamma-interferon-inducible lysosomal thiol reductase (EC 1.8.-.-) (Gamma-interferon-inducible protein IP-30) (Legumaturain)	IFI30 GILT IP30	Homo sapiens (Human)		Complete proteome; Direct protein sequencing; Disulfide bond; Glycoprotein; Immunity; Lysosome; Oxidoreductase; Redox-active center; Reference proteome; Secreted; Signal
SRR342017_TR25891_c0_g1_i6_len=1583	NA	NA	NA	NA	NA	PF07712.9^SURNod19^Stress up-regulated Nod 19^22-365^E:1.7e-169	0,016	1,265	0	3,982	0	2,799	0	2,864	0,666	0,269	.	.	.	.	.	.
SRR342017_TR27234_c0_g1_i1_len=2294	PME40_ARATH	Q:523-1962,H:37-518	55.56%ID	E:0	Probable pectinesterase/pectinesterase inhibitor 40	PF04043.12^PMEI^Plant invertase/pectin methylesterase inhibitor^63-210^E:1e-26`PF01095.16^Pectinesterase^Pectinesterase^258-555^E:1.2e-144	0,275	0,455	0	4,223	0	2,457	0	3,527	0,832	-0,328	PME40_ARATH	Probable pectinesterase/pectinesterase inhibitor 40 [Includes: Pectinesterase inhibitor 40 (Pectin methylesterase inhibitor 40); Pectinesterase 40 (PE 40) (EC 3.1.1.11) (Pectin methylesterase 40) (AtPME40)]	PME40 ARATH40 At4g02320 T14P8.1	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Glycan metabolism; pectin degradation; 2-dehydro-3-deoxy-D-gluconate from pectin: step 1/5.	Aspartyl esterase; Cell wall; Cell wall biogenesis/degradation; Complete proteome; Disulfide bond; Glycoprotein; Hydrolase; Reference proteome; Secreted; Signal
SRR342019_TR2072_c0_g1_i7_len=1858	TI10A_ARATH	Q:1316-687,H:4-219	39.74%ID	E:1e-30	Protein TIFY 10A	PF06200.11^tify^tify domain^105-137^E:3.1e-19`PF09425.7^CCT_2^Divergent CCT motif^192-209^E:7.1e-08	0,003	3,129	0	4,956	0	2,747	0	2,362	1	0,274	TI10A_ARATH	Protein TIFY 10A (Jasmonate ZIM domain-containing protein 1)	TIFY10A JAZ1 At1g19180 T29M8.5	Arabidopsis thaliana (Mouse-ear cress)		3D-structure; Alternative splicing; Complete proteome; Jasmonic acid signaling pathway; Nucleus; Plant defense; Reference proteome; Transcription; Transcription regulation; Ubl conjugation
SRR342019_TR2192_c0_g1_i1_len=1163	NA	NA	NA	NA	NA	.	0,118	2,274	0	4,084	0	5,027	0	5,546	1	0,107	.	.	.	.	.	.
SRR342019_TR2192_c0_g2_i2_len=1054	IAA26_ARATH	Q:1020-307,H:60-267	48.8%ID	E:4e-60	Auxin-responsive protein IAA26	PF02309.13^AUX_IAA^AUX/IAA family^20-142^E:4.7e-34	0,732	0,555	0	3,109	0	4,361	0	4,952	1	0,328	IAA26_ARATH	Auxin-responsive protein IAA26 (Indoleacetic acid-induced protein 26) (Phytochrome-associated protein 1)	IAA26 PAP1 At3g16500 MDC8.13	Arabidopsis thaliana (Mouse-ear cress)		Auxin signaling pathway; Complete proteome; Nucleus; Reference proteome; Repressor; Transcription; Transcription regulation
SRR342019_TR2738_c0_g1_i1_len=1423	ACMAT_VITLA	Q:1301-873,H:10-150	62.07%ID	E:1e-47	Methanol O-anthraniloyltransferase	PF02458.12^Transferase^Transferase family^6-147^E:1.4e-23	1	-0,052	0	3,048	0	5,159	0	5,419	0,732	0,682	ACMAT_VITLA	Methanol O-anthraniloyltransferase (EC 2.3.1.232) (Anthraniloyl-CoA:methanol acyltransferase) (Benzyl alcohol O-benzoyltransferase) (EC 2.3.1.196)	AMAT	Vitis labrusca (Concord grape)		Acyltransferase; Direct protein sequencing; Transferase
SRR342019_TR2870_c0_g7_i15_len=3527	AFS1_MALDO	Q:2531-3382,H:274-559	54.7%ID	E:2e-95	(E,E)-alpha-farnesene synthase	PF03936.13^Terpene_synth_C^Terpene synthase family, metal binding domain^1-158^E:6.8e-43	1	0,494	0	5,248	0	5,755	0	6,206	1	1,017	AFS1_MALDO	(E,E)-alpha-farnesene synthase (MdASF1) (EC 4.2.3.46) (Prenyltransferase) (EC 2.5.1.-)	AFS1 AFAR	Malus domestica (Apple) (Pyrus malus)		Cytoplasm; Lyase; Magnesium; Manganese; Metal-binding; Potassium; Transferase
SRR342019_TR3398_c0_g1_i2_len=810	GSTUI_ARATH	Q:699-133,H:38-227	68.95%ID	E:9e-87	Glutathione S-transferase U18	PF13417.3^GST_N_3^Glutathione S-transferase, N-terminal domain^4-47^E:1.8e-07`PF02798.17^GST_N^Glutathione S-transferase, N-terminal domain^11-47^E:8.8e-10`PF00043.22^GST_C^Glutathione S-transferase, C-terminal domain^68-169^E:5.3e-08	0,75	-0,108	0	3,082	0	1,298	0	1,331	0,319	-1,115	GSTUI_ARATH	Glutathione S-transferase U18 (AtGSTU18) (EC 2.5.1.18) (GST class-tau member 18) (Glutathione S-transferase 29)	GSTU18 GST29 At1g10360 F14N23.24	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Cytoplasm; Detoxification; Reference proteome; Transferase
SRR342019_TR5096_c2_g6_i2_len=878	NA	NA	NA	NA	NA	PF14368.3^LTP_2^Probable lipid transfer^13-104^E:2.2e-19	0,481	0,186	0	2,871	0	1,939	0	1,94	1	-1,56	.	.	.	.	.	.
SRR342019_TR7445_c2_g3_i2_len=1912	SPEA_BACSU	Q:282-1715,H:7-474	35.14%ID	E:5e-82	Arginine decarboxylase	PF01276.17^OKR_DC_1^Orn/Lys/Arg decarboxylase, major domain^63-430^E:1.5e-65`PF00155.18^Aminotran_1_2^Aminotransferase class I and II^125-261^E:2e-10`PF00266.16^Aminotran_5^Aminotransferase class-V^125-289^E:2.2e-08`PF01212.18^Beta_elim_lyase^Beta-eliminating lyase^126-258^E:6.8e-05`PF01053.17^Cys_Met_Meta_PP^Cys/Met metabolism PLP-dependent enzyme^128-290^E:2.3e-05`PF01041.14^DegT_DnrJ_EryC1^DegT/DnrJ/EryC1/StrS aminotransferase family^138-264^E:9.4e-09`PF05889.10^SepSecS^O-phosphoseryl-tRNA(Sec) selenium transferase, SepSecS^160-288^E:1.1e-06`PF03711.12^OKR_DC_1_C^Orn/Lys/Arg decarboxylase, C-terminal domain^471-533^E:1.4e-08	0,21	-0,352	0	4,838	0	6,487	0	7,839	0,842	0,101	SPEA_BACSU	Arginine decarboxylase (EC 4.1.1.19)	speA cad BSU14630	Bacillus subtilis (strain 168)	PATHWAY: Amine and polyamine biosynthesis; agmatine biosynthesis; agmatine from L-arginine: step 1/1.	Complete proteome; Cytoplasm; Decarboxylase; Lyase; Polyamine biosynthesis; Putrescine biosynthesis; Pyridoxal phosphate; Reference proteome; Spermidine biosynthesis
SRR342019_TR9202_c0_g3_i1_len=330	NA	NA	NA	NA	NA	.	0,732	0,608	0	4,921	0	1,992	0	1,559	0,129	-2,81	.	.	.	.	.	.
SRR342019_TR11375_c0_g1_i2_len=1989	NA	NA	NA	NA	NA	PF05542.8^DUF760^Protein of unknown function (DUF760)^87-165^E:1.2e-	0,594	0,254	0	2,475	0	1,383	0	2,158	0,123	0,722						

[illegible]	NA	NA	NA	NA	NA	17`PF05542.8^DUF760^Protein of unknown function (DUF760)^260-345^E:2.7e-14	[illegible]	[illegible]	0	[illegible]	0	[illegible]	0	[illegible]	[illegible]	[illegible]	.	.	.	.	.	.
SRR342019_TR12005_c1_g2_i2_len=1751	TRPB_CAMAC	Q:1292-72,H:85-456	60.24%ID	E:4e-174	Tryptophan synthase beta chain 2, chloroplastic	PF00291.22^PALP^Pyridoxal-phosphate dependent enzyme^154-438^E:1.7e-40	0,254	3,585	0	9,378	0	6,809	0	7,882	1	-0,345	TRPB_CAMAC	Tryptophan synthase beta chain 2, chloroplastic (EC 4.2.1.20)	TSB	Camptotheca acuminata (Happy tree)	PATHWAY: Amino-acid biosynthesis; L-tryptophan biosynthesis; L-tryptophan from chorismate: step 5/5.	Amino-acid biosynthesis; Aromatic amino acid biosynthesis; Chloroplast; Lyase; Plastid; Pyridoxal phosphate; Transit peptide; Tryptophan biosynthesis
SRR342019_TR13660_c2_g2_i11_len=1714	B2_DAUCA	Q:918-466,H:55-205	92.05%ID	E:1e-97	B2 protein	PF10539.6^Dev_Cell_Death^Development and cell death domain^199-326^E:2.2e-41	0,317	0,542	0	2,036	0	1,744	0	1,897	0,334	0,31	B2_DAUCA	B2 protein		Daucus carota (Wild carrot)		
SRR342019_TR14141_c0_g4_i2_len=1188	PTR53_ARATH	Q:1004-6,H:27-359	56.59%ID	E:9e-134	Protein NRT1/ PTR FAMILY 2.11	PF00854.18^PTR2^POT family^95-338^E:3e-38	0,517	1,151	0	4,775	0	5,14	0	5,588	0,381	1,424	PTR53_ARATH	Protein NRT1/ PTR FAMILY 2.11 (AtNPF2.11) (Nitrate transporter 1.10) (Protein GLUCOSINOLATE TRANSPORTER-2)	NPF2.11 GTR2 NRT1.10 At5g62680 MRG21.10	Arabidopsis thaliana (Mouse-ear cress)		Cell membrane; Complete proteome; Membrane; Reference proteome; Transmembrane; Transmembrane helix; Transport
SRR342019_TR15113_c3_g1_i4_len=2062	PRS2_SOLTU	Q:1925-1470,H:1-155	35.67%ID	E:5e-22	Pathogenesis-related protein STH-2	PF00407.16^Bet_v_1^Pathogenesis-related protein Bet v I family^1-147^E:4e-13	0,316	0,678	0	1,905	0	1,76	0	1,456	1	0	PRS2_SOLTU	Pathogenesis-related protein STH-2	STH-2	Solanum tuberosum (Potato)		Complete proteome; Pathogenesis-related protein; Plant defense; Reference proteome
SRR342019_TR16511_c1_g3_i1_len=1606	TIP13_ARATH	Q:102-857,H:1-252	79.76%ID	E:2e-139	Aquaporin TIP1-3	PF00230.17^MIP^Major intrinsic protein^14-234^E:6.5e-74	0,005	6,253	0	5,759	0	4,293	0	2,543	1	0,197	TIP13_ARATH	Aquaporin TIP1-3 (Gamma-tonoplast intrinsic protein 3) (Gamma-TIP3) (Tonoplast intrinsic protein 1-3) (AtTIP1;3) [Cleaved into: Aquaporin TIP1-3, N-terminally processed]	TIP1-3 At4g01470 F11O4.1	Arabidopsis thaliana (Mouse-ear cress)		Acetylation; Complete proteome; Membrane; Reference proteome; Repeat; Stress response; Transmembrane; Transmembrane helix; Transport; Vacuole
SRR342019_TR22279_c1_g4_i2_len=1337	GSTF_HYOMU	Q:910-272,H:2-212	68.54%ID	E:3e-103	Glutathione S-transferase	PF02798.17^GST_N^Glutathione S-transferase, N-terminal domain^8-79^E:1.7e-15`PF13417.3^GST_N_3^Glutathione S-transferase, N-terminal domain^10-85^E:6.5e-13`PF13409.3^GST_N_2^Glutathione S-transferase, N-terminal domain^14-78^E:1.6e-05`PF00043.22^GST_C^Glutathione S-transferase, C-terminal domain^114-207^E:1.8e-15`PF13410.3^GST_C_2^Glutathione S-transferase, C-terminal domain^135-201^E:2e-08`PF14497.3^GST_C_3^Glutathione S-transferase, C-terminal domain^141-208^E:5.4e-05	0,009	0,614	0	3,141	0	2,53	0	2,086	0,071	0,822	GSTF_HYOMU	Glutathione S-transferase (EC 2.5.1.18) (25 kDa auxin-binding protein) (GST class-phi)		Hyoscyamus muticus (Egyptian henbane)		Auxin signaling pathway; Direct protein sequencing; Transferase
SRR342019_TR23181_c0_g1_i1_len=4456	GLR34_ARATH	Q:1032-3785,H:3-932	63.25%ID	E:0	Glutamate receptor 3.4	PF13458.3^Peripla_BP_6^Periplasmic binding protein^53-412^E:3e-22`PF01094.25^ANF_receptor^Receptor family ligand binding region^60-417^E:2e-82`PF10613.6^Lig_chan-Glu_bd^Ligated ion channel L-glutamate- and glycine-binding site^483-581^E:1.3e-10`PF00497.17^SBP_bac_3^Bacterial extracellular solute-binding proteins, family 3^491-820^E:1.8e-21`PF00060.23^Lig_chan^Ligand-gated ion channel^598-852^E:3.2e-36	0,012	1,294	0	2,615	0	2,567	0	2,834	1	-0,122	GLR34_ARATH	Glutamate receptor 3.4 (AtGLR4) (Ligand-gated ion channel 3.4)	GLR3.4 GLR4 GLUR3 At1g05200 YUP8H12.19	Arabidopsis thaliana (Mouse-ear cress)		Alternative splicing; Cell membrane; Chloroplast; Complete proteome; Glycoprotein; Ion channel; Ion transport; Ligand-gated ion channel; Membrane; Plastid; Receptor; Reference proteome; Signal; Stress response; Transmembrane; Transmembrane helix; Transport
SRR342019_TR23718_c0_g2_i1_len=2559	AIM1_ARATH	Q:2329-212,H:7-712	74.65%ID	E:0	Peroxisomal fatty acid beta-oxidation multifunctional protein AIM1	PF00378.17^ECH_1^Enoyl-CoA hydratase/isomerase^84-285^E:5.8e-37`PF16113.2^ECH_2^Enoyl-CoA hydratase/isomerase^89-270^E:6.9e-20`PF02737.15^3HCDH_N^3-hydroxyacyl-CoA dehydrogenase, NAD binding domain^381-559^E:8.4e-58`PF00725.19^3HCDH^3-hydroxyacyl-CoA dehydrogenase, C-terminal domain^562-655^E:3.8e-19`PF00725.19^3HCDH^3-hydroxyacyl-CoA dehydrogenase, C-terminal domain^694-774^E:0.00023	0,135	0,614	0	3,914	0,001	1,591	0	1,718	1	-0,229	AIM1_ARATH	Peroxisomal fatty acid beta-oxidation multifunctional protein AIM1 (Protein ABNORMAL INFLORESCENCE MERISTEM 1) (AtAIM1) [Includes: Enoyl-CoA hydratase/3-2-trans-enoyl-CoA isomerase/3-hydroxybutyryl-CoA epimerase (EC 4.2.1.17) (EC 5.1.2.3) (EC 5.3.3.8); 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35)]	AIM1 At4g29010 F19B15.40	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Lipid metabolism; fatty acid beta-oxidation.	Complete proteome; Fatty acid metabolism; Isomerase; Lipid metabolism; Lyase; Multifunctional enzyme; NAD; Oxidoreductase; Peroxisome; Reference proteome
SRR342019_TR27096_c0_g1_i1_len=1477	DBR_TOBAC	Q:259-1290,H:1-343	82.56%ID	E:0	2-alkenal reductase (NADP(+)-dependent)	PF16884.2^ADH_N_2^N-terminal domain of oxidoreductase^8-116^E:1.6e-26`PF00107.23^ADH_zinc_N^Zinc-binding dehydrogenase^166-293^E:1.6e-24`PF13602.3^ADH_zinc_N_2^Zinc-binding dehydrogenase^200-337^E:1.7e-07	0,745	0,112	0	1,188	0	0,917	0,001	0,88	0,458	0,234	DBR_TOBAC	2-alkenal reductase (NADP(+)-dependent) (EC 1.3.1.102) (Alkenal double bound reductase) (Allyl-alcohol dehydrogenase) (EC 1.1.1.54) (Allylic alcohol dehydrogenase 1) (allyl-ADH1) (Flavin-free double bond reductase) (NtDBR) (Pulegone reductase) (NtRed-1)	DBR	Nicotiana tabacum (Common tobacco)		3D-structure; Direct protein sequencing; NADP; Oxidoreductase
SRR342019_TR32476_c0_g1_i1_len=1833	UFOG6_FRAAN	Q:1610-198,H:3-478	52.99%ID	E:8e-176	UDP-glucose flavonoid 3-O-glucosyltransferase 6 {ECO:0000303|PubMed:18487633}	PF00201.15^UDPGT^UDP-glucoronosyl and UDP-glucosyl transferase^260-397^E:1.3e-21	0,38	0,556	0	2,736	0	0,933	0	1,339	0,239	1,104	UFOG6_FRAAN	UDP-glucose flavonoid 3-O-glucosyltransferase 6 (EC 2.4.1.91) (Flavonol 3-O-glucosyltransferase 6) (FaGT6)	GT6	Fragaria ananassa (Strawberry)		Glycosyltransferase; Transferase
SRR342019_TR36177_c0_g4_i1_len=741	NA	NA	NA	NA	NA	PF13833.3^EF-hand_8^EF-hand domain pair^21-45^E:0.031`PF00036.29^EF-hand_1^EF hand^23-50^E:4.7e-07`PF13405.3^EF-hand_6^EF-hand domain^23-50^E:8.9e-07`PF13202.3^EF-hand_5^EF hand^24-46^E:2.1e-06`PF13202.3^EF-hand_5^EF hand^64-83^E:0.012	0,286	0,899	0	2,664	0	2,514	0	2,654	0,212	-1,069	.	.	.	.	.	.
SRR342019_TR39103_c0_g2_i1_len=1363	SRG1_ARATH	Q:1291-347,H:17-333	38.51%ID	E:2e-68	Protein SRG1	PF14226.3^DIOX_N^non-haem dioxygenase in morphine synthesis N-terminal^52-158^E:4.3e-24`PF03171.17^2OG-FeII_Oxy^2OG-Fe(II) oxygenase superfamily^206-303^E:5.5e-28	0,254	3,607	0	6,024	0	7,465	0	5,217	1	-1,033	SRG1_ARATH	Protein SRG1 (AtSRG1) (Protein SENESCENCE-RELATED GENE 1)	SRG1 At1g17020 F20D23.28 F6I1.30	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Iron; Metal-binding; Oxidoreductase; Reference proteome
SRR342022_TR1215_c4_g6_i6_len=760	PRS2_SOLTU	Q:671-204,H:1-155	36.88%ID	E:2e-25	Pathogenesis-related protein STH-2	PF00407.16^Bet_v_1^Pathogenesis-related protein Bet v I family^30-179^E:1.1e-11	0,3	0,239	0	3,053	0	1,465	0	1,496	1	0,073	PRS2_SOLTU	Pathogenesis-related protein STH-2	STH-2	Solanum tuberosum (Potato)		Complete proteome; Pathogenesis-related protein; Plant defense; Reference proteome
SRR342022_TR2129_c0_g2_i2_len=1572	PLA17_ARATH	Q:311-1387,H:148-514	69.65%ID	E:0	Phospholipase A1-Igamma3, chloroplastic	PF01764.22^Lipase_3^Lipase (class 3)^103-259^E:1.2e-39	0,017	1,238	0	3,572	0	2,511	0	2,891	0,107	0,798	PLA17_ARATH	Phospholipase A1-Igamma3, chloroplastic (EC 3.1.1.-)	At1g51440 F5D21.19	Arabidopsis thaliana (Mouse-ear cress)		Chloroplast; Complete proteome; Hydrolase; Lipid degradation; Lipid metabolism; Plastid; Reference proteome; Transit peptide
SRR342022_TR2238_c7_g1_i2_len=2722	SABP2_TOBAC	Q:1032-262,H:5-259	44.15%ID	E:6e-61	Salicylic acid-binding protein 2	PF12146.5^Hydrolase_4^Serine aminopeptidase, S33^147-270^E:1.5e-07`PF00561.17^Abhydrolase_1^alpha/beta hydrolase fold^150-260^E:1.4e-10`PF12697.4^Abhydrolase_6^Alpha/beta hydrolase family^151-225^E:6.2e-06	0,732	0,897	0	1,548	0	1,274	0	1,982	1	1,354	SABP2_TOBAC	Salicylic acid-binding protein 2 (NtSABP2) (EC 3.1.1.-) (Methyl salicylate esterase)	SABP2	Nicotiana tabacum (Common tobacco)		3D-structure; Hydrolase; Immunity; Innate immunity; Plant defense
SRR342022_TR2984_c0_g5_i6_len=3797	DOX1_ARATH	Q:58-1767,H:1-565	71.28%ID	E:0	Alpha-dioxygenase 1	PF02403.19^Seryl_tRNA_N^Seryl-tRNA synthetase N-terminal domain^1-112^E:1.1e-26`PF00587.22^tRNA-synt_2b^tRNA synthetase class II core domain (G, H, P, S and T)^221-407^E:1.6e-35	0,76	0,566	0	3,896	0	5,33	0	6,15	0,517	-0,806	DOX1_ARATH	Alpha-dioxygenase 1 (Alpha DOX1) (EC 1.14.99.-) (Fatty acid dioxygenase AlphaDOX1) (Pathogen-induced oxygenase) (Plant alpha dioxygenase 1)	DOX1 DIOX1 PADOX-1 PIOX At3g01420 T13O15.6	Arabidopsis thaliana (Mouse-ear cress)		3D-structure; Complete proteome; Dioxygenase; Fatty acid biosynthesis; Fatty acid metabolism; Glycoprotein; Hypersensitive response; Iron; Lipid biosynthesis; Lipid metabolism; Metal-binding; Oxidoreductase; Oxylipin biosynthesis; Peroxidase; Plant defense; Reference proteome; Signal
SRR342022_TR6106_c0_g1_i1_len=509	NA	NA	NA	NA	NA	.	0,299	1,615	0	7,181	0	4,567	0	5,256	1	3,206	.	.	.	.	.	.
SRR342022_TR12801_c0_g3_i13_len=1371	MTDH_FRAAN	Q:1270-248,H:15-355	64.52%ID	E:2e-146	Probable mannitol dehydrogenase	PF08240.9^ADH_N^Alcohol dehydrogenase GroES-like domain^5-90^E:1.3e-15`PF00107.23^ADH_zinc_N^Zinc-binding dehydrogenase^134-257^E:2.2e-16	0,002	1,722	0	4,416	0	3,664	0	2,475	1	-0,015	MTDH_FRAAN	Probable mannitol dehydrogenase (EC 1.1.1.255) (NAD-dependent mannitol dehydrogenase)	CAD	Fragaria ananassa (Strawberry)		Metal-binding; NAD; Oxidoreductase; Zinc
SRR342022_TR13754_c0_g1_i2_len=952	RAE1C_ARATH	Q:263-868,H:15-216	93.07%ID	E:1e-118	Ras-related protein RABE1c	PF00025.18^Arf^ADP-ribosylation factor family^16-163^E:2.1e-15`PF00071.19^Ras^Ras family^17-178^E:1.6e-66`PF08477.10^Roc^Ras of Complex, Roc, domain of DAPkinase^17-132^E:4.6e-35`PF04670.9^Gtr1_RagA^Gtr1/RagA G protein conserved region^17-132^E:4.5e-05`PF01926.20^MMR_HSR1^50S ribosome-binding GTPase^18-128^E:4.7e-05	0,086	-0,97	0	7,651	0	7,822	0	7,548	0,049	1,391	RAE1C_ARATH	Ras-related protein RABE1c (AtRABE1c) (Ras-related protein Ara-3) (Ras-related protein Rab8A) (AtRab8A)	RABE1C ARA-3 RAB8A At3g46060 F12M12.30	Arabidopsis thaliana (Mouse-ear cress)		Cell membrane; Complete proteome; GTP-binding; Golgi apparatus; Lipoprotein; Membrane; Nucleotide-binding; Prenylation; Protein transport; Reference proteome; Transport
SRR342022_TR13846_c1_g2_i2_len=1683	FRI1_ARATH	Q:1545-790,H:6-255	65.08%ID	E:1e-96	Ferritin-1, chloroplastic	PF00210.21^Ferritin^Ferritin-like domain^95-238^E:6.1e-32	0,443	0,241	0	2,078	0	1,737	0	1,646	1	-0,407	FRI1_ARATH	Ferritin-1, chloroplastic (AtFer1) (EC 1.16.3.1)	FER1 At5g01600 F7A7.120	Arabidopsis thaliana (Mouse-ear cress)		Chloroplast; Complete proteome; Iron; Iron storage; Metal-binding; Oxidoreductase; Plastid; Reference proteome; Transit peptide
SRR342022_TR18252_c2_g4_i1_len=1124	NA	NA	NA	NA	NA	PF06747.10^CHCH^CHCH domain^158-192^E:1.8e-08	0,44	-0,198	0	0,892	0	1,217	0	1,063	0,184	-0,329	.	.	.	.	.	.
SRR342022_TR23364_c0_g1_i1_len=3450	CLPD_ARATH	Q:1412-3112,H:375-943	73.86%ID	E:0	Chaperone protein ClpD, chloroplastic {ECO:0000303|PubMed:11299370}	PF07724.11^AAA_2^AAA domain (Cdc48 subfamily)^226-401^E:9.5e-52`PF00158.23^Sigma54_activat^Sigma-54 interaction domain^228-346^E:0.00017`PF07728.11^AAA_5^AAA domain (dynein-related subfamily)^231-351^E:7.3e-12`PF00004.26^AAA^ATPase family associated with various cellular activities (AAA)^231-339^E:1e-06`PF10431.6^ClpB_D2-small^C-terminal, D2-small domain, of ClpB protein^407-486^E:7.4e-23	0,04	1,339	0	2,475	0	2,571	0	2,502	1	-0,064	CLPD_ARATH	Chaperone protein ClpD, chloroplastic (EC 3.6.1.3) (ATP-dependent Clp protease ATP-binding subunit ClpD homolog) (Casein lytic proteinase D) (ERD1 protein) (Protein EARLY RESPONSIVE TO DEHYDRATION 1) (Protein SENESCENCE ASSOCIATED GENE 15)	CLPD ERD1 SAG15 At5g51070 K3K7.27	Arabidopsis thaliana (Mouse-ear cress)		ATP-binding; Chaperone; Chloroplast; Complete proteome; Hydrolase; Nucleotide-binding; Plastid; Reference proteome; Repeat; Stress response; Transit peptide
SRR342022_TR27951_c0_g1_i1_len=798	NA	NA	NA	NA	NA	PF00582.23^Usp^Universal stress protein family^48-193^E:2.9e-26	0,051	1,135	0	2,636	0	2,542	0	2,234	1	-1,281	.	.	.	.	.	.
SRR342022_TR30528_c1_g2_i1_len=2981	MSL3_ARATH	Q:845-2551,H:42-659	57.84%ID	E:0	Mechanosensitive ion channel protein 3, chloroplastic	PF00924.15^MS_channel^Mechanosensitive ion channel^241-448^E:5.7e-30	0,001	1,348	0	3,09	0	2,642	0	2,498	1	0,451	MSL3_ARATH	Mechanosensitive ion channel protein 3, chloroplastic (Mechanosensitive channel of small conductance-like 3) (MscS-Like protein 3)	MSL3 At1g58200 F16M22.2 T18I24.11	Arabidopsis thaliana (Mouse-ear cress)		Chloroplast; Complete proteome; Ion channel; Ion transport; Membrane; Phosphoprotein; Plastid; Reference proteome; Transit peptide; Transmembrane; Transmembrane helix; Transport
SRR342022_TR30552_c2_g5_i5_len=4084	NA	NA	NA	NA	NA	PF07712.9^SURNod19^Stress up-regulated Nod 19^34-404^E:4.3e-186	0,298	0,679	0	2,891	0	2,512	0	2,536	0,832	-0,21	.	.	.	.	.	.
SRR342022_TR32777_c0_g2_i1_len=1741	RFS6_ARATH	Q:60-1610,H:261-749	73.17%ID	E:0	Probable galactinol--sucrose galactosyltransferase 6	PF05691.9^Raffinose_syn^Raffinose synthase or seed imbibition protein Sip1^9-518^E:8.1e-222	0,034	0,684	0	2,24	0	1,733	0	1,662	0,085	0,472	RFS6_ARATH	Probable galactinol--sucrose galactosyltransferase 6 (EC 2.4.1.82) (Protein DARK INDUCIBLE 10) (Raffinose synthase 6)	RFS6 DIN10 RS6 At5g20250 F5O24.140	Arabidopsis thaliana (Mouse-ear cress)		Alternative splicing; Carbohydrate metabolism; Complete proteome; Glycosyltransferase; Reference proteome; Transferase
SRR342022_TR33006_c0_g1_i1_len=616	ASPGB_ARATH	Q:153-614,H:3-156	85.71%ID	E:5e-93	Probable isoaspartyl peptidase/L-asparaginase 2	PF01112.15^Asparaginase_2^Asparaginase^5-155^E:8.3e-53	0,165	-0,762	0	5,674	0	4,922	0	6,843	0,254	-2,687	ASPGB_ARATH	Probable isoaspartyl peptidase/L-asparaginase 2 (EC 3.4.19.5) (L-asparagine amidohydrolase 2) [Cleaved into: Isoaspartyl peptidase/L-asparaginase 2 subunit alpha; Isoaspartyl peptidase/L-asparaginase 2 subunit beta]	At3g16150 MSL1.19	Arabidopsis thaliana (Mouse-ear cress)		Alternative splicing; Autocatalytic cleavage; Complete proteome; Hydrolase; Protease; Reference proteome
SRR342022_TR34054_c2_g1_i1_len=1654	NA	NA	NA	NA	NA	PF04640.11^PLATZ^PLATZ transcription factor^28-99^E:1.9e-29	0,052	1,621	0	2,472	0	2,55	0	2,562	1	0,253	.	.	.	.	.	.
SRR342022_TR34536_c1_g4_i1_len=2142	C98A2_SOYBN	Q:1644-181,H:22-509	85.66%ID	E:0	Cytochrome P450 98A2	PF00067.19^p450^Cytochrome P450^29-481^E:3.2e-102	0,115	0,742	0	3,582	0,001	1,106	0	1,772	0,278	0,759	C98A2_SOYBN	Cytochrome P450 98A2 (EC 1.14.-.-)	CYP98A2	Glycine max (Soybean) (Glycine hispida)		Complete proteome; Heme; Iron; Membrane; Metal-binding; Monooxygenase; Oxidoreductase; Reference proteome; Transmembrane; Transmembrane helix
SRR342023_TR798_c1_g19_i3_len=1000	MES9_ARATH	Q:175-942,H:2-254	42.97%ID	E:2e-64	Methylesterase 9	PF00561.17^Abhydrolase_1^alpha/beta hydrolase fold^45-284^E:4.1e-15`PF12697.4^Abhydrolase_6^Alpha/beta hydrolase family^46-289^E:8.1e-17`PF12146.5^Hydrolase_4^Serine aminopeptidase, S33^46-156^E:1.5e-12	0,816	-0,154	0	4,227	0	2,563	0	3,506	0,001	1,522	MES9_ARATH	Methylesterase 9 (AtMES9) (EC 3.1.1.-)	MES9 At4g37150 AP22.78 C7A10.210	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Hydrolase; Immunity; Innate immunity; Plant defense; Reference proteome
SRR342023_TR1587_c2_g1_i2_len=4884	PHT14_ARATH	Q:2814-4337,H:1-508	84.45%ID	E:0	Inorganic phosphate transporter 1-4	PF00083.21^Sugar_tr^Sugar (and other) transporter^25-515^E:5e-49`PF07690.13^MFS_1^Major Facilitator Superfamily^69-457^E:2.1e-21	0,066	1,022	0	4,307	0	7,933	0	6,842	1	-0,773	PHT14_ARATH	Inorganic phosphate transporter 1-4 (AtPht1;4) (H(+)/Pi cotransporter)	PHT1-4 PHT4 PT2 At2g38940 T7F6.11	Arabidopsis thaliana (Mouse-ear cress)		Cell membrane; Complete proteome; Membrane; Phosphate transport; Phosphoprotein; Reference proteome; Symport; Transmembrane; Transmembrane helix; Transport
SRR342023_TR1698_c2_g1_i1_len=1005	KIC_ARATH	Q:727-431,H:21-119	72.73%ID	E:3e-45	Calcium-binding protein KIC	PF13833.3^EF-hand_8^EF-hand domain pair^43-94^E:5.3e-16	0,237	0,44	0	4,728	0	2,816	0	2,473	1	0	KIC_ARATH	Calcium-binding protein KIC (KCBP-interacting calcium-binding protein)	KIC At2g46600 F13A10.13	Arabidopsis thaliana (Mouse-ear cress)		3D-structure; Calcium; Complete proteome; Metal-binding; Reference proteome
SRR342023_TR2241_c0_g3_i1_len=522	NA	NA	NA	NA	NA	.	0,76	-0,576	0	4,26	0	3,812	0	4,063	0,732	0,769	.	.	.	.	.	.
SRR342023_TR16666_c0_g1_i5_len=4417	LOX5_ARATH	Q:228-2852,H:34-886	67.99%ID	E:0	Linoleate 9S-lipoxygenase 5, chloroplastic	PF01477.20^PLAT^PLAT/LH2 domain^81-173^E:2.1e-15`PF00305.16^Lipoxygenase^Lipoxygenase^187-624^E:2.2e-197	0,866	0,085	0	2,759	0	2,029	0	3,36	1	1,128	LOX5_ARATH	Linoleate 9S-lipoxygenase 5, chloroplastic (EC 1.13.11.58) (Lipoxygenase 5) (AtLOX5)	LOX5 At3g22400 MCB17.13	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Lipid metabolism; oxylipin biosynthesis. {ECO:0000255|PROSITE-ProRule:PRU00726}.	Chloroplast; Complete proteome; Dioxygenase; Fatty acid biosynthesis; Fatty acid metabolism; Iron; Lipid biosynthesis; Lipid metabolism; Metal-binding; Oxidoreductase; Oxylipin biosynthesis; Plastid; Reference proteome
SRR342023_TR18599_c2_g5_i10_len=3676	DGAT2_ARATH	Q:745-1554,H:46-314	71.85%ID	E:5e-135	Diacylglycerol O-acyltransferase 2	PF03547.15^Mem_trans^Membrane transport protein^11-405^E:7.7e-65	0,017	2,06	0	3,653	0	5,904	0	5,67	0,239	1,585	DGAT2_ARATH	Diacylglycerol O-acyltransferase 2 (EC 2.3.1.20)	DGAT2 At3g51520 F26O13.160	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Glycerolipid metabolism; triacylglycerol biosynthesis.	Acyltransferase; Complete proteome; Endoplasmic reticulum; Glycerol metabolism; Glycoprotein; Lipid biosynthesis; Lipid metabolism; Membrane; Reference proteome; Transferase; Transmembrane; Transmembrane helix
SRR342023_TR19871_c0_g1_i2_len=1614	BBD1_ARATH	Q:551-1231,H:94-320	77.97%ID	E:1e-127	Bifunctional nuclease 1	PF02577.11^DNase-RNase^Bifunctional nuclease^44-158^E:2.2e-22	0,539	0,221	0	2,922	0	2,861	0	3,99	0,899	0,071	BBD1_ARATH	Bifunctional nuclease 1 (AtBBD1) (EC 3.1.-.-)	BBD1 At1g75380 F1B16.9 F1B16_15	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Hydrolase; Nuclease; Nucleus; Reference proteome
SRR342023_TR19929_c1_g1_i2_len=1377	PT504_ARATH	Q:334-1245,H:6-309	81.25%ID	E:0	Probable sugar phosphate/phosphate translocator At5g04160	PF08449.8^UAA^UAA transporter family^17-310^E:4.9e-14`PF03151.13^TPT^Triose-phosphate Transporter family^20-309^E:7.3e-46	0,763	-0,257	0	2,096	0	3,312	0	4,943	1	-0,046	PT504_ARATH	Probable sugar phosphate/phosphate translocator At5g04160	At5g04160 F21E1.80	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Membrane; Pyruvate; Reference proteome; Sugar transport; Transmembrane; Transmembrane helix; Transport
SRR342023_TR22818_c0_g2_i1_len=446	NA	NA	NA	NA	NA	.	0,112	1,129	0	4,739	0	4,862	0	5,38	0,581	-0,356	.	.	.	.	.	.
SRR342023_TR27035_c0_g1_i1_len=2028	ERDL4_ARATH	Q:304-1767,H:1-488	77.71%ID	E:0	Sugar transporter ERD6-like 4	PF00083.21^Sugar_tr^Sugar (and other) transporter^52-484^E:2.4e-99`PF07690.13^MFS_1^Major Facilitator Superfamily^62-435^E:7.3e-25	0,398	0,403	0	2,003	0	1,578	0	2,22	0,847	0,14	ERDL4_ARATH	Sugar transporter ERD6-like 4	At1g19450 F18O14.22	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Membrane; Reference proteome; Sugar transport; Transmembrane; Transmembrane helix; Transport
SRR342023_TR28027_c0_g2_i1_len=1586	NA	NA	NA	NA	NA	.	0,328	0,414	0	3,153	0	4,218	0	4,89	0,904	0,1	.	.	.	.	.	.
SRR342023_TR28680_c0_g1_i3_len=1608	C71DC_CATRO	Q:744-142,H:296-492	72.14%ID	E:1e-89	Tabersonine 16-hydroxylase	PF00067.19^p450^Cytochrome P450^1-173^E:8.4e-59	0,002	1,226	0,001	1,168	0	2,253	0	1,827	0,316	0,659	C71DC_CATRO	Tabersonine 16-hydroxylase (EC 1.14.13.73) (Cytochrome P450 71D12) (Fragment)	CYP71D12	Catharanthus roseus (Madagascar periwinkle) (Vinca rosea)	PATHWAY: Alkaloid biosynthesis; vindoline biosynthesis; vindoline from tabersonine: step 1/6.	Endoplasmic reticulum; Heme; Iron; Metal-binding; Monooxygenase; NADP; Oxidoreductase
SRR342023_TR29509_c0_g3_i3_len=2067	C7D55_HYOMU	Q:228-1592,H:49-502	52.3%ID	E:5e-163	Premnaspirodiene oxygenase	PF00067.19^p450^Cytochrome P450^33-486^E:1.3e-101	0,004	0,803	0	1,271	0	1,832	0	1,779	0,007	0,876	C7D55_HYOMU	Premnaspirodiene oxygenase (HPO) (EC 1.14.13.121) (Cytochrome P450 71D55)	CYP71D55	Hyoscyamus muticus (Egyptian henbane)		Heme; Iron; Membrane; Metal-binding; Monooxygenase; NADP; Oxidoreductase; Transmembrane; Transmembrane helix
SRR342023_TR29531_c0_g9_i2_len=1198	TSJT1_TOBAC	Q:186-626,H:1-148	44.3%ID	E:3e-35	Stem-specific protein TSJT1	PF12481.5^DUF3700^Aluminium induced protein^63-287^E:2.6e-89`PF13522.3^GATase_6^Glutamine amidotransferase domain^113-229^E:2.5e-08`PF13537.3^GATase_7^Glutamine amidotransferase domain^121-233^E:5.9e-11	0,412	0,213	0	1,361	0	1,12	0	1,458	0,002	0,986	TSJT1_TOBAC	Stem-specific protein TSJT1	TSJT1	Nicotiana tabacum (Common tobacco)		
SRR342023_TR30981_c0_g1_i1_len=940	BH147_ARATH	Q:395-832,H:49-201	56.69%ID	E:3e-46	Transcription factor bHLH147	.	0,007	1,004	0	2,369	0	1,856	0	2,028	1	-0,07	BH147_ARATH	Transcription factor bHLH147 (ATBS1 interacting factor 3) (Basic helix-loop-helix protein 147) (AtbHLH147) (bHLH 147) (Transcription factor EN 142) (bHLH transcription factor bHLH147)	BHLH147 AIF3 EN142 At3g17100 K14A17.17	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; DNA-binding; Nucleus; Reference proteome; Transcription; Transcription regulation
SRR342023_TR31426_c6_g4_i1_len=2314	TT12_ARATH	Q:1448-2062,H:289-493	44.88%ID	E:2e-41	.	PF01554.15^MatE^MatE^40-198^E:9.9e-24	0,76	0,698	0	2,214	0	3,258	0	3,689	1	-0,149	DTX41_ARATH	Protein DETOXIFICATION 41 (AtDTX41) (Multidrug and toxic compound extrusion protein 41) (MATE protein 41) (Protein TANNIN-DEFICIENT SEED 3) (Protein TRANSPARENT TESTA 12)	DTX41 TDS3 TT12 At3g59030 F17J16_80	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Secondary metabolite biosynthesis; flavonoid biosynthesis.	Antiport; Complete proteome; Flavonoid biosynthesis; Membrane; Reference proteome; Transmembrane; Transmembrane helix; Transport; Vacuole
SRR342023_TR31454_c5_g6_i1_len=732	PRS2_SOLTU	Q:660-205,H:1-155	36.94%ID	E:4e-24	Pathogenesis-related protein STH-2	PF00407.16^Bet_v_1^Pathogenesis-related protein Bet v I family^25-171^E:4e-13	0,002	0,704	0	2,569	0	1,524	0	1,546	1	0,342	PRS2_SOLTU	Pathogenesis-related protein STH-2	STH-2	Solanum tuberosum (Potato)		Complete proteome; Pathogenesis-related protein; Plant defense; Reference proteome
SRR646572_TR25887_c0_g2_i5_len=1422	HS217_ARATH	Q:645-1154,H:9-184	54.55%ID	E:6e-59	21.7 kDa class VI heat shock protein	PF00011.18^HSP20^Hsp20/alpha crystallin family^87-179^E:1.4e-10	0,094	1,158	0	1,905	0	1,854	0	1,828	1	0,126	HS217_ARATH	21.7 kDa class VI heat shock protein (21.7 kDa heat shock protein) (AtHsp21.7)	HSP21.7 At5g54660 MRB17.16	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Cytoplasm; Reference proteome; Stress response
SRR646572_TR35126_c0_g1_i1_len=1004	NA	NA	NA	NA	NA	PF12507.5^HCMV_UL139^Human Cytomegalovirus UL139 protein^22-139^E:1.7e-20	0,025	1,981	0	4,343	0	5,187	0	6,247	1	-3,501	.	.	.	.	.	.
SRR646572_TR35841_c0_g1_i1_len=752	NLTP_HELAN	Q:622-272,H:1-116	52.54%ID	E:6e-27	Non-specific lipid-transfer protein	PF14368.3^LTP_2^Probable lipid transfer^15-105^E:1.4e-05`PF00234.19^Tryp_alpha_amyl^Protease inhibitor/seed storage/LTP family^30-113^E:1e-07	0,341	0,207	0	0,899	0	2,823	0	1,673	0,146	0,506	NLTP_HELAN	Non-specific lipid-transfer protein (LTP) (NsLTP) (SDI-9)		Helianthus annuus (Common sunflower)		Disulfide bond; Lipid-binding; Signal; Transport
SRR646596_TR595_c0_g2_i1_len=1576	BH014_ARATH	Q:1381-143,H:39-421	35.22%ID	E:6e-59	Transcription factor bHLH14	PF14215.3^bHLH-MYC_N^bHLH-MYC and R2R3-MYB transcription factors N-terminal^26-185^E:1.4e-33`PF00010.23^HLH^Helix-loop-helix DNA-binding domain^260-305^E:2.1e-10	1	0,358	0	5,634	0	10,779	0	11,579	1	0	BH014_ARATH	Transcription factor bHLH14 (Basic helix-loop-helix protein 14) (AtbHLH14) (bHLH 14) (Transcription factor EN 33) (bHLH transcription factor bHLH014)	BHLH14 EN33 At4g00870 A_TM018A10.7 T18A10.17	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; DNA-binding; Nucleus; Reference proteome; Transcription; Transcription regulation
SRR646596_TR1244_c0_g1_i11_len=3593	SYK_ARATH	Q:292-1899,H:80-615	81.34%ID	E:0	.	PF01336.22^tRNA_anti-codon^OB-fold nucleic acid binding domain^88-166^E:2.9e-13`PF00152.17^tRNA-synt_2^tRNA synthetases class II (D, K and N)^206-555^E:2.8e-82	0,955	0,038	0	1,743	0	3,068	0	2,836	0,575	-0,198	SYKC_ARATH	Lysine--tRNA ligase, cytoplasmic (EC 6.1.1.6) (Lysyl-tRNA synthetase) (LysRS) (Lysyl-tRNA synthetase 1) (AtKRS-1)	At3g11710 T19F11.11	Arabidopsis thaliana (Mouse-ear cress)		ATP-binding; Acetylation; Aminoacyl-tRNA synthetase; Calcium; Coiled coil; Complete proteome; Cytoplasm; DNA-binding; Ligase; Metal-binding; Nucleotide-binding; Protein biosynthesis; Reference proteome
SRR646596_TR1756_c1_g1_i1_len=932	NA	NA	NA	NA	NA	PF01221.15^Dynein_light^Dynein light chain type 1^65-158^E:2.3e-26	1	2,138	0	7,114	0	5,34	0	6,238	1	0,555	.	.	.	.	.	.
SRR646596_TR2215_c0_g1_i1_len=805	IPRT1_CATRO	Q:152-631,H:1-157	68.75%ID	E:2e-66	Probable intracellular pathogenesis-related protein T1	PF00407.16^Bet_v_1^Pathogenesis-related protein Bet v I family^5-157^E:1.1e-19	0,76	0,576	0	7,742	0	7,24	0	3,097	0,027	-2,429	IPRT1_CATRO	Probable intracellular pathogenesis-related protein T1	PCKR3	Catharanthus roseus (Madagascar periwinkle) (Vinca rosea)		Direct protein sequencing; Glycoprotein; Pathogenesis-related protein; Plant defense
SRR646596_TR4674_c0_g1_i1_len=1491	ACMAT_VITLA	Q:1365-34,H:10-449	48.89%ID	E:3e-151	Methanol O-anthraniloyltransferase	PF02458.12^Transferase^Transferase family^6-437^E:6.3e-68	0,094	1,235	0	5,457	0	6,815	0	7,492	0,16	1,326	ACMAT_VITLA	Methanol O-anthraniloyltransferase (EC 2.3.1.232) (Anthraniloyl-CoA:methanol acyltransferase) (Benzyl alcohol O-benzoyltransferase) (EC 2.3.1.196)	AMAT	Vitis labrusca (Concord grape)		Acyltransferase; Direct protein sequencing; Transferase
SRR646596_TR4958_c0_g1_i3_len=2289	TRXH2_TOBAC	Q:763-503,H:30-116	82.76%ID	E:2e-42	Thioredoxin H-type 2	.	0,381	2,69	0	6,128	0	3,311	0	3,594	1	0,101	TRXH2_TOBAC	Thioredoxin H-type 2 (Trx-H2)		Nicotiana tabacum (Common tobacco)		Cytoplasm; Disulfide bond; Electron transport; Redox-active center; Transport
SRR646596_TR5611_c0_g1_i1_len=2176	NA	NA	NA	NA	NA	.	0,045	1,547	0	4,445	0	4,941	0	5,779	0,732	-0,713	.	.	.	.	.	.
SRR646596_TR8408_c0_g1_i1_len=1358	COMT1_CAPAN	Q:165-1220,H:9-359	54.55%ID	E:9e-133	Caffeic acid 3-O-methyltransferase	PF08100.8^Dimerisation^Dimerisation domain^32-83^E:1.4e-19`PF00891.15^Methyltransf_2^O-methyltransferase^128-346^E:3.4e-73	0,158	1,681	0	7,647	0	9,866	0	10,755	1	2,501	COMT1_CAPAN	Caffeic acid 3-O-methyltransferase (CAOMT) (COMT) (EC 2.1.1.68) (S-adenosysl-L-methionine:caffeic acid 3-O-methyltransferase)	COMT	Capsicum annuum (Bell pepper)	PATHWAY: Aromatic compound metabolism; phenylpropanoid biosynthesis.	Lignin biosynthesis; Methyltransferase; S-adenosyl-L-methionine; Transferase
SRR646596_TR12950_c0_g1_i2_len=1785	OPR3_SOLLC	Q:499-1647,H:9-390	79.37%ID	E:0	12-oxophytodienoate reductase 3	PF00724.17^Oxidored_FMN^NADH:flavin oxidoreductase / NADH oxidase family^10-359^E:4.7e-87	0,029	0,756	0	4,044	0	1,886	0	2,659	0,173	-0,674	OPR3_SOLLC	12-oxophytodienoate reductase 3 (EC 1.3.1.42) (12-oxophytodienoate-10,11-reductase 3) (OPDA-reductase 3) (LeOPR3)	OPR3	Solanum lycopersicum (Tomato) (Lycopersicon esculentum)	PATHWAY: Lipid metabolism; oxylipin biosynthesis.	3D-structure; Complete proteome; FMN; Fatty acid biosynthesis; Fatty acid metabolism; Flavoprotein; Lipid biosynthesis; Lipid metabolism; NADP; Oxidoreductase; Oxylipin biosynthesis; Peroxisome; Reference proteome
SRR646596_TR15830_c3_g1_i27_len=1817	FAD3E_TOBAC	Q:477-1571,H:12-374	76.16%ID	E:0	Omega-3 fatty acid desaturase, endoplasmic reticulum	PF11960.5^DUF3474^Domain of unknown function (DUF3474)^6-62^E:7.5e-26`PF00487.21^FA_desaturase^Fatty acid desaturase^77-328^E:4.4e-33	0,44	0,948	0	4,506	0	3,79	0	4,436	0,593	-0,669	FAD3E_TOBAC	Omega-3 fatty acid desaturase, endoplasmic reticulum (EC 1.14.19.-)	FAD3	Nicotiana tabacum (Common tobacco)	PATHWAY: Lipid metabolism; polyunsaturated fatty acid biosynthesis.	Endoplasmic reticulum; Fatty acid biosynthesis; Fatty acid metabolism; Lipid biosynthesis; Lipid metabolism; Membrane; Oxidoreductase; Transmembrane; Transmembrane helix
SRR646596_TR18446_c0_g1_i2_len=3570	NA	NA	NA	NA	NA	PF12507.5^HCMV_UL139^Human Cytomegalovirus UL139 protein^25-142^E:3.2e-21	0,076	2,389	0	5,604	0	6,615	0	7,389	1	0,826	.	.	.	.	.	.
SRR646596_TR19493_c0_g2_i1_len=747	NA	NA	NA	NA	NA	.	0,226	2,488	0	6,235	0	6,499	0	7,173	1	-0,541	.	.	.	.	.	.
SRR646596_TR19548_c2_g1_i1_len=1319	CLH2_ARATH	Q:71-916,H:5-299	42.14%ID	E:1e-55	Chlorophyllase-2, chloroplastic	PF07224.8^Chlorophyllase^Chlorophyllase^23-317^E:6.3e-90`PF12740.4^Chlorophyllase2^Chlorophyllase enzyme^53-301^E:3.7e-87`PF03403.10^PAF-AH_p_II^Platelet-activating factor acetylhydrolase, isoform II^60-99^E:2.4e-06	0,001	2,468	0	4,395	0	4,504	0	4,544	1	0,067	CLH2_ARATH	Chlorophyllase-2, chloroplastic (AtCLH2) (EC 3.1.1.14) (Chlorophyll-chlorophyllido hydrolase 2) (Chlase 2)	CLH2 At5g43860 MQD19.22	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Porphyrin-containing compound metabolism; chlorophyll degradation.	Chlorophyll catabolism; Chloroplast; Complete proteome; Hydrolase; Membrane; Plastid; Reference proteome; Transit peptide
SRR646596_TR20372_c1_g1_i8_len=3816	AFS1_MALDO	Q:2823-3686,H:274-563	54.3%ID	E:2e-95	(E,E)-alpha-farnesene synthase	PF03936.13^Terpene_synth_C^Terpene synthase family, metal binding domain^1-158^E:7.1e-43	1	2,176	0	9,401	0	9,488	0	10,228	1	0	AFS1_MALDO	(E,E)-alpha-farnesene synthase (MdASF1) (EC 4.2.3.46) (Prenyltransferase) (EC 2.5.1.-)	AFS1 AFAR	Malus domestica (Apple) (Pyrus malus)		Cytoplasm; Lyase; Magnesium; Manganese; Metal-binding; Potassium; Transferase
SRR646596_TR20372_c1_g1_i16_len=1360	TPS7_RICCO	Q:474-1358,H:50-340	48.47%ID	E:5e-82	Alpha-farnesene synthase	PF01397.18^Terpene_synth^Terpene synthase, N-terminal domain^5-102^E:7.3e-24`PF03936.13^Terpene_synth_C^Terpene synthase family, metal binding domain^135-235^E:3.2e-37	1	1,217	0	6,243	0	9,605	0	10,798	1	0	TPS7_RICCO	Alpha-farnesene synthase (EC 4.2.3.46) ((E,E)-alpha-farnesene synthase) (Terpene synthase 7) (RcSeTPS7)	TPS7 RCOM_0906600	Ricinus communis (Castor bean)		Complete proteome; Lyase; Magnesium; Metal-binding; Reference proteome
SRR646596_TR25164_c0_g1_i3_len=1751	NA	NA	NA	NA	NA	PF00892.17^EamA^EamA-like transporter family^172-297^E:3.3e-09`PF00892.17^EamA^EamA-like transporter family^307-456^E:2.6e-13	0,001	1,701	0	2,539	0	3,116	0	3,48	0,407	0,622	.	.	.	.	.	.
SRR646596_TR25397_c0_g2_i2_len=1677	TRPB_CAMAC	Q:1193-87,H:85-456	66.4%ID	E:0	Tryptophan synthase beta chain 2, chloroplastic	PF00291.22^PALP^Pyridoxal-phosphate dependent enzyme^154-481^E:1e-50	0,003	2,239	0	8,623	0	8,115	0	9,2	1	1,074	TRPB_CAMAC	Tryptophan synthase beta chain 2, chloroplastic (EC 4.2.1.20)	TSB	Camptotheca acuminata (Happy tree)	PATHWAY: Amino-acid biosynthesis; L-tryptophan biosynthesis; L-tryptophan from chorismate: step 5/5.	Amino-acid biosynthesis; Aromatic amino acid biosynthesis; Chloroplast; Lyase; Plastid; Pyridoxal phosphate; Transit peptide; Tryptophan biosynthesis
SRR646596_TR26170_c0_g1_i1_len=2541	TRPE_ARATH	Q:341-1489,H:50-434	68.05%ID	E:0	Anthranilate synthase alpha subunit 1, chloroplastic	PF04715.10^Anth_synt_I_N^Anthranilate synthase component I, N terminal region^153-307^E:7.3e-28`PF00425.15^Chorismate_bind^chorismate binding enzyme^368-502^E:3.4e-36	1	-0,302	0	4,243	0	4,791	0	5,537	1	0,315	TRPE_ARATH	Anthranilate synthase alpha subunit 1, chloroplastic (EC 4.1.3.27) (Anthranilate synthase component 1-1) (Anthranilate synthase component I-1) (Protein A-METHYL TRYPTOPHAN RESISTANT 1) (Protein JASMONATE-INDUCED DEFECTIVE LATERAL ROOT 1) (Protein TRYPTOPHAN BIOSYNTHESIS 5) (Protein WEAK ETHYLENE INSENSITIVE 2)	ASA1 AMT1 JDL1 TRP5 WEI2 At5g05730 MJJ3.14	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Amino-acid biosynthesis; L-tryptophan biosynthesis; L-tryptophan from chorismate: step 1/5.	Acetylation; Alternative splicing; Amino-acid biosynthesis; Aromatic amino acid biosynthesis; Chloroplast; Complete proteome; Lyase; Plastid; Reference proteome; Transit peptide; Tryptophan biosynthesis
SRR646596_TR28644_c0_g1_i2_len=2039	GPX1_PEA	Q:1895-1161,H:1-236	70.45%ID	E:5e-105	Phospholipid hydroperoxide glutathione peroxidase, chloroplastic	PF08534.7^Redoxin^Redoxin^85-160^E:4e-08`PF00255.16^GSHPx^Glutathione peroxidase^88-196^E:4.9e-44`PF00578.18^AhpC-TSA^AhpC/TSA family^88-150^E:4.3e-09	0,132	2,814	0	5,162	0	5,611	0	6,106	1	0,012	GPX1_PEA	Phospholipid hydroperoxide glutathione peroxidase, chloroplastic (PHGPx) (EC 1.11.1.12)		Pisum sativum (Garden pea)		Chloroplast; Oxidoreductase; Peroxidase; Plastid; Transit peptide
SRR646596_TR28759_c0_g2_i1_len=2422	DOX1_ARATH	Q:89-2119,H:1-639	65.74%ID	E:0	Alpha-dioxygenase 1	PF03098.12^An_peroxidase^Animal haem peroxidase^123-381^E:1.2e-55	0,517	0,975	0	4,672	0	7,802	0	8,592	0,299	-1,153	DOX1_ARATH	Alpha-dioxygenase 1 (Alpha DOX1) (EC 1.14.99.-) (Fatty acid dioxygenase AlphaDOX1) (Pathogen-induced oxygenase) (Plant alpha dioxygenase 1)	DOX1 DIOX1 PADOX-1 PIOX At3g01420 T13O15.6	Arabidopsis thaliana (Mouse-ear cress)		3D-structure; Complete proteome; Dioxygenase; Fatty acid biosynthesis; Fatty acid metabolism; Glycoprotein; Hypersensitive response; Iron; Lipid biosynthesis; Lipid metabolism; Metal-binding; Oxidoreductase; Oxylipin biosynthesis; Peroxidase; Plant defense; Reference proteome; Signal
SRR646596_TR28759_c0_g2_i2_len=2322	DOX1_ARATH	Q:89-1159,H:1-353	74.02%ID	E:0	Alpha-dioxygenase 1	PF03098.12^An_peroxidase^Animal haem peroxidase^123-381^E:1.2e-55	1	0,538	0	4,239	0	7,312	0	8,244	0,629	-1,622	DOX1_ARATH	Alpha-dioxygenase 1 (Alpha DOX1) (EC 1.14.99.-) (Fatty acid dioxygenase AlphaDOX1) (Pathogen-induced oxygenase) (Plant alpha dioxygenase 1)	DOX1 DIOX1 PADOX-1 PIOX At3g01420 T13O15.6	Arabidopsis thaliana (Mouse-ear cress)		3D-structure; Complete proteome; Dioxygenase; Fatty acid biosynthesis; Fatty acid metabolism; Glycoprotein; Hypersensitive response; Iron; Lipid biosynthesis; Lipid metabolism; Metal-binding; Oxidoreductase; Oxylipin biosynthesis; Peroxidase; Plant defense; Reference proteome; Signal
SRR646596_TR28962_c0_g1_i6_len=1981	C72A1_CATRO	Q:1104-265,H:245-524	97.86%ID	E:0	Secologanin synthase	PF00067.19^p450^Cytochrome P450^93-235^E:2.5e-16	0,158	1,626	0	5,843	0	4,053	0	3,669	1	1,667	C72A1_CATRO	Secologanin synthase (SLS) (EC 1.3.3.9) (CYPLXXII) (Cytochrome P450 72A1)	CYP72A1 CYP72 P450CR3	Catharanthus roseus (Madagascar periwinkle) (Vinca rosea)	PATHWAY: Alkaloid biosynthesis; secologanin biosynthesis.	Alkaloid metabolism; Heme; Iron; Membrane; Metal-binding; Monooxygenase; NADP; Oxidoreductase; Transmembrane; Transmembrane helix; Vacuole
SRR646596_TR30017_c1_g3_i2_len=3962	TPS7_RICCO	Q:353-1129,H:74-334	48.88%ID	E:1e-72	Alpha-farnesene synthase	PF01397.18^Terpene_synth^Terpene synthase, N-terminal domain^2-74^E:4.5e-10`PF03936.13^Terpene_synth_C^Terpene synthase family, metal binding domain^103-195^E:1.3e-27	1	0,347	0	6,678	0	7,852	0	9,252	1	0	TPS7_RICCO	Alpha-farnesene synthase (EC 4.2.3.46) ((E,E)-alpha-farnesene synthase) (Terpene synthase 7) (RcSeTPS7)	TPS7 RCOM_0906600	Ricinus communis (Castor bean)		Complete proteome; Lyase; Magnesium; Metal-binding; Reference proteome
SRR646596_TR32139_c1_g1_i1_len=1808	NA	NA	NA	NA	NA	PF03060.12^NMO^Nitronate monooxygenase^6-74^E:9.6e-13`PF00478.22^IMPDH^IMP dehydrogenase / GMP reductase domain^26-207^E:5.2e-08`PF03060.12^NMO^Nitronate monooxygenase^76-319^E:1.3e-42`PF01070.15^FMN_dh^FMN-dependent dehydrogenase^117-199^E:1e-07	0,051	1,074	0	2,897	0	3,307	0	2,985	0,679	-0,433	.	.	.	.	.	.
SRR646596_TR32486_c0_g1_i1_len=2139	NA	NA	NA	NA	NA	.	0,005	0,88	0	2,034	0	1,846	0	1,63	0,077	0,601	.	.	.	.	.	.
SRR646604_TR1107_c0_g1_i3_len=4655	PR5_ARATH	Q:1058-366,H:7-239	55.27%ID	E:2e-63	Pathogenesis-related protein 5	PF01764.22^Lipase_3^Lipase (class 3)^412-548^E:7.3e-26	0,707	0,415	0	2,137	0	3,781	0	4,689	1	-0,241	PR5_ARATH	Pathogenesis-related protein 5 (PR-5)	At1g75040 F9E10.11	Arabidopsis thaliana (Mouse-ear cress)		Apoplast; Complete proteome; Direct protein sequencing; Disulfide bond; Pathogenesis-related protein; Plant defense; Reference proteome; Secreted; Signal
SRR646604_TR2744_c0_g1_i3_len=1139	VSR1_ARATH	Q:111-872,H:357-612	79.69%ID	E:1e-136	Vacuolar-sorting receptor 1	.	0,046	0,863	0	3,194	0	3,012	0	3,377	0,601	0,264	VSR1_ARATH	Vacuolar-sorting receptor 1 (AtVSR1) (BP80-like protein b) (AtBP80b) (Epidermal growth factor receptor-like protein 1) (AtELP) (AtELP1) (Spot 3 protein)	VSR1 BP80B ELP ELP1 At3g52850 F8J2.20	Arabidopsis thaliana (Mouse-ear cress)		3D-structure; Calcium; Complete proteome; Cytoplasmic vesicle; Disulfide bond; EGF-like domain; Glycoprotein; Golgi apparatus; Membrane; Protein transport; Reference proteome; Repeat; Signal; Transmembrane; Transmembrane helix; Transport
SRR646604_TR2963_c0_g1_i1_len=4284	AB15B_ARATH	Q:4146-409,H:1-1238	72.32%ID	E:0	ABC transporter B family member 15	PF00664.20^ABC_membrane^ABC transporter transmembrane region^36-308^E:6.3e-46`PF00005.24^ABC_tran^ABC transporter^382-530^E:2.5e-33`PF00664.20^ABC_membrane^ABC transporter transmembrane region^683-952^E:1.2e-51`PF00005.24^ABC_tran^ABC transporter^1024-1172^E:9.8e-33	0,147	0,974	0	2,691	0	3,56	0	4,512	0,76	0,649	AB15B_ARATH	ABC transporter B family member 15 (ABC transporter ABCB.15) (AtABCB15) (Multidrug resistance protein 13) (P-glycoprotein 15)	ABCB15 MDR13 PGP15 At3g28345 MZF16.16	Arabidopsis thaliana (Mouse-ear cress)		ATP-binding; Complete proteome; Glycoprotein; Membrane; Nucleotide-binding; Reference proteome; Repeat; Transmembrane; Transmembrane helix; Transport
SRR646604_TR4901_c0_g1_i3_len=2933	DGAT2_ARATH	Q:550-1125,H:2-194	65.8%ID	E:2e-83	Diacylglycerol O-acyltransferase 2	PF03982.10^DAGAT^Diacylglycerol acyltransferase^52-204^E:4.8e-37	0,286	0,901	0	4,209	0	4,823	0	5,552	1	0,368	DGAT2_ARATH	Diacylglycerol O-acyltransferase 2 (EC 2.3.1.20)	DGAT2 At3g51520 F26O13.160	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Glycerolipid metabolism; triacylglycerol biosynthesis.	Acyltransferase; Complete proteome; Endoplasmic reticulum; Glycerol metabolism; Glycoprotein; Lipid biosynthesis; Lipid metabolism; Membrane; Reference proteome; Transferase; Transmembrane; Transmembrane helix
SRR646604_TR5072_c0_g2_i4_len=1750	SDC1_ARATH	Q:217-1422,H:83-482	61.69%ID	E:0	Serine decarboxylase	PF00282.16^Pyridoxal_deC^Pyridoxal-dependent decarboxylase conserved domain^74-370^E:9.2e-25	0,629	0,817	0	7,699	0	10,156	0	11,636	1	0	SDC1_ARATH	Serine decarboxylase (AtSDC) (EC 4.1.1.-) (Protein EMBRYO DEFECTIVE 1075) (Serine decarboxylase 1) (AtSDC1)	SDC EMB1075 SDC1 At1g43710 F2J6.7	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Cytoplasm; Decarboxylase; Lyase; Pyridoxal phosphate; Reference proteome
SRR646604_TR5846_c0_g1_i1_len=2084	NA	NA	NA	NA	NA	PF06813.10^Nodulin-like^Nodulin-like^74-319^E:6.2e-94`PF07690.13^MFS_1^Major Facilitator Superfamily^397-603^E:5.4e-12	0,299	1,191	0	5,006	0	7,644	0	8,552	1	0,694	.	.	.	.	.	.
SRR646604_TR6389_c0_g2_i1_len=773	BH035_ARATH	Q:690-52,H:5-215	53.18%ID	E:3e-70	Transcription factor bHLH35	PF00010.23^HLH^Helix-loop-helix DNA-binding domain^78-120^E:9.7e-12	0,01	2,425	0	4,705	0	2,776	0	3,64	1	0,923	BH035_ARATH	Transcription factor bHLH35 (Basic helix-loop-helix protein 35) (AtbHLH35) (bHLH 35) (Transcription factor EN 41) (bHLH transcription factor bHLH035)	BHLH35 EN41 At5g57150 MUL3.10	Arabidopsis thaliana (Mouse-ear cress)		Alternative splicing; Complete proteome; DNA-binding; Nucleus; Reference proteome; Transcription; Transcription regulation
SRR646604_TR7319_c0_g1_i1_len=1992	NA	NA	NA	NA	NA	PF00106.22^adh_short^short chain dehydrogenase^6-194^E:2.2e-25`PF13561.3^adh_short_C2^Enoyl-(Acyl carrier protein) reductase^17-253^E:1.7e-41	0,066	5,326	0	7,623	0	10,479	0	11,195	1	0	.	.	.	.	.	.
SRR646604_TR8743_c0_g2_i1_len=1590	PNC1_ARATH	Q:1197-241,H:1-320	73.44%ID	E:7e-144	Peroxisomal adenine nucleotide carrier 1	PF00153.24^Mito_carr^Mitochondrial carrier protein^7-97^E:1.6e-13`PF00153.24^Mito_carr^Mitochondrial carrier protein^105-188^E:8.5e-09`PF00153.24^Mito_carr^Mitochondrial carrier protein^202-295^E:2.2e-16	0,517	0,921	0	3,898	0	3,52	0	4,23	1	0,542	PNC1_ARATH	Peroxisomal adenine nucleotide carrier 1 (AtPNC1)	PNC1 At3g05290 T12H1.26	Arabidopsis thaliana (Mouse-ear cress)		Antiport; Complete proteome; Membrane; Peroxisome; Reference proteome; Repeat; Transmembrane; Transmembrane helix; Transport
SRR646604_TR9738_c0_g2_i5_len=2691	NA	NA	NA	NA	NA	.	1	1,785	0	4,88	0	7,364	0	7,747	1	0,614	.	.	.	.	.	.
SRR646604_TR10507_c0_g1_i1_len=1120	NA	NA	NA	NA	NA	PF06884.8^DUF1264^Protein of unknown function (DUF1264)^84-250^E:2.8e-69	0,005	4,269	0	6,112	0	7,181	0	5,858	0,118	1,659	.	.	.	.	.	.
SRR646604_TR11282_c0_g1_i1_len=1551	NA	NA	NA	NA	NA	PF04117.9^Mpv17_PMP22^Mpv17 / PMP22 family^250-311^E:1.9e-17	0,187	1,224	0	3,486	0	4,182	0	4,937	1	-0,486	.	.	.	.	.	.
SRR646604_TR22369_c0_g2_i29_len=2732	FAD3E_SOYBN	Q:801-505,H:246-321	68.69%ID	E:9e-68	Omega-3 fatty acid desaturase, endoplasmic reticulum	PF11960.5^DUF3474^Domain of unknown function (DUF3474)^6-62^E:1.6e-26`PF00487.21^FA_desaturase^Fatty acid desaturase^77-152^E:4.8e-13	0,118	2,067	0	4,846	0	5,188	0	5,431	1	-0,103	FAD3E_SOYBN	Omega-3 fatty acid desaturase, endoplasmic reticulum (EC 1.14.19.-)	FAD3	Glycine max (Soybean) (Glycine hispida)	PATHWAY: Lipid metabolism; polyunsaturated fatty acid biosynthesis.	Complete proteome; Endoplasmic reticulum; Fatty acid biosynthesis; Fatty acid metabolism; Lipid biosynthesis; Lipid metabolism; Membrane; Oxidoreductase; Reference proteome; Transmembrane; Transmembrane helix
SRR646604_TR24012_c0_g1_i1_len=426	NA	NA	NA	NA	NA	.	0,489	0,527	0	3,438	0	1,886	0	2,647	0,142	0,76	.	.	.	.	.	.
SRR646604_TR24656_c0_g2_i3_len=2411	TRPE_ARATH	Q:2056-422,H:50-595	71.48%ID	E:0	Anthranilate synthase alpha subunit 1, chloroplastic	PF04715.10^Anth_synt_I_N^Anthranilate synthase component I, N terminal region^158-312^E:1.3e-27`PF00425.15^Chorismate_bind^chorismate binding enzyme^373-645^E:3.2e-81	0,854	-0,257	0	4,651	0	3,239	0	4,255	1	0,284	TRPE_ARATH	Anthranilate synthase alpha subunit 1, chloroplastic (EC 4.1.3.27) (Anthranilate synthase component 1-1) (Anthranilate synthase component I-1) (Protein A-METHYL TRYPTOPHAN RESISTANT 1) (Protein JASMONATE-INDUCED DEFECTIVE LATERAL ROOT 1) (Protein TRYPTOPHAN BIOSYNTHESIS 5) (Protein WEAK ETHYLENE INSENSITIVE 2)	ASA1 AMT1 JDL1 TRP5 WEI2 At5g05730 MJJ3.14	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Amino-acid biosynthesis; L-tryptophan biosynthesis; L-tryptophan from chorismate: step 1/5.	Acetylation; Alternative splicing; Amino-acid biosynthesis; Aromatic amino acid biosynthesis; Chloroplast; Complete proteome; Lyase; Plastid; Reference proteome; Transit peptide; Tryptophan biosynthesis
SRR646604_TR25379_c0_g1_i2_len=1322	NA	NA	NA	NA	NA	.	0,001	2,079	0	3,164	0	3,281	0	4,014	0,593	0,706	.	.	.	.	.	.
SRR646604_TR26737_c2_g1_i2_len=3166	CSCL4_ARATH	Q:776-2590,H:1-606	79.04%ID	E:0	CSC1-like protein At3g21620	PF13967.3^RSN1_TM^Late exocytosis, associated with Golgi transport^7-176^E:3.5e-52`PF14703.3^PHM7_cyt^Cytosolic domain of 10TM putative phosphate transporter^197-359^E:5.8e-49`PF02714.12^RSN1_7TM^Calcium-dependent channel, 7TM region, putative phosphate^370-612^E:1.3e-70	0,381	1,649	0	5,125	0,001	5,229	0	5,919	1	0,105	CSCL4_ARATH	CSC1-like protein At3g21620	At3g21620 MIL23.19	Arabidopsis thaliana (Mouse-ear cress)		Calcium; Complete proteome; Ion channel; Ion transport; Membrane; Reference proteome; Transmembrane; Transmembrane helix; Transport
SRR646604_TR26737_c2_g1_i7_len=3093	CSCL4_ARATH	Q:1814-3067,H:300-717	79.67%ID	E:0	CSC1-like protein At3g21620	PF14703.3^PHM7_cyt^Cytosolic domain of 10TM putative phosphate transporter^4-64^E:4.2e-14`PF02714.12^RSN1_7TM^Calcium-dependent channel, 7TM region, putative phosphate^75-347^E:9.3e-84	0,239	1,311	0	4,526	0	4,494	0	5,55	0,76	-0,566	CSCL4_ARATH	CSC1-like protein At3g21620	At3g21620 MIL23.19	Arabidopsis thaliana (Mouse-ear cress)		Calcium; Complete proteome; Ion channel; Ion transport; Membrane; Reference proteome; Transmembrane; Transmembrane helix; Transport
SRR646604_TR27677_c0_g1_i4_len=2620	PPH_ARATH	Q:474-1334,H:3-285	57.29%ID	E:7e-101	Pheophytinase, chloroplastic	PF00561.17^Abhydrolase_1^alpha/beta hydrolase fold^157-295^E:1.1e-11`PF12697.4^Abhydrolase_6^Alpha/beta hydrolase family^159-314^E:7.6e-13	1	0,812	0	4,643	0	8,285	0	8,771	1	-0,402	PPH_ARATH	Pheophytinase, chloroplastic (EC 3.1.1.-) (Pheophytin pheophorbide hydrolase) (Protein CO-REGULATED WITH NYE1)	PPH CRN1 At5g13800 MAC12.25	Arabidopsis thaliana (Mouse-ear cress)		Chlorophyll catabolism; Chloroplast; Complete proteome; Hydrolase; Membrane; Plastid; Reference proteome; Thylakoid; Transit peptide
SRR646604_TR27677_c0_g1_i6_len=2779	PPH_ARATH	Q:999-2414,H:3-472	59.37%ID	E:0	Pheophytinase, chloroplastic	PF00561.17^Abhydrolase_1^alpha/beta hydrolase fold^168-450^E:1.8e-13`PF12697.4^Abhydrolase_6^Alpha/beta hydrolase family^170-456^E:4.9e-18	0,502	1,99	0	5,338	0	4,753	0	5,393	1	0,169	PPH_ARATH	Pheophytinase, chloroplastic (EC 3.1.1.-) (Pheophytin pheophorbide hydrolase) (Protein CO-REGULATED WITH NYE1)	PPH CRN1 At5g13800 MAC12.25	Arabidopsis thaliana (Mouse-ear cress)		Chlorophyll catabolism; Chloroplast; Complete proteome; Hydrolase; Membrane; Plastid; Reference proteome; Thylakoid; Transit peptide
SRR646604_TR28091_c0_g2_i1_len=1576	DAT_CATRO	Q:1547-237,H:8-439	79.22%ID	E:0	Deacetylvindoline O-acetyltransferase	PF02458.12^Transferase^Transferase family^13-437^E:8.5e-65	1	2,57	0	7,308	0	7,055	0	6,949	1	0	DAT_CATRO	Deacetylvindoline O-acetyltransferase (EC 2.3.1.107) (Acetyl-coenzyme A:deacetylvindoline 4-O-acetyltransferase)	DAT	Catharanthus roseus (Madagascar periwinkle) (Vinca rosea)	PATHWAY: Alkaloid biosynthesis; vindoline biosynthesis; vindoline from tabersonine: step 6/6.	Acyltransferase; Coiled coil; Direct protein sequencing; Transferase
SRR646604_TR28167_c0_g2_i1_len=906	NA	NA	NA	NA	NA	PF05899.9^Cupin_3^Protein of unknown function (DUF861)^46-124^E:9.7e-32	0,187	1,153	0	3,85	0	2,562	0	2,926	1	-0,204	.	.	.	.	.	.
SRR646604_TR28322_c0_g1_i1_len=2020	C79D1_MANES	Q:406-1842,H:69-540	57.83%ID	E:0	Valine N-monooxygenase 1	PF00067.19^p450^Cytochrome P450^47-509^E:7.2e-76	1	0,076	0	3,357	0	7,366	0	8,243	0,629	1,397	C79D1_MANES	Valine N-monooxygenase 1 (EC 1.14.13.118) (Cytochrome P450 79D1)	CYP79D1	Manihot esculenta (Cassava) (Jatropha manihot)		Direct protein sequencing; Endoplasmic reticulum; Heme; Iron; Membrane; Metal-binding; Microsome; Monooxygenase; NADP; Oxidoreductase; Transmembrane; Transmembrane helix
SRR646604_TR28953_c0_g1_i1_len=1888	HQGT_RAUSE	Q:126-1565,H:5-470	79.38%ID	E:0	Hydroquinone glucosyltransferase	PF00201.15^UDPGT^UDP-glucoronosyl and UDP-glucosyl transferase^271-448^E:2.8e-21	0,052	1,494	0	5,318	0	2,294	0	2,587	0,02	1,118	HQGT_RAUSE	Hydroquinone glucosyltransferase (EC 2.4.1.218) (Arbutin synthase)	AS	Rauvolfia serpentina (Serpentine wood) (Ophioxylon serpentinum)		Direct protein sequencing; Glycosyltransferase; Transferase
						PF05368.10^NmrA^NmrA-like family^8-169^E:6e-42`PF01370.18^Epimerase^NAD dependent																

SRR646604_TR29137_c0_g1_i10_len=1773	EGS1_OCIBA	Q:108-632,H:7-181	69.71%ID	E:5e-81	Eugenol synthase 1	epimerase/dehydratase family^8-86^E:5.1e-06`PF01073.16^3Beta_HSD^3-beta hydroxysteroid dehydrogenase/isomerase family^9-98^E:1.2e-05`PF13460.3^NAD_binding_10^NAD(P)H-binding^12-149^E:1.6e-12	0,015	1,744	0	2,839	0	5,954	0	6,135	1	0,392	EGS1_OCIBA	Eugenol synthase 1 (EC 1.1.1.318)	EGS1	Ocimum basilicum (Sweet basil)	PATHWAY: Aromatic compound metabolism; phenylpropanoid biosynthesis.	3D-structure; NADP; Oxidoreductase; Phenylpropanoid metabolism
SRR646604_TR29855_c0_g1_i1_len=1229	DIOX3_PAPSO	Q:208-768,H:171-358	54.79%ID	E:1e-66	Codeine O-demethylase	PF03171.17^2OG-FeII_Oxy^2OG-Fe(II) oxygenase superfamily^29-125^E:7e-26	0,254	4,492	0	7,018	0	8,684	0	8,047	1	0	DIOX3_PAPSO	Codeine O-demethylase (EC 1.14.11.32)	CODM DIOX3	Papaver somniferum (Opium poppy)	PATHWAY: Alkaloid biosynthesis; morphine biosynthesis.	Alkaloid metabolism; Dioxygenase; Iron; Metal-binding; Methyltransferase; Oxidoreductase; Transferase
SRR646604_TR29872_c1_g1_i8_len=3925	C79D3_LOTJA	Q:176-1624,H:45-530	53.89%ID	E:3e-175	Isoleucine N-monooxygenase 1	PF00067.19^p450^Cytochrome P450^43-510^E:3.4e-84	1	-0,162	0	2,278	0	5,325	0	6,664	0,798	-0,455	C79D3_LOTJA	Isoleucine N-monooxygenase 1 (EC 1.14.13.117) (Cytochrome P450 79D3)	CYP79D3	Lotus japonicus (Lotus corniculatus var. japonicus)		Endoplasmic reticulum; Heme; Iron; Membrane; Metal-binding; Microsome; Monooxygenase; NADP; Oxidoreductase; Transmembrane; Transmembrane helix
SRR646604_TR30246_c1_g1_i3_len=2865	LOX31_SOLTU	Q:2778-49,H:1-914	79.35%ID	E:0	Linoleate 13S-lipoxygenase 3-1, chloroplastic	PF01477.20^PLAT^PLAT/LH2 domain^157-242^E:8e-13`PF00305.16^Lipoxygenase^Lipoxygenase^255-922^E:5.1e-303	0,088	1,564	0	4,912	0	3,981	0	4,539	1	0	LOX31_SOLTU	Linoleate 13S-lipoxygenase 3-1, chloroplastic (EC 1.13.11.12)	LOX3.1 LOX-H3	Solanum tuberosum (Potato)	PATHWAY: Lipid metabolism; oxylipin biosynthesis. {ECO:0000255|PROSITE-ProRule:PRU00726}.	Chloroplast; Complete proteome; Dioxygenase; Fatty acid biosynthesis; Fatty acid metabolism; Iron; Lipid biosynthesis; Lipid metabolism; Metal-binding; Oxidoreductase; Oxylipin biosynthesis; Plastid; Reference proteome; Thylakoid; Transit peptide
SRR646604_TR31106_c0_g1_i1_len=1331	NA	NA	NA	NA	NA	.	0,502	2,317	0	6,067	0	7,562	0	8,749	1	-0,305	.	.	.	.	.	.
SRR646604_TR33445_c0_g2_i1_len=1210	NA	NA	NA	NA	NA	PF02519.11^Auxin_inducible^Auxin responsive protein^84-154^E:4.4e-21	0,461	1,256	0	3,351	0	3,775	0	4,488	1	-0,086	.	.	.	.	.	.
SRR646604_TR37105_c3_g1_i5_len=4576	SDP1_ARATH	Q:1037-2467,H:1-474	83.05%ID	E:0	Triacylglycerol lipase SDP1	PF11815.5^DUF3336^Domain of unknown function (DUF3336)^99-229^E:2.7e-29`PF01734.19^Patatin^Patatin-like phospholipase^236-430^E:1.2e-18	0,312	0,92	0	2,379	0	5,785	0	6,023	0,798	0,348	SDP1_ARATH	Triacylglycerol lipase SDP1 (EC 3.1.1.3) (Protein SUGAR-DEPENDENT 1)	SDP1 At5g04040 F8F6.10 F8F6.250	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Glycerol metabolism; Glycoprotein; Hydrolase; Lipid degradation; Lipid droplet; Lipid metabolism; Membrane; Reference proteome; Transmembrane; Transmembrane helix
SRR646604_TR37251_c0_g1_i1_len=852	MIRA_SYNDU	Q:119-676,H:30-217	38.14%ID	E:2e-31	Miraculin	PF00197.15^Kunitz_legume^Trypsin and protease inhibitor^46-224^E:3.4e-47	0,502	2,962	0	6,93	0	11,361	0	7,397	1	0	MIRA_SYNDU	Miraculin (MIR)		Synsepalum dulcificum (Miracle fruit) (Richadella dulcifica)		Direct protein sequencing; Disulfide bond; Glycoprotein; Signal; Taste-modifying protein
SRR646604_TR38185_c0_g1_i1_len=1662	NAC72_ARATH	Q:135-881,H:1-241	73.02%ID	E:2e-122	NAC domain-containing protein 72	PF02365.12^NAM^No apical meristem (NAM) protein^59-183^E:8e-26	0,694	0,395	0	1,927	0	2,078	0	2,337	0,505	0,392	NAC72_ARATH	NAC domain-containing protein 72 (ANAC072) (Protein RESPONSIVE TO DESICCATION 26)	NAC072 RD26 At4g27410 F27G19.10	Arabidopsis thaliana (Mouse-ear cress)		Alternative splicing; Complete proteome; DNA-binding; Nucleus; Reference proteome; Transcription; Transcription regulation
SRR646604_TR38644_c1_g1_i8_len=3869	AFS1_MALDO	Q:1177-314,H:274-563	54.3%ID	E:3e-95	(E,E)-alpha-farnesene synthase	PF03936.13^Terpene_synth_C^Terpene synthase family, metal binding domain^1-158^E:7.1e-43	1	2,333	0	6,834	0	7,73	0	8,737	1	-0,245	AFS1_MALDO	(E,E)-alpha-farnesene synthase (MdAFS1) (EC 4.2.3.46) (Prenyltransferase) (EC 2.5.1.-)	AFS1 AFAR	Malus domestica (Apple) (Pyrus malus)		Cytoplasm; Lyase; Magnesium; Manganese; Metal-binding; Potassium; Transferase
SRR648705_TR7373_c0_g1_i1_len=1827	NAC2_ARATH	Q:1522-626,H:2-289	62.21%ID	E:4e-111	NAC domain-containing protein 2	PF02365.12^NAM^No apical meristem (NAM) protein^22-145^E:4.8e-27	0,01	2,599	0	8,341	0	3,604	0	4,99	1	0,883	NAC2_ARATH	NAC domain-containing protein 2 (ANAC002)	NAC002 ATAF1 At1g01720 T1N6.12	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; DNA-binding; Nucleus; Reference proteome; Transcription; Transcription regulation
SRR648705_TR9374_c0_g2_i2_len=2661	HSP83_IPONI	Q:2440-329,H:1-703	95.88%ID	E:0	Heat shock protein 83	PF13589.3^HATPase_c_3^Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase^30-151^E:2.8e-09`PF02518.23^HATPase_c^Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase^32-186^E:1.1e-16`PF00183.15^HSP90^Hsp90 protein^189-699^E:1.2e-241	0,781	-0,422	0,001	2,473	0	1,17	0,001	1,065	1	0,2	HSP83_IPONI	Heat shock protein 83	HSP83A	Ipomoea nil (Japanese morning glory) (Pharbitis nil)		ATP-binding; Chaperone; Cytoplasm; Nucleotide-binding; Stress response
SRR648705_TR11052_c0_g1_i3_len=1379	CBSX1_ARATH	Q:974-465,H:65-234	74.12%ID	E:8e-85	CBS domain-containing protein CBSX1, chloroplastic	PF00571.25^CBS^CBS domain^76-130^E:8.2e-13`PF00571.25^CBS^CBS domain^170-223^E:7.4e-18	0,004	1,66	0	3,718	0	3,046	0	2,168	0,226	2,682	CBSX1_ARATH	CBS domain-containing protein CBSX1, chloroplastic (CBS domain-containing protein 2) (AtCDCP2) (Protein LOSS OF THE TIMING OF ET AND JA BIOSYNTHESIS 2) (AtLEJ2)	CBSX1 CDCP2 At4g36910 AP22.61 C7A10.450	Arabidopsis thaliana (Mouse-ear cress)		3D-structure; Acetylation; CBS domain; Chloroplast; Complete proteome; Plastid; Reference proteome; Repeat; Transit peptide
SRR648705_TR12139_c0_g1_i1_len=4526	VSR1_ARATH	Q:4162-2318,H:3-621	76.9%ID	E:0	Vacuolar-sorting receptor 1	PF02225.19^PA^PA domain^92-161^E:2.1e-09`PF12662.4^cEGF^Complement Clr-like EGF-like^498-517^E:3.7e-07`PF07645.12^EGF_CA^Calcium-binding EGF domain^514-545^E:0.00012	0,409	0,4	0	2,525	0	1,848	0	2,277	0,691	0,255	VSR1_ARATH	Vacuolar-sorting receptor 1 (AtVSR1) (BP80-like protein b) (AtBP80b) (Epidermal growth factor receptor-like protein 1) (AtELP) (AtELP1) (Spot 3 protein)	VSR1 BP80B ELP ELP1 At3g52850 F8J2.20	Arabidopsis thaliana (Mouse-ear cress)		3D-structure; Calcium; Complete proteome; Cytoplasmic vesicle; Disulfide bond; EGF-like domain; Glycoprotein; Golgi apparatus; Membrane; Protein transport; Reference proteome; Repeat; Signal; Transmembrane; Transmembrane helix; Transport
SRR648705_TR12587_c0_g1_i1_len=2064	PTR21_ARATH	Q:1838-75,H:31-617	53.3%ID	E:0	Protein NRT1/ PTR FAMILY 2.13	PF07690.13^MFS_1^Major Facilitator Superfamily^115-580^E:7.8e-09`PF00854.18^PTR2^POT family^170-599^E:9.8e-82	1	1,428	0	7,148	0	3,545	0	2,623	1	0,377	PTR21_ARATH	Protein NRT1/ PTR FAMILY 2.13 (AtNPF2.13) (Nitrate transporter 1.7)	NPF2.13 NRT1.7 At1g69870 T17F3.10	Arabidopsis thaliana (Mouse-ear cress)		Cell membrane; Complete proteome; Membrane; Nitrate assimilation; Reference proteome; Symport; Transmembrane; Transmembrane helix; Transport
SRR648705_TR13222_c0_g2_i1_len=584	NA	NA	NA	NA	NA	.	0,059	1,553	0	3,607	0	6,151	0	6,57	1	-0,167	.	.	.	.	.	.
SRR648705_TR15518_c0_g1_i1_len=1550	NA	NA	NA	NA	NA	PF06200.11^tify^tify domain^37-67^E:6.5e-18`PF09425.7^CCT_2^Divergent CCT motif^127-151^E:2.6e-13	0,014	2,841	0	5,374	0	5,673	0	5,747	0,76	-0,46	.	.	.	.	.	.
SRR648705_TR17063_c0_g2_i2_len=1722	UGT9_GARJA	Q:265-1581,H:1-437	56.59%ID	E:3e-174	Beta-D-glucosyl crocetin beta-1,6-glucosyltransferase	PF00201.15^UDPGT^UDP-glucoronosyl and UDP-glucosyl transferase^263-395^E:9.9e-21	1	0,376	0	3,566	0	1,452	0	2,38	0,643	-0,455	UGT9_GARJA	Beta-D-glucosyl crocetin beta-1,6-glucosyltransferase (EC 2.4.1.330) (UDP-glucose glucosyltransferase 9) (GjUGT9) (UDP-glycosyltransferase 94E5)	UGT94E5 UGT9	Gardenia jasminoides (Cape jasmine) (Gardenia augusta)		Glycosyltransferase; Transferase
SRR648705_TR18211_c0_g1_i2_len=900	SGRM_PEA	Q:292-771,H:1-159	75.78%ID	E:4e-76	Non-functional protein STAY-GREEN, chloroplastic	PF12638.4^Staygreen^Staygreen protein^54-171^E:1.4e-35	1	0,911	0	5,386	0	3,844	0	3,744	1	0,382	SGRM_PEA	Non-functional protein STAY-GREEN, chloroplastic (Protein STAYGREEN)	SGR	Pisum sativum (Garden pea)		Chloroplast; Plastid; Transit peptide
SRR648705_TR18346_c2_g1_i1_len=2673	NA	NA	NA	NA	NA	.	1	0,705	0	4,935	0	1,566	0	2,076	0,629	1,609	.	.	.	.	.	.
SRR648705_TR25572_c0_g2_i1_len=721	NA	NA	NA	NA	NA	.	0,402	1,088	0	2,32	0	3,52	0	2,321	0,074	0,98	.	.	.	.	.	.
SRR648705_TR26993_c0_g1_i2_len=2232	CBP22_HORVU	Q:468-1766,H:1-436	70.18%ID	E:0	Serine carboxypeptidase II-2	PF00450.19^Peptidase_S10^Serine carboxypeptidase^45-461^E:5.7e-147	0,031	0,652	0	1,425	0	2,533	0	2,813	0,439	0,329	CBP22_HORVU	Serine carboxypeptidase II-2 (EC 3.4.16.6) (CP-MII.2) [Cleaved into: Serine carboxypeptidase II-2 chain A; Serine carboxypeptidase II-2 chain B] (Fragment)	CXP;2-2	Hordeum vulgare (Barley)		Carboxypeptidase; Direct protein sequencing; Disulfide bond; Glycoprotein; Hydrolase; Protease; Zymogen
SRR648705_TR33071_c0_g1_i1_len=1721	NA	NA	NA	NA	NA	PF00564.21^PB1^PB1 domain^29-114^E:6.1e-17	1	0,543	0	4,217	0	3,915	0	4,737	1	0,057	.	.	.	.	.	.
SRR648705_TR34167_c1_g1_i1_len=1738	NA	NA	NA	NA	NA	PF04720.9^PDDEXK_6^PDDEXK-like family of unknown function^61-248^E:9.1e-65	0,025	3,566	0	5,491	0	4,071	0	3,786	1	1,504	.	.	.	.	.	.
SRR648705_TR38568_c0_g1_i2_len=675	NA	NA	NA	NA	NA	.	0,003	3,077	0	3,847	0	5,017	0,001	3,774	1	-0,149	.	.	.	.	.	.
SRR648705_TR38919_c0_g2_i4_len=2033	NOTUM_MOUSE	Q:1758-721,H:107-456	27.32%ID	E:2e-21	Palmitoleoyl-protein carboxylesterase NOTUM {ECO:0000250|UniProtKB:Q6P988}	PF03283.10^PAE^Pectinacetylesterase^21-372^E:2.1e-168	0,679	0,452	0	2,335	0	1,223	0,001	1,097	1	-0,285	NOTUM_MOUSE	Palmitoleoyl-protein carboxylesterase NOTUM (EC 3.1.1.-)	Notum	Mus musculus (Mouse)		Alternative splicing; Complete proteome; Glycoprotein; Hydrolase; Phosphoprotein; Reference proteome; Secreted; Serine esterase; Signal; Wnt signaling pathway
SRR648705_TR42618_c0_g1_i1_len=1167	OFP8_ARATH	Q:312-112,H:154-220	64.18%ID	E:4e-21	Transcription repressor OFP8	PF04844.10^Ovate^Transcriptional repressor, ovate^243-299^E:1.8e-20	1	0,086	0	6,258	0	5,678	0	6,951	1	0,194	OFP8_ARATH	Transcription repressor OFP8 (Ovate family protein 8) (AtOFP8)	OFP8 At5g19650 T29J13	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Nucleus; Reference proteome; Repressor; Transcription; Transcription regulation
SRR648705_TR43591_c0_g1_i19_len=3515	NA	NA	NA	NA	NA	PF12146.5^Hydrolase_4^Serine aminopeptidase, S33^37-157^E:2.2e-34`PF00561.17^Abhydrolase_1^alpha/beta hydrolase fold^39-148^E:1.1e-11`PF12697.4^Abhydrolase_6^Alpha/beta hydrolase family^43-149^E:1.5e-09	0,044	2,036	0	4,385	0	3,363	0	3,609	1	-0,015	.	.	.	.	.	.
SRR648705_TR44780_c0_g1_i1_len=1654	QOR1_ECOLI	Q:234-1205,H:1-327	47.4%ID	E:1e-89	Quinone oxidoreductase 1	PF08240.9^ADH_N^Alcohol dehydrogenase GroES-like domain^106-164^E:2.5e-08`PF00107.23^ADH_zinc_N^Zinc-binding dehydrogenase^229-342^E:3e-27`PF13602.3^ADH_zinc_N_2^Zinc-binding dehydrogenase^262-399^E:1.1e-20	0,352	0,323	0	1,525	0	2,372	0	2,468	0,931	0,075	QOR1_ECOLI	Quinone oxidoreductase 1 (EC 1.6.5.5) (NADPH:quinone reductase 1) (Zeta-crystallin homolog protein)	qorA hcz qor qor1 b4051 JW4011	Escherichia coli (strain K12)		3D-structure; Complete proteome; NADP; Oxidoreductase; Reference proteome
SRR648707_TR337_c1_g1_i1_len=1430	Y8948_DICDI	Q:817-53,H:15-261	32.32%ID	E:1e-30	Putative methyltransferase DDB_G0268948	PF13649.3^Methyltransf_25^Methyltransferase domain^37-128^E:9.1e-10`PF13847.3^Methyltransf_31^Methyltransferase domain^37-138^E:4.5e-08`PF08241.9^Methyltransf_11^Methyltransferase domain^39-132^E:1.3e-10`PF08242.9^Methyltransf_12^Methyltransferase domain^39-132^E:2.2e-08	0,237	0,44	0	2,409	0	1,971	0	2,627	0,781	0,621	Y8948_DICDI	Putative methyltransferase DDB_G0268948 (EC 2.1.1.-)	DDB_G0268948	Dictyostelium discoideum (Slime mold)		Complete proteome; Methyltransferase; Reference proteome; S-adenosyl-L-methionine; Transferase
SRR648707_TR3152_c0_g1_i1_len=1530	NAC72_ARATH	Q:139-885,H:1-241	73.02%ID	E:9e-124	NAC domain-containing protein 72	PF02365.12^NAM^No apical meristem (NAM) protein^61-185^E:4.9e-26	1	1,725	0	6,803	0	7,009	0	6,911	1	2,162	NAC72_ARATH	NAC domain-containing protein 72 (ANAC072) (Protein RESPONSIVE TO DESICCATION 26)	NAC072 RD26 At4g27410 F27G19.10	Arabidopsis thaliana (Mouse-ear cress)		Alternative splicing; Complete proteome; DNA-binding; Nucleus; Reference proteome; Transcription; Transcription regulation
SRR648707_TR3906_c1_g1_i2_len=1814	SRG1_ARATH	Q:1606-599,H:16-358	39.19%ID	E:7e-69	Protein SRG1	PF14226.3^DIOX_N^non-haem dioxygenase in morphine synthesis N-terminal^53-158^E:1e-25`PF03171.17^2OG-FeII_Oxy^2OG-Fe(II) oxygenase superfamily^207-303^E:4.6e-23	0,016	2,313	0	5,542	0	4,248	0	3,122	1	0	SRG1_ARATH	Protein SRG1 (AtSRG1) (Protein SENESCENCE-RELATED GENE 1)	SRG1 At1g17020 F20D23.28 F6I1.30	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Iron; Metal-binding; Oxidoreductase; Reference proteome
SRR648707_TR4594_c0_g2_i1_len=986	IKU2_ARATH	Q:259-981,H:24-272	48.8%ID	E:7e-65	Receptor-like protein kinase HAIKU2	PF08263.9^LRRNT_2^Leucine rich repeat N-terminal domain^40-78^E:2e-10`PF13855.3^LRR_8^Leucine rich repeat^206-265^E:1.5e-06`PF00560.30^LRR_1^Leucine Rich Repeat^207-228^E:0.62	0,286	1,02	0	6,819	0	7,329	0	7,207	1	-0,743	IKU2_ARATH	Receptor-like protein kinase HAIKU2 (EC 2.7.11.1)	IKU2 At3g19700 MMB12.19	Arabidopsis thaliana (Mouse-ear cress)		ATP-binding; Complete proteome; Glycoprotein; Kinase; Leucine-rich repeat; Membrane; Nucleotide-binding; Phosphoprotein; Receptor; Reference proteome; Repeat; Serine/threonine-protein kinase; Signal; Transferase; Transmembrane; Transmembrane helix
SRR648707_TR9115_c0_g1_i1_len=463	NA	NA	NA	NA	NA	.	0,129	4,993	0	5,555	0	5,167	0	5,419	1	-3,182	.	.	.	.	.	.
SRR648707_TR9982_c0_g1_i1_len=1004	NA	NA	NA	NA	NA	.	1	-2,698	0	7,591	0	5,731	0	4,502	1	0,56	.	.	.	.	.	.
SRR648707_TR12944_c0_g1_i1_len=910	PTI5_SOLLC	Q:793-347,H:1-143	62.82%ID	E:8e-42	Pathogenesis-related genes transcriptional activator PTI5	PF00847.17^AP2^AP2 domain^66-116^E:6e-15	0,111	1,453	0	5,11	0	6,736	0	7,744	1	1,243	PTI5_SOLLC	Pathogenesis-related genes transcriptional activator PTI5 (PTO-interacting protein 5)	PTI5	Solanum lycopersicum (Tomato) (Lycopersicon esculentum)		Activator; Complete proteome; DNA-binding; Nucleus; Plant defense; Reference proteome; Transcription; Transcription regulation
SRR648707_TR15942_c0_g1_i1_len=1178	RFS6_ARATH	Q:804-40,H:1-263	73%ID	E:5e-133	Probable galactinol--sucrose galactosyltransferase 6	PF05691.9^Raffinose_syn^Raffinose synthase or seed imbibition protein Sip1^108-365^E:7.9e-107	0,856	0,08	0	3,744	0	1,548	0	1,768	0,402	1,204	RFS6_ARATH	Probable galactinol--sucrose galactosyltransferase 6 (EC 2.4.1.82) (Protein DARK INDUCIBLE 10) (Raffinose synthase 6)	RFS6 DIN10 RS6 At5g20250 F5O24.140	Arabidopsis thaliana (Mouse-ear cress)		Alternative splicing; Carbohydrate metabolism; Complete proteome; Glycosyltransferase; Reference proteome; Transferase
SRR648707_TR16177_c0_g2_i1_len=1206	NA	NA	NA	NA	NA	PF13639.3^zf-RING_2^Ring finger domain^115-160^E:3.9e-11`PF17123.2^zf-RING_11^RING-like zinc finger^115-145^E:6.3e-07`PF14634.3^zf-RING_5^zinc-RING finger domain^115-161^E:1.1e-06`PF13923.3^zf-C3HC4_2^Zinc finger, C3HC4 type (RING finger)^116-159^E:8.2e-07`PF00097.22^zf-C3HC4^Zinc finger, C3HC4 type (RING finger)^116-159^E:1.4e-05`PF12861.4^zf-ANAPC11^Anaphase-promoting complex subunit 11 RING-H2 finger^116-164^E:3.6e-05`PF13445.3^zf-RING_UBOX^RING-type zinc-finger^116-157^E:0.00092	0,133	1,13	0	3,788	0	4,196	0	4,696	1	-0,486	.	.	.	.	.	.
SRR648707_TR20187_c0_g3_i6_len=4057	MATE3_ARATH	Q:772-2133,H:60-541	60.58%ID	E:5e-165	.	PF01554.15^MatE^MatE^122-289^E:5.8e-11`PF14667.3^Polysacc_synt_C^Polysaccharide biosynthesis C-terminal domain^247-338^E:5.6e-07`PF01554.15^MatE^MatE^361-491^E:7.5e-12	0,014	1,804	0	4,283	0	3,866	0	4,086	0,444	0,477	DTX45_ARATH	Protein DETOXIFICATION 45, chloroplastic (AtDTX45) (Multidrug and toxic compound extrusion protein 45) (MATE protein 45)	DTX45 At4g38380 F22I13.150	Arabidopsis thaliana (Mouse-ear cress)		Chloroplast; Complete proteome; Membrane; Plastid; Reference proteome; Transit peptide; Transmembrane; Transmembrane helix; Transport
SRR648707_TR22697_c0_g1_i1_len=1576	DIOX3_PAPSO	Q:1078-425,H:140-358	54.34%ID	E:9e-86	Codeine O-demethylase	PF03171.17^2OG-FeII_Oxy^2OG-Fe(II) oxygenase superfamily^85-181^E:1.4e-25	0,129	4,163	0	6,722	0	8,369	0	7,459	1	0	DIOX3_PAPSO	Codeine O-demethylase (EC 1.14.11.32)	CODM DIOX3	Papaver somniferum (Opium poppy)	PATHWAY: Alkaloid biosynthesis; morphine biosynthesis.	Alkaloid metabolism; Dioxygenase; Iron; Metal-binding; Methyltransferase; Oxidoreductase; Transferase
SRR648707_TR22784_c0_g2_i2_len=1914	NAC2_ARATH	Q:657-1520,H:1-289	69.49%ID	E:4e-133	NAC domain-containing protein 2	PF02365.12^NAM^No apical meristem (NAM) protein^8-131^E:1.4e-27	0,032	1,292	0	3,568	0	3,273	0	3,67	0,444	0,467	NAC2_ARATH	NAC domain-containing protein 2 (ANAC002)	NAC002 ATAF1 At1g01720 T1N6.12	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; DNA-binding; Nucleus; Reference proteome; Transcription; Transcription regulation
SRR648707_TR23814_c0_g1_i1_len=2005	CNR8_MAIZE	Q:342-917,H:38-233	68.5%ID	E:2e-87	Cell number regulator 8	PF04749.14^PLAC8^PLAC8 family^71-209^E:5.9e-21	0,506	0,212	0	1,569	0	1,275	0	1,197	0,816	0,112	CNR8_MAIZE	Cell number regulator 8 (ZmCNR08)	CNR8 SAT5	Zea mays (Maize)		Complete proteome; Membrane; Reference proteome; Transmembrane; Transmembrane helix
SRR648707_TR23832_c1_g1_i1_len=1601	NA	NA	NA	NA	NA	PF04640.11^PLATZ^PLATZ transcription factor^69-140^E:2.8e-29	0,003	1,438	0	2,249	0	2,516	0	2,565	0,174	0,567	.	.	.	.	.	.
SRR648707_TR25545_c1_g1_i1_len=1181	NA	NA	NA	NA	NA	.	0,066	3,071	0	4,827	0	3,516	0	3,29	0,461	1,121	.	.	.	.	.	.
SRR648707_TR27118_c0_g1_i2_len=1921	MDAR_SOLLC	Q:122-1423,H:1-433	86.41%ID	E:0	Monodehydroascorbate reductase	PF07992.11^Pyr_redox_2^Pyridine nucleotide-disulphide oxidoreductase^47-362^E:6e-56`PF00070.24^Pyr_redox^Pyridine nucleotide-disulphide oxidoreductase^205-287^E:9.7e-14	0,22	0,313	0	2,302	0	1,66	0	1,665	0,034	-0,567	MDAR_SOLLC	Monodehydroascorbate reductase (MDAR) (EC 1.6.5.4) (Ascorbate free radical reductase) (AFR reductase)	AFRR	Solanum lycopersicum (Tomato) (Lycopersicon esculentum)		Complete proteome; Cytoplasm; FAD; Flavoprotein; NAD; Oxidoreductase; Redox-active center; Reference proteome
SRR648707_TR29077_c0_g2_i1_len=629	NA	NA	NA	NA	NA	.	0,189	2,076	0	6,342	0	6,759	0	6,93	0,356	-1,103	.	.	.	.	.	.
SRR648707_TR30848_c0_g1_i1_len=1760	AB7I_ARATH	Q:1701-226,H:1-475	54.36%ID	E:2e-173	Protein ABCI7, chloroplastic	PF01458.14^UPF0051^Uncharacterized protein family (UPF0051)^242-467^E:2.2e-59	0,292	0,271	0,001	0,94	0	0,891	0,001	0,876	0,143	0,499	AB7I_ARATH	Protein ABCI7, chloroplastic (ABC transporter I family member 7) (ABC transporter ABCI.7) (AtABCI7) (Non-intrinsic ABC protein 6) (Plastid SufD-like protein)	ABCI7 NAP6 At1g32500 F5D14.28	Arabidopsis thaliana (Mouse-ear cress)		Chloroplast; Complete proteome; Plastid; Reference proteome; Transit peptide
SRR648707_TR32619_c0_g1_i1_len=465	NA	NA	NA	NA	NA	.	0,132	2,615	0	4,528	0	5,285	0	5,482	1	0	.	.	.	.	.	.
SRR648707_TR33467_c0_g1_i1_len=2068	C81E1_GLYEC	Q:1822-479,H:54-493	47.02%ID	E:2e-147	Isoflavone 2'-hydroxylase	PF00067.19^p450^Cytochrome P450^30-485^E:1.8e-91	0,021	1,652	0	4,825	0	3,744	0	3,242	1	0,211	C81E1_GLYEC	Isoflavone 2'-hydroxylase (EC 1.14.13.89) (CYP GE-3) (Cytochrome P450 81E1) (Cytochrome P450 91A4)	CYP81E1 CYP91A4	Glycyrrhiza echinata (Licorice)		Heme; Iron; Membrane; Metal-binding; Monooxygenase; NADP; Oxidoreductase
SRR648707_TR34170_c0_g1_i1_len=611	NA	NA	NA	NA	NA	.	0,564	0,448	0	3,51	0	5,478	0	5,928	0,402	-1,169	.	.	.	.	.	.
SRR648707_TR34684_c0_g2_i2_len=2163	C81E8_MEDTR	Q:510-1436,H:176-490	45.37%ID	E:2e-105	Cytochrome P450 81E8 {ECO:0000303|PubMed:14617078}	PF00067.19^p450^Cytochrome P450^25-290^E:5.5e-67	1	-0,039	0	3,352	0	4,58	0	5,652	0,56	0,902	C81E8_MEDTR	Cytochrome P450 81E8 (EC 1.14.13.-)	CYP81E8	Medicago truncatula (Barrel medic) (Medicago tribuloides)		Heme; Iron; Membrane; Metal-binding; Monooxygenase; NADP; Oxidoreductase; Transmembrane; Transmembrane helix
SRR648707_TR36394_c2_g1_i5_len=1389	PIP27_MAIZE	Q:155-1018,H:1-287	82.01%ID	E:5e-150	Aquaporin PIP2-7	PF00230.17^MIP^Major intrinsic protein^34-269^E:3.2e-83	0,043	3,29	0	8,934	0	5,884	0	4,596	1	1,168	PIP27_MAIZE	Aquaporin PIP2-7 (Plasma membrane intrinsic protein 2-7) (ZmPIP2-7) (ZmPIP2;7)	PIP2-7	Zea mays (Maize)		Cell membrane; Complete proteome; Membrane; Reference proteome; Repeat; Transmembrane; Transmembrane helix; Transport
SRR648707_TR37199_c0_g1_i3_len=1848	NA	NA	NA	NA	NA	PF03547.15^Mem_trans^Membrane transport protein^10-408^E:6.7e-83	0,381	0,786	0	2,995	0	5,115	0	4,742	1	-0,025	.	.	.	.	.	.
SRR648707_TR37528_c0_g1_i1_len=1469	ATL51_ARATH	Q:230-1066,H:1-296	45.87%ID	E:3e-61	RING-H2 finger protein ATL51	PF13639.3^zf-RING_2^Ring finger domain^134-177^E:8.4e-14`PF17123.2^zf-RING_11^RING-like zinc finger^134-163^E:3.6e-10`PF13923.3^zf-C3HC4_2^Zinc finger, C3HC4 type (RING finger)^134-176^E:1.1e-06`PF00097.22^zf-C3HC4^Zinc finger, C3HC4 type (RING finger)^135-176^E:0.00011	0,006	1,726	0	2,336	0	1,803	0	1,742	0,299	1,549	ATL51_ARATH	RING-H2 finger protein ATL51	ATL51 At3g03550 T12J13.17 T21P5.3	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Protein modification; protein ubiquitination.	Complete proteome; Membrane; Metal-binding; Reference proteome; Transmembrane; Transmembrane helix; Ubl conjugation pathway; Zinc; Zinc-finger
SRR648707_TR39385_c1_g1_i11_len=2270	DCAM_CATRO	Q:710-1780,H:1-357	100%ID	E:0	S-adenosylmethionine decarboxylase proenzyme	PF01536.13^SAM_decarbox^Adenosylmethionine decarboxylase^9-332^E:9.8e-110	0,107	0,407	0	1,727	0	0,867	0	1,025	0,674	0,105	DCAM_CATRO	S-adenosylmethionine decarboxylase proenzyme (AdoMetDC) (SAMDC) (EC 4.1.1.50) [Cleaved into: S-adenosylmethionine decarboxylase alpha chain; S-adenosylmethionine decarboxylase beta chain]	SAMDC	Catharanthus roseus (Madagascar periwinkle) (Vinca rosea)	PATHWAY: Amine and polyamine biosynthesis; S-adenosylmethioninamine biosynthesis; S-adenosylmethioninamine from S-adenosyl-L-methionine: step 1/1.	Autocatalytic cleavage; Decarboxylase; Lyase; Polyamine biosynthesis; Pyruvate; S-adenosyl-L-methionine; Schiff base; Spermidine biosynthesis; Zymogen
SRR648707_TR40821_c0_g1_i1_len=1711	T184C_BOVIN	Q:364-1215,H:39-325	29.93%ID	E:1e-35	Transmembrane protein 184C	PF03619.13^Solute_trans_a^Organic solute transporter Ostalpha^9-275^E:1e-68	0,002	0,973	0	3,555	0	2,256	0	2,103	0,189	0,553	T184C_BOVIN	Transmembrane protein 184C (Transmembrane protein 34)	TMEM184C TMEM34	Bos taurus (Bovine)		Complete proteome; Membrane; Reference proteome; Transmembrane; Transmembrane helix
SRR924147_TR2336_c0_g1_i1_len=1470	HIDM_GLYEC	Q:200-1144,H:12-327	47.37%ID	E:9e-98	2-hydroxyisoflavanone dehydratase	PF00135.25^COesterase^Carboxylesterase family^58-179^E:3.3e-07`PF07859.10^Abhydrolase_3^alpha/beta hydrolase fold^73-299^E:8.4e-38	0,06	0,807	0	2,47	0	2,274	0	2,352	0,458	0,451	HIDM_GLYEC	2-hydroxyisoflavanone dehydratase (EC 3.1.1.1) (EC 4.2.1.105) (Carboxylesterase HIDM)	HIDM	Glycyrrhiza echinata (Licorice)	PATHWAY: Secondary metabolite biosynthesis; flavonoid biosynthesis.	Flavonoid biosynthesis; Hydrolase; Lyase
SRR924147_TR11424_c0_g2_i1_len=1050	CRPM2_ARATH	Q:890-285,H:1-203	65.52%ID	E:2e-87	Cold-regulated 413 plasma membrane protein 2	PF05562.8^WCOR413^Cold acclimation protein WCOR413^9-189^E:8.3e-85	1	1,367	0	7,769	0	5,298	0	4,34	1	0	CRPM2_ARATH	Cold-regulated 413 plasma membrane protein 2 (AtCOR413-PM2)	COR413PM2 At3g50830 F18B3.110	Arabidopsis thaliana (Mouse-ear cress)		Cell membrane; Complete proteome; Membrane; Reference proteome; Transmembrane; Transmembrane helix
SRR924147_TR15016_c0_g1_i1_len=1466	ANXD1_ARATH	Q:1318-371,H:1-317	67.51%ID	E:9e-157	Annexin D1	PF00191.17^Annexin^Annexin^16-79^E:1.1e-21`PF00191.17^Annexin^Annexin^87-152^E:3.7e-17`PF00191.17^Annexin^Annexin^171-231^E:2.5e-14	0,226	0,414	0	2,356	0	2,482	0	2,04	0,007	0,933	ANXD1_ARATH	Annexin D1 (AnnAt1) (Annexin A1)	ANN1 ANNAT1 ANX23-ATH ATOXY5 OXY5 At1g35720 F14D7.2	Arabidopsis thaliana (Mouse-ear cress)		3D-structure; Acetylation; Annexin; Calcium; Calcium/phospholipid-binding; Complete proteome; Cytoplasm; Membrane; Reference proteome; Repeat; Stress response
SRR924147_TR31078_c1_g2_i2_len=2112	WRKY6_ARATH	Q:1994-546,H:1-498	50.84%ID	E:4e-98	WRKY transcription factor 6	PF03106.12^WRKY^WRKY DNA -binding domain^318-375^E:9.9e-27	0,118	2,328	0	3,797	0	4,395	0	5,02	1	0,106	WRKY6_ARATH	WRKY transcription factor 6 (WRKY DNA-binding protein 6) (AtWRKY6)	WRKY6 At1g62300 F19K23.22	Arabidopsis thaliana (Mouse-ear cress)		Activator; Complete proteome; DNA-binding; Ethylene signaling pathway; Nucleus; Reference proteome; Repressor; Transcription; Transcription regulation
SRR924147_TR32903_c0_g1_i1_len=1616	SGRW_PEA	Q:1237-515,H:1-236	71.07%ID	E:3e-115	Protein STAY-GREEN, chloroplastic	PF12638.4^Staygreen^Staygreen protein^54-205^E:3.3e-58	0,103	1,637	0	4,905	0	4,382	0	4,361	1	3,301	SGRW_PEA	Protein STAY-GREEN, chloroplastic (Protein STAYGREEN)	SGR	Pisum sativum (Garden pea)		Chloroplast; Plastid; Transit peptide
SRR924148_TR4179_c0_g2_i4_len=1472	TRPA2_ARATH	Q:266-1153,H:11-312	76.16%ID	E:6e-146	Tryptophan synthase alpha chain, chloroplastic	PF00290.17^Trp_syntA^Tryptophan synthase alpha chain^61-316^E:1.1e-95`PF00977.18^His_biosynth^Histidine biosynthesis protein^242-291^E:3.3e-06	0,001	0,781	0	2,39	0	1,073	0,001	0,945	1	0,009	TRPA2_ARATH	Tryptophan synthase alpha chain, chloroplastic (EC 4.2.1.20) (Indole-3-glycerol-phosphate lyase, chloroplastic) (EC 4.1.2.8) (Protein TRYPTOPHAN-REQUIRING 3)	TSA1 TRP3 TSA2 At3g54640 T14E10.210	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Amino-acid biosynthesis; L-tryptophan biosynthesis; L-tryptophan from chorismate: step 5/5.	Amino-acid biosynthesis; Aromatic amino acid biosynthesis; Auxin biosynthesis; Chloroplast; Complete proteome; Lyase; Plastid; Reference proteome; Transit peptide; Tryptophan biosynthesis
SRR924148_TR9505_c0_g2_i1_len=1093	NA	NA	NA	NA	NA	.	0,155	1,13	0	2,199	0	2,255	0,001	2,157	0,643	0,442	.	.	.	.	.	.
SRR924148_TR10819_c2_g2_i1_len=1467	NA	NA	NA	NA	NA	PF00076.19^RRM_1^RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)^19-84^E:3e-08`PF13893.3^RRM_5^RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)^37-83^E:0.076	1	0,473	0	3,741	0	1,896	0	2,296	1	-0,357	.	.	.	.	.	.
SRR924148_TR12464_c0_g1_i1_len=521	NA	NA	NA	NA	NA	.	0,006	1,784	0	6,885	0	7,671	0	8,087	0,56	-0,734	.	.	.	.	.	.
SRR924148_TR16409_c0_g2_i1_len=1271	NA	NA	NA	NA	NA	.	1	1,234	0	2,342	0	1,85	0	1,871	0,017	5,796	.	.	.	.	.	.
SRR924148_TR20364_c1_g4_i12_len=3184	GATLA_ARATH	Q:866-1369,H:37-195	46.47%ID	E:3e-36	Probable galacturonosyltransferase-like 10	PF05542.8^DUF760^Protein of unknown function (DUF760)^87-165^E:1.3e-17`PF05542.8^DUF760^Protein of unknown function (DUF760)^260-363^E:1.5e-26	0,663	0,519	0	2,058	0	2,417	0	3,526	0,656	-0,32	GATLA_ARATH	Probable galacturonosyltransferase-like 10 (EC 2.4.1.-) (Galactinol synthase 8) (AtGolS8) (GolS-8)	GATL10 GOLS8 At3g28340 MZF16.17	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Glycan metabolism; pectin biosynthesis.	Cell wall biogenesis/degradation; Complete proteome; Glycoprotein; Glycosyltransferase; Golgi apparatus; Membrane; Reference proteome; Signal-anchor; Transferase; Transmembrane; Transmembrane helix
SRR924148_TR26351_c1_g4_i1_len=2386	HSP7C_PETHY	Q:140-2086,H:1-651	92.35%ID	E:0	Heat shock cognate 70 kDa protein	PF00012.17^HSP70^Hsp70 protein^9-618^E:5e-270`PF06723.10^MreB_Mbl^MreB/Mbl protein^131-380^E:2.8e-14	0,16	1,296	0	4,402	0	1,366	0	1,205	0,798	0,291	HSP7C_PETHY	Heat shock cognate 70 kDa protein	HSP70	Petunia hybrida (Petunia)		ATP-binding; Nucleotide-binding; Stress response
SRR924148_TR26351_c2_g2_i1_len=1560	HSP72_SOLLC	Q:1558-272,H:218-644	94.41%ID	E:0	Heat shock cognate 70 kDa protein 2	PF00012.17^HSP70^Hsp70 protein^1-401^E:3.5e-157	0,212	0,509	0	1,184	0	1,07	0	0,968	0,017	-4,469	HSP72_SOLLC	Heat shock cognate 70 kDa protein 2	HSC-2	Solanum lycopersicum (Tomato) (Lycopersicon esculentum)		ATP-binding; Complete proteome; Nucleotide-binding; Reference proteome; Stress response
SRR924148_TR26518_c0_g1_i4_len=1979	SCP31_ARATH	Q:1517-186,H:16-471	65.79%ID	E:0	Serine carboxypeptidase-like 31	PF00450.19^Peptidase_S10^Serine carboxypeptidase^46-467^E:3.3e-136	0,008	2,858	0	4,626	0	2,519	0	2,269	1	-0,755	SCP31_ARATH	Serine carboxypeptidase-like 31 (EC 3.4.16.-)	SCPL31 At1g11080 T19D16.4	Arabidopsis thaliana (Mouse-ear cress)		Alternative splicing; Carboxypeptidase; Complete proteome; Disulfide bond; Glycoprotein; Hydrolase; Protease; Reference proteome; Secreted; Signal
SRR924148_TR26932_c1_g3_i1_len=1664	GSTUI_ARATH	Q:510-875,H:5-127	74.8%ID	E:3e-79	Glutathione S-transferase U18	PF02798.17^GST_N^Glutathione S-transferase, N-terminal domain^6-77^E:1.1e-16`PF13417.3^GST_N_3^Glutathione S-transferase, N-terminal domain^8-77^E:4.6e-16`PF13409.3^GST_N_2^Glutathione S-transferase, N-terminal domain^14-77^E:1.6e-07	0,889	0,073	0	3,528	0	1,276	0	1,4	0,865	-0,065	GSTUI_ARATH	Glutathione S-transferase U18 (AtGSTU18) (EC 2.5.1.18) (GST class-tau member 18) (Glutathione S-transferase 29)	GSTU18 GST29 At1g10360 F14N23.24	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Cytoplasm; Detoxification; Reference proteome; Transferase
SRR924148_TR27396_c0_g2_i1_len=612	NA	NA	NA	NA	NA	.	0,08	1,378	0	3,489	0	3,365	0	2,968	1	-0,16	.	.	.	.	.	.
SRR924148_TR28419_c0_g3_i5_len=1480	PIP1_SOLLC	Q:347-1192,H:1-282	86.52%ID	E:5e-178	Probable aquaporin PIP-type pTOM75	PF00230.17^MIP^Major intrinsic protein^45-274^E:1e-83	0,021	0,547	0	2,265	0	1,553	0	0,861	0,74	0,084	PIP1_SOLLC	Probable aquaporin PIP-type pTOM75 (Ripening-associated membrane protein) (RAMP)		Solanum lycopersicum (Tomato) (Lycopersicon esculentum)		Cell membrane; Complete proteome; Membrane; Reference proteome; Repeat; Stress response; Transmembrane; Transmembrane helix; Transport
SRR924148_TR30626_c0_g2_i1_len=2780	MFPA_CUCSA	Q:292-2457,H:4-725	80.19%ID	E:0	Glyoxysomal fatty acid beta-oxidation multifunctional protein MFP-a	PF00378.17^ECH_1^Enoyl-CoA hydratase/isomerase^14-209^E:6.7e-40`PF16113.2^ECH_2^Enoyl-CoA hydratase/isomerase^26-192^E:3.2e-24`PF02737.15^3HCDH_N^3-hydroxyacyl-CoA dehydrogenase, NAD binding domain^312-490^E:1.5e-60`PF00725.19^3HCDH^3-hydroxyacyl-CoA dehydrogenase, C-terminal domain^493-586^E:9.3e-21	0,194	0,418	0	1,598	0	2,241	0	2,633	0,394	0,325	MFPA_CUCSA	Glyoxysomal fatty acid beta-oxidation multifunctional protein MFP-a [Includes: Enoyl-CoA hydratase/3-2-trans-enoyl-CoA isomerase/3-hydroxybutyryl-CoA epimerase (EC 4.2.1.17) (EC 5.1.2.3) (EC 5.3.3.8); 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35)]		Cucumis sativus (Cucumber)	PATHWAY: Lipid metabolism; fatty acid beta-oxidation.	Fatty acid metabolism; Glyoxysome; Isomerase; Lipid metabolism; Lyase; Multifunctional enzyme; NAD; Oxidoreductase; Peroxisome
SRR924148_TR37688_c0_g1_i1_len=1718	YQJG_ECOLI	Q:331-1284,H:15-328	46.77%ID	E:2e-90	Glutathionyl-hydroquinone reductase YqjG	PF13409.3^GST_N_2^Glutathione S-transferase, N-terminal domain^89-196^E:1.2e-19`PF14497.3^GST_C_3^Glutathione S-transferase, C-terminal domain^233-315^E:0.00011`PF00043.22^GST_C^Glutathione S-transferase, C-terminal domain^238-317^E:1.2e-07`PF13410.3^GST_C_2^Glutathione S-transferase, C-terminal domain^244-311^E:1.2e-09	0,239	0,446	0,001	1,248	0	1,556	0,001	1,459	0,927	0,073	YQJG_ECOLI	Glutathionyl-hydroquinone reductase YqjG (GS-HQR) (EC 1.8.-.-)	yqjG b3102 JW3073	Escherichia coli (strain K12)		3D-structure; Complete proteome; Oxidoreductase; Reference proteome
SRR924148_TR40931_c0_g1_i1_len=2638	IDN2_ARATH	Q:2174-336,H:21-637	51.61%ID	E:0	Protein INVOLVED IN DE NOVO 2 {ECO:0000303|PubMed:19915591}	PF03470.11^zf-XS^XS zinc finger domain^48-91^E:8.6e-19`PF03468.11^XS^XS domain^120-231^E:3.7e-38`PF03469.11^XH^XH domain^508-636^E:4.9e-53	0,045	0,667	0	2,707	0	2,863	0	3,358	0,84	0,227	IDN2_ARATH	Protein INVOLVED IN DE NOVO 2 (Protein RNA-DIRECTED DNA METHYLATION 12)	IDN2 RDM12 At3g48670 T8P19.180	Arabidopsis thaliana (Mouse-ear cress)		3D-structure; Coiled coil; Complete proteome; RNA-binding; RNA-mediated gene silencing; Reference proteome
SRR1271857_TR20542_c0_g1_i4_len=1910	ALMT9_ARATH	Q:501-1742,H:134-566	52.64%ID	E:3e-134	Aluminum-activated malate transporter 9	PF11744.5^ALMT^Aluminium activated malate transporter^2-392^E:2.6e-123	0,283	0,442	0,004	1,466	0	4,296	0	3,965	0	7,319	ALMT9_ARATH	Aluminum-activated malate transporter 9 (AtALMT9)	ALMT9 At3g18440 MYF24.16	Arabidopsis thaliana (Mouse-ear cress)		Chloride; Complete proteome; Ion channel; Ion transport; Membrane; Reference proteome; Transmembrane; Transmembrane helix; Transport; Vacuole
SRR1271857_TR40574_c0_g1_i3_len=1027	KIRO_ACTDE	Q:713-270,H:1-148	46.62%ID	E:1e-33	Kirola {ECO:0000303|PubMed:21309790}	PF00407.16^Bet_v_1^Pathogenesis-related protein Bet v I family^31-174^E:2.3e-32	0,907	0,026	0,874	0,036	0	0,881	0	0,759	0	1,125	KIRO_ACTDE	Kirola (allergen Act d 11)		Actinidia deliciosa (Kiwi)		3D-structure; Acetylation; Allergen; Direct protein sequencing; Polymorphism
SRR1271857_TR40877_c0_g1_i1_len=1170	ANX4_FRAAN	Q:1070-135,H:1-314	63.38%ID	E:1e-141	Annexin-like protein RJ4	PF00191.17^Annexin^Annexin^15-76^E:9.7e-20`PF00191.17^Annexin^Annexin^87-149^E:7.1e-09`PF00191.17^Annexin^Annexin^168-231^E:3.5e-11`PF00191.17^Annexin^Annexin^245-307^E:5.1e-18	1	-0,104	0,189	2	0	1,937	0	2,213	0	2,154	ANX4_FRAAN	Annexin-like protein RJ4		Fragaria ananassa (Strawberry)		Annexin; Calcium; Calcium/phospholipid-binding; Repeat
SRR1271858_TR14181_c0_g1_i2_len=692	KIRO_ACTDE	Q:650-228,H:8-148	46.81%ID	E:2e-31	Kirola {ECO:0000303|PubMed:21309790}	PF00407.16^Bet_v_1^Pathogenesis-related protein Bet v I family^18-154^E:6.5e-32	0,118	0,335	0,764	-0,071	0	1,691	0	1,068	0	0,781	KIRO_ACTDE	Kirola (allergen Act d 11)		Actinidia deliciosa (Kiwi)		3D-structure; Acetylation; Allergen; Direct protein sequencing; Polymorphism
SRR342017_TR7655_c0_g7_i10_len=2440	C76B6_CATRO	Q:999-2396,H:32-493	50.64%ID	E:3e-154	Geraniol 8-hydroxylase	PF00067.19^p450^Cytochrome P450^2-423^E:1.7e-96	0,027	2,464	0,593	0,667	0	1,245	0	1,335	0	1,472	C76B6_CATRO	Geraniol 8-hydroxylase (EC 1.14.13.152) (Cytochrome P450 76B6) (Geraniol 10-hydroxylase) (CrG10H)	CYP76B6 G10H	Catharanthus roseus (Madagascar periwinkle) (Vinca rosea)		Direct protein sequencing; Endoplasmic reticulum; Heme; Iron; Membrane; Metal-binding; Monooxygenase; NADP; Oxidoreductase; Transmembrane; Transmembrane helix
SRR342019_TR1547_c0_g2_i1_len=1144	NA	NA	NA	NA	NA	PF13833.3^EF-hand_8^EF-hand domain pair^36-96^E:3.5e-05`PF13202.3^EF-hand_5^EF hand^76-94^E:0.14	0,58	0,246	0,502	0,333	0,001	1,401	0	1,507	0,001	4,381	.	.	.	.	.	.
SRR342019_TR14878_c1_g2_i3_len=1789	DAT_CATRO	Q:73-1389,H:1-439	99.77%ID	E:0	Deacetylvindoline O-acetyltransferase	PF02458.12^Transferase^Transferase family^35-456^E:3.6e-66	0,437	0,193	0,43	0,22	0	1,74	0	1,44	0	1,026	DAT_CATRO	Deacetylvindoline O-acetyltransferase (EC 2.3.1.107) (Acetyl-coenzyme A:deacetylvindoline 4-O-acetyltransferase)	DAT	Catharanthus roseus (Madagascar periwinkle) (Vinca rosea)	PATHWAY: Alkaloid biosynthesis; vindoline biosynthesis; vindoline from tabersonine: step 6/6.	Acyltransferase; Coiled coil; Direct protein sequencing; Transferase
SRR646604_TR35379_c0_g2_i1_len=2307	PTR18_ARATH	Q:105-1883,H:1-593	55.85%ID	E:0	Protein NRT1/ PTR FAMILY 3.1	PF00854.18^PTR2^POT family^98-533^E:1.1e-94	1	0,606	1	0,804	0	1,809	0	1,723	0	3,04	PTR18_ARATH	Protein NRT1/ PTR FAMILY 3.1 (AtNPF3.1)	NPF3.1 NITR At1g68570 F24J5.19	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Membrane; Nitrate assimilation; Reference proteome; Transmembrane; Transmembrane helix; Transport
SRR924148_TR8082_c0_g2_i1_len=1811	AAT_AQUAE	Q:407-1555,H:4-394	28.43%ID	E:2e-37	Aspartate aminotransferase	PF00155.18^Aminotran_1_2^Aminotransferase class I and II^31-380^E:1.6e-49`PF01053.17^Cys_Met_Meta_PP^Cys/Met metabolism PLP-dependent enzyme^91-207^E:9.4e-05	0,87	-0,166	0,16	-0,648	0	1,989	0	1,84	0	2,311	AAT_AQUAE	Aspartate aminotransferase (AspAT) (EC 2.6.1.1) (Transaminase A)	aspC aq_1969	Aquifex aeolicus (strain VF5)		Aminotransferase; Complete proteome; Cytoplasm; Pyridoxal phosphate; Reference proteome; Transferase
SRR1144633_TR1228_c0_g2_i1_len=1493	PUP3_ARATH	Q:357-1304,H:5-321	45.74%ID	E:6e-81	Purine permease 3	PF16913.2^PUNUT^Purine nucleobase transmembrane transport^23-345^E:4.7e-99	0	2,695	0	7,485	0	7,08	0	8,434	1	0,468	PUP3_ARATH	Purine permease 3 (AtPUP3)	PUP3 At1g28220 F3H9.12	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Membrane; Reference proteome; Transmembrane; Transmembrane helix; Transport
SRR1144633_TR5772_c0_g3_i2_len=991	CYB5_TOBAC	Q:728-324,H:1-135	86.67%ID	E:3e-69	Cytochrome b5	PF00173.25^Cyt-b5^Cytochrome b5-like Heme/Steroid binding domain^9-80^E:1.1e-26	0	9,072	0	8,748	0	1,567	0	1,328	1	-1,052	CYB5_TOBAC	Cytochrome b5		Nicotiana tabacum (Common tobacco)		Electron transport; Endoplasmic reticulum; Heme; Iron; Membrane; Metal-binding; Microsome; Transmembrane; Transmembrane helix; Transport
SRR1144633_TR32951_c0_g1_i1_len=1954	CIPKB_ARATH	Q:1689-442,H:13-422	60.38%ID	E:5e-175	CBL-interacting serine/threonine-protein kinase 11	PF00069.22^Pkinase^Protein kinase domain^25-279^E:4.8e-76`PF07714.14^Pkinase_Tyr^Protein tyrosine kinase^27-275^E:3.6e-41`PF14531.3^Kinase-like^Kinase-like^121-264^E:2.7e-08`PF03822.11^NAF^NAF domain^315-367^E:5.5e-14	0	2,577	0	4,336	0	1,661	0	1,684	1	1,052	CIPKB_ARATH	CBL-interacting serine/threonine-protein kinase 11 (EC 2.7.11.1) (SNF1-related kinase 3.22) (SOS2-like protein kinase PKS5) (SOS3-interacting protein 4)	CIPK11 PKS5 SIP4 SnRK3.22 At2g30360 T9D9.17	Arabidopsis thaliana (Mouse-ear cress)		ATP-binding; Complete proteome; Kinase; Magnesium; Manganese; Nucleotide-binding; Phosphoprotein; Reference proteome; Serine/threonine-protein kinase; Transferase
SRR1144633_TR36204_c0_g1_i1_len=1331	NA	NA	NA	NA	NA	.	0,001	4,428	0	6,683	0	5,146	0	6,29	0,502	2,653	.	.	.	.	.	.
SRR1144634_TR9978_c0_g1_i1_len=585	NA	NA	NA	NA	NA	.	0,001	1,742	0	2,301	0	2,322	0	1,849	1	0	.	.	.	.	.	.
SRR1144634_TR10670_c0_g2_i11_len=898	ARGE_ARATH	Q:679-191,H:278-438	65.64%ID	E:2e-71	Acetylornithine deacetylase	.	0	3,061	0	4,602	0	5,701	0	4,122	0,005	0,978	ARGE_ARATH	Acetylornithine deacetylase (EC 3.5.1.16) (N-acetylornithinase) (AO) (Acetylornithinase) (NAO)	At4g17830 dl4945w T6K21	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Amino-acid biosynthesis; L-arginine biosynthesis; L-ornithine from N(2)-acetyl-L-ornithine (linear): step 1/1.	Alternative splicing; Amino-acid biosynthesis; Arginine biosynthesis; Cobalt; Complete proteome; Hydrolase; Metal-binding; Reference proteome; Zinc
SRR1144634_TR17599_c0_g1_i1_len=761	P2B11_ARATH	Q:23-520,H:88-255	36.05%ID	E:5e-22	F-box protein PP2-B11	PF14299.3^PP2^Phloem protein 2^15-173^E:1.8e-31	0	4,363	0	9,065	0	9,084	0	6,679	1	-0,025	P2B11_ARATH	F-box protein PP2-B11 (Protein PHLOEM PROTEIN 2-LIKE B11) (AtPP2-B11) (SKP1-interacting partner 12)	PP2B11 SKIP12 At1g80110 F18B13.19	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Protein modification; protein ubiquitination.	Complete proteome; Nucleus; Reference proteome; Ubl conjugation pathway
SRR1144634_TR28611_c0_g1_i1_len=775	NA	NA	NA	NA	NA	PF13419.3^HAD_2^Haloacid dehalogenase-like hydrolase^5-101^E:1.8e-18`PF00702.23^Hydrolase^haloacid dehalogenase-like hydrolase^6-94^E:1.6e-08`PF13242.3^Hydrolase_like^HAD-hyrolase-like^56-103^E:9.5e-07	0	2,098	0	2,763	0	2,349	0	2,541	0,025	3,634	.	.	.	.	.	.
SRR122236_TR27004_c0_g2_i2_len=735	CYTI_VIGUN	Q:93-377,H:1-95	70.53%ID	E:6e-41	Cysteine proteinase inhibitor	.	0	1,265	0	2,314	0	1,866	0	1,2	0,683	0,116	CYTI_VIGUN	Cysteine proteinase inhibitor (Cystatin)		Vigna unguiculata (Cowpea)		3D-structure; Protease inhibitor; Thiol protease inhibitor
SRR122238_TR813_c0_g1_i1_len=1167	TIP13_ARATH	Q:1022-267,H:1-252	79.76%ID	E:1e-141	Aquaporin TIP1-3	PF00230.17^MIP^Major intrinsic protein^14-234^E:6.5e-74	0	3,722	0	5,184	0	4,884	0	3,164	1	0,398	TIP13_ARATH	Aquaporin TIP1-3 (Gamma-tonoplast intrinsic protein 3) (Gamma-TIP3) (Tonoplast intrinsic protein 1-3) (AtTIP1;3) [Cleaved into: Aquaporin TIP1-3, N-terminally processed]	TIP1-3 At4g01470 F11O4.1	Arabidopsis thaliana (Mouse-ear cress)		Acetylation; Complete proteome; Membrane; Reference proteome; Repeat; Stress response; Transmembrane; Transmembrane helix; Transport; Vacuole
SRR122238_TR2609_c0_g1_i1_len=1753	ARGE_ARATH	Q:1679-375,H:1-438	68.34%ID	E:0	Acetylornithine deacetylase	PF01546.25^Peptidase_M20^Peptidase family M20/M25/M40^119-456^E:8.8e-31`PF07687.11^M20_dimer^Peptidase dimerisation domain^227-341^E:3.6e-12	0	2,44	0	3,703	0	4,817	0	4,473	0,007	1,003	ARGE_ARATH	Acetylornithine deacetylase (EC 3.5.1.16) (N-acetylornithinase) (AO) (Acetylornithinase) (NAO)	At4g17830 dl4945w T6K21	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Amino-acid biosynthesis; L-arginine biosynthesis; L-ornithine from N(2)-acetyl-L-ornithine (linear): step 1/1.	Alternative splicing; Amino-acid biosynthesis; Arginine biosynthesis; Cobalt; Complete proteome; Hydrolase; Metal-binding; Reference proteome; Zinc
SRR122238_TR9216_c1_g1_i2_len=1145	SWT12_ARATH	Q:87-746,H:10-236	60.79%ID	E:2e-89	Bidirectional sugar transporter SWEET12 {ECO:0000303|PubMed:21107422}	PF03083.13^MtN3_slv^Sugar efflux transporter for intercellular exchange^12-96^E:4.7e-25`PF04193.11^PQ-loop^PQ loop repeat^14-67^E:9.2e-05`PF03083.13^MtN3_slv^Sugar efflux transporter for intercellular exchange^132-214^E:4e-26	0	2,902	0	3,397	0	1,639	0	1,767	0,84	0,351	SWT12_ARATH	Bidirectional sugar transporter SWEET12 (AtSWEET12) (MtN3-like protein) (Protein SUGARS WILL EVENTUALLY BE EXPORTED TRANSPORTERS 12)	SWEET12 MTN3 At5g23660 MQM1.8	Arabidopsis thaliana (Mouse-ear cress)		Cell membrane; Complete proteome; Developmental protein; Membrane; Reference proteome; Repeat; Sugar transport; Transmembrane; Transmembrane helix; Transport
SRR122238_TR17062_c0_g1_i5_len=1342	TI10A_ARATH	Q:1128-397,H:4-253	38.02%ID	E:7e-39	Protein TIFY 10A	PF06200.11^tify^tify domain^105-137^E:4.2e-19`PF09425.7^CCT_2^Divergent CCT motif^192-217^E:3.4e-13	0	2,506	0	4,269	0	2,706	0	2,714	0,906	0,076	TI10A_ARATH	Protein TIFY 10A (Jasmonate ZIM domain-containing protein 1)	TIFY10A JAZ1 At1g19180 T29M8.5	Arabidopsis thaliana (Mouse-ear cress)		3D-structure; Alternative splicing; Complete proteome; Jasmonic acid signaling pathway; Nucleus; Plant defense; Reference proteome; Transcription; Transcription regulation; Ubl conjugation
SRR122238_TR19465_c0_g3_i2_len=1290	NA	NA	NA	NA	NA	PF00106.22^adh_short^short chain dehydrogenase^6-194^E:2.2e-25`PF13561.3^adh_short_C2^Enoyl-(Acyl carrier protein) reductase^17-253^E:1.7e-41	0	1,851	0	4,853	0	6,794	0	7,56	0,679	-0,322	.	.	.	.	.	.
SRR122238_TR21630_c0_g1_i3_len=1535	NA	NA	NA	NA	NA	PF06200.11^tify^tify domain^98-128^E:1e-17`PF09425.7^CCT_2^Divergent CCT motif^188-212^E:4e-13	0	4,513	0	5,824	0	4,914	0	4,98	1	-0,165	.	.	.	.	.	.
SRR122238_TR21949_c0_g1_i1_len=1290	FNSI_PETCR	Q:1175-195,H:1-333	34.82%ID	E:1e-66	Flavone synthase	PF14226.3^DIOX_N^non-haem dioxygenase in morphine synthesis N-terminal^76-180^E:2.3e-27`PF03171.17^2OG-FeII_Oxy^2OG-Fe(II) oxygenase superfamily^228-326^E:6.9e-29	0	3,469	0	4,861	0	3,012	0	2,676	0,629	-1,435	FNSI_PETCR	Flavone synthase (EC 1.14.11.22) (Flavone synthase I)	FNSI	Petroselinum crispum (Parsley) (Petroselinum hortense)	PATHWAY: Secondary metabolite biosynthesis; flavonoid biosynthesis.	Cytoplasm; Flavonoid biosynthesis; Iron; Metal-binding; Oxidoreductase; Vitamin C
SRR122238_TR24079_c0_g2_i5_len=1499	NA	NA	NA	NA	NA	PF06200.11^tify^tify domain^120-151^E:1.8e-16`PF09425.7^CCT_2^Divergent CCT motif^258-278^E:5.7e-09	0	1,555	0	3,15	0	2,407	0	2,951	0,017	-5,782	.	.	.	.	.	.
SRR122238_TR24079_c0_g2_i9_len=1403	NA	NA	NA	NA	NA	PF06200.11^tify^tify domain^88-119^E:1.6e-16`PF09425.7^CCT_2^Divergent CCT motif^226-246^E:5e-09	0	2,066	0	2,985	0	2,141	0	2,419	0,115	0,784	.	.	.	.	.	.
SRR122238_TR26146_c1_g2_i2_len=1477	B2_DAUCA	Q:541-996,H:54-205	80.92%ID	E:4e-90	B2 protein	PF10539.6^Dev_Cell_Death^Development and cell death domain^202-328^E:2.1e-41	0	1,136	0	1,356	0	1,663	0	1,554	0,022	0,544	B2_DAUCA	B2 protein		Daucus carota (Wild carrot)		
SRR122238_TR26400_c0_g1_i2_len=974	NA	NA	NA	NA	NA	PF04570.11^zf-FLZ^zinc-finger of the FCS-type, C2-C2^69-113^E:2.8e-19	0	2,085	0	3,041	0	3,955	0	3,717	1	0,155	.	.	.	.	.	.
SRR122238_TR27056_c0_g1_i5_len=2087	NA	NA	NA	NA	NA	PF03959.10^FSH1^Serine hydrolase (FSH1)^10-203^E:1.5e-47	0	1,75	0	2,327	0	1,998	0	2,931	1	-0,325	.	.	.	.	.	.
SRR122238_TR33818_c0_g1_i1_len=1720	U91A1_ARATH	Q:1595-213,H:9-466	57.42%ID	E:0	UDP-glycosyltransferase 91A1	PF00201.15^UDPGT^UDP-glucoronosyl and UDP-glucosyl transferase^275-444^E:2.7e-17	0	2,053	0	3,476	0	4,717	0	5,372	0,258	0,911	U91A1_ARATH	UDP-glycosyltransferase 91A1 (EC 2.4.1.-)	UGT91A1 At2g22590 T9I22.3	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Glycosyltransferase; Reference proteome; Transferase
SRR122238_TR37682_c0_g1_i1_len=548	NA	NA	NA	NA	NA	.	0	4,101	0	6,102	0	10,678	0	7,884	1	0	.	.	.	.	.	.
SRR122238_TR45263_c0_g1_i3_len=1590	DRL29_ARATH	Q:775-179,H:617-816	54.23%ID	E:3e-59	Probable disease resistance protein At4g33300	PF05659.8^RPW8^Arabidopsis broad-spectrum mildew resistance protein RPW8^38-165^E:2.6e-14`PF00931.19^NB-ARC^NB-ARC domain^221-288^E:5.7e-11	0	2,288	0	3,391	0	4,653	0	4,971	1	-0,035	DRL29_ARATH	Probable disease resistance protein At4g33300	At4g33300 F17M5.60	Arabidopsis thaliana (Mouse-ear cress)		ATP-binding; Coiled coil; Complete proteome; Leucine-rich repeat; Nucleotide-binding; Plant defense; Reference proteome; Repeat
SRR122238_TR47400_c1_g1_i3_len=1577	C72A1_CATRO	Q:106-1575,H:1-490	97.35%ID	E:0	Secologanin synthase	PF00067.19^p450^Cytochrome P450^90-490^E:2.6e-84	0	1,026	0	3,308	0	1,365	0	1,052	0,067	0,613	C72A1_CATRO	Secologanin synthase (SLS) (EC 1.3.3.9) (CYPLXXII) (Cytochrome P450 72A1)	CYP72A1 CYP72 P450CR3	Catharanthus roseus (Madagascar periwinkle) (Vinca rosea)	PATHWAY: Alkaloid biosynthesis; secologanin biosynthesis.	Alkaloid metabolism; Heme; Iron; Membrane; Metal-binding; Monooxygenase; NADP; Oxidoreductase; Transmembrane; Transmembrane helix; Vacuole
[illegible]	[illegible]	Q:200-403,H:1-	[illegible]	[illegible]	[illegible]		[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]		Prunus armeniaca (Apricot)		[illegible]

[illegible]	[illegible]	68	[illegible]	[illegible]	Non-specific lipid-transfer protein 2	.	0	[illegible]	0	[illegible]	0	[illegible]	0	[illegible]	[illegible]	[illegible]	[illegible]	Non-specific lipid-transfer protein 2 (LTP 2)		(Armeniaca vulgaris)		Direct protein sequencing; Lipid-binding; Transport
SRR122238_TR50696_c0_g1_i1_len=606	GRXC9_ARATH	Q:480-94,H:11-137	54.2%ID	E:3e-40	Glutaredoxin-C9	PF00462.21^Glutaredoxin^Glutaredoxin^47-115^E:2.5e-09	0	7,782	0	2,539	0	1,94	0	3,574	0,262	-0,536	GRXC9_ARATH	Glutaredoxin-C9 (AtGrxC9) (Protein ROXY 19)	GRXC9 GRX480 ROXY19 At1g28480 F3M18.8	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Cytoplasm; Disulfide bond; Electron transport; Nucleus; Redox-active center; Reference proteome; Transport
SRR122238_TR65873_c1_g1_i1_len=574	CNR8_MAIZE	Q:272-571,H:38-140	65.42%ID	E:4e-39	Cell number regulator 8	PF04749.14^PLAC8^PLAC8 family^71-140^E:7.1e-09	0,001	1,533	0	4,65	0	1,673	0	2,001	0,02	0,854	CNR8_MAIZE	Cell number regulator 8 (ZmCNR08)	CNR8 SAT5	Zea mays (Maize)		Complete proteome; Membrane; Reference proteome; Transmembrane; Transmembrane helix
SRR122238_TR75737_c0_g1_i4_len=1213	AOC4_ARATH	Q:868-308,H:64-248	66.67%ID	E:2e-73	Allene oxide cyclase 4, chloroplastic	PF06351.8^Allene_ox_cyc^Allene oxide cyclase^77-249^E:1.7e-91	0	1,961	0	5,566	0	2,937	0	2,978	0,093	-1,044	AOC4_ARATH	Allene oxide cyclase 4, chloroplastic (EC 5.3.99.6)	AOC4 At1g13280 T6J4.4 T6J4_23	Arabidopsis thaliana (Mouse-ear cress)		Chloroplast; Complete proteome; Isomerase; Plastid; Reference proteome; Transit peptide
SRR1271857_TR30546_c0_g1_i1_len=1649	NA	NA	NA	NA	NA	PF00388.16^PI-PLC-X^Phosphatidylinositol-specific phospholipase C, X domain^81-174^E:2.6e-09	0	1,396	0	1,532	0	1,967	0	1,791	0,84	0,066	.	.	.	.	.	.
SRR1271857_TR32512_c2_g1_i3_len=1413	NA	NA	NA	NA	NA	PF06200.11^tify^tify domain^108-139^E:1.7e-16`PF09425.7^CCT_2^Divergent CCT motif^246-266^E:5.4e-09	0	1,565	0	3,732	0	1,67	0	1,967	1	-0,133	.	.	.	.	.	.
SRR1271857_TR37691_c0_g1_i3_len=1157	NA	NA	NA	NA	NA	PF06232.8^ATS3^Embryo-specific protein 3, (ATS3)^30-132^E:4.1e-07`PF01477.20^PLAT^PLAT/LH2 domain^36-153^E:2.2e-14	0	0,813	0	3,151	0	4,17	0	3,746	0,895	0,05	.	.	.	.	.	.
SRR1271858_TR9171_c0_g1_i1_len=639	TRXH2_ARATH	Q:144-506,H:11-130	52.07%ID	E:1e-44	Thioredoxin H2	PF14595.3^Thioredoxin_9^Thioredoxin^10-124^E:6.7e-06`PF04756.10^OST3_OST6^OST3 / OST6 family, transporter family^19-127^E:1.5e-06`PF00085.17^Thioredoxin^Thioredoxin^35-127^E:2e-29`PF13098.3^Thioredoxin_2^Thioredoxin-like domain^40-119^E:9.4e-07`PF00578.18^AhpC-TSA^AhpC/TSA family^42-119^E:8.7e-05	0	2,854	0	6,429	0	4,886	0	5,499	0,461	-1,107	TRXH2_ARATH	Thioredoxin H2 (AtTrxh2) (Thioredoxin 2) (AtTRX2)	TRX2 At5g39950 MYH19.14	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Cytoplasm; Disulfide bond; Electron transport; Mitochondrion; Redox-active center; Reference proteome; Transport
SRR1271858_TR16116_c0_g1_i3_len=1778	LDOX_MALDO	Q:1382-567,H:10-281	37.82%ID	E:9e-58	Leucoanthocyanidin dioxygenase	PF14226.3^DIOX_N^non-haem dioxygenase in morphine synthesis N-terminal^56-167^E:6e-33`PF03171.17^2OG-FeII_Oxy^2OG-Fe(II) oxygenase superfamily^216-292^E:5.6e-15	0	5,829	0	12,489	0	3,773	0	2,766	1	0	LDOX_MALDO	Leucoanthocyanidin dioxygenase (LDOX) (Leucocyanidin oxygenase) (EC 1.14.11.19) (Anthocyanidin synthase) (Leucoanthocyanidin hydroxylase)	ANS	Malus domestica (Apple) (Pyrus malus)	PATHWAY: Pigment biosynthesis; anthocyanin biosynthesis.	Dioxygenase; Flavonoid biosynthesis; Iron; Metal-binding; Oxidoreductase; Vitamin C
SRR1271858_TR21137_c0_g1_i1_len=1857	GDL71_ARATH	Q:1545-604,H:39-352	59.37%ID	E:9e-134	GDSL esterase/lipase At5g03610	PF00657.19^Lipase_GDSL^GDSL-like Lipase/Acylhydrolase^55-356^E:3e-12	0	1,691	0	5,304	0	2,997	0	3,135	0,534	0,374	GDL71_ARATH	GDSL esterase/lipase At5g03610 (EC 3.1.1.-) (Extracellular lipase At5g03610)	At5g03610 F17C15.30	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Glycoprotein; Hydrolase; Lipid degradation; Lipid metabolism; Reference proteome; Secreted; Signal
SRR1271858_TR43396_c1_g1_i1_len=2203	PTR28_ARATH	Q:1893-175,H:4-569	63.08%ID	E:0	Protein NRT1/ PTR FAMILY 5.6	PF07690.13^MFS_1^Major Facilitator Superfamily^91-516^E:6.2e-09`PF00854.18^PTR2^POT family^112-534^E:1e-94	0	4,942	0	9,905	0	4,653	0	4,55	1	0,15	PTR28_ARATH	Protein NRT1/ PTR FAMILY 5.6 (AtNPF5.6)	NPF5.6 At2g37900 T8P21.19	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Membrane; Phosphoprotein; Reference proteome; Transmembrane; Transmembrane helix; Transport
SRR1271858_TR49971_c0_g1_i7_len=2709	NA	NA	NA	NA	NA	PF06200.11^tify^tify domain^65-96^E:9.6e-17	0,001	2,18	0	3,069	0	2,691	0	2,938	0,11	0,589	.	.	.	.	.	.
SRR1271858_TR49971_c0_g1_i26_len=3146	NA	NA	NA	NA	NA	PF09425.7^CCT_2^Divergent CCT motif^100-120^E:1.8e-09	0	2,496	0	2,779	0	3,051	0	3,143	0,875	0,083	.	.	.	.		.
SRR1271858_TR57498_c0_g2_i1_len=846	GSTX4_TOBAC	Q:58-579,H:47-221	72.57%ID	E:4e-89	Probable glutathione S-transferase	PF02798.17^GST_N^Glutathione S-transferase, N-terminal domain^16-50^E:1.2e-09`PF13417.3^GST_N_3^Glutathione S-transferase, N-terminal domain^18-54^E:6.7e-07`PF00043.22^GST_C^Glutathione S-transferase, C-terminal domain^89-167^E:3.2e-11`PF13410.3^GST_C_2^Glutathione S-transferase, C-terminal domain^96-161^E:2.4e-12	0	1,444	0	2,694	0	1,059	0,001	0,737	0,021	0,621	GSTX4_TOBAC	Probable glutathione S-transferase (EC 2.5.1.18) (Auxin-induced protein PCNT107)		Nicotiana tabacum (Common tobacco)		Auxin signaling pathway; Transferase
SRR1271859_TR797_c0_g1_i1_len=914	SRG1_ARATH	Q:817-56,H:16-279	46.97%ID	E:2e-81	Protein SRG1	PF14226.3^DIOX_N^non-haem dioxygenase in morphine synthesis N-terminal^56-136^E:1.5e-19`PF03171.17^2OG-FeII_Oxy^2OG-Fe(II) oxygenase superfamily^197-262^E:1.3e-14	0	6,992	0	6,778	0	10,204	0	10,199	1	1,039	SRG1_ARATH	Protein SRG1 (AtSRG1) (Protein SENESCENCE-RELATED GENE 1)	SRG1 At1g17020 F20D23.28 F6I1.30	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Iron; Metal-binding; Oxidoreductase; Reference proteome
SRR1271859_TR7358_c0_g1_i1_len=2680	FAO2_LOTJA	Q:2002-137,H:119-748	62.11%ID	E:0	Long-chain-alcohol oxidase FAO2	PF00732.16^GMC_oxred_N^GMC oxidoreductase^91-353^E:2.4e-69`PF05199.10^GMC_oxred_C^GMC oxidoreductase^442-575^E:1.2e-19	0	5,799	0	4,59	0	2,293	0	2,447	0,402	1,137	FAO2_LOTJA	Long-chain-alcohol oxidase FAO2 (EC 1.1.3.20) (Long-chain fatty alcohol oxidase 2)	FAO2	Lotus japonicus (Lotus corniculatus var. japonicus)		FAD; Flavoprotein; Membrane; Oxidoreductase; Transmembrane; Transmembrane helix
SRR1271859_TR11727_c0_g1_i1_len=974	NA	NA	NA	NA	NA	PF06232.8^ATS3^Embryo-specific protein 3, (ATS3)^30-132^E:2.4e-08`PF01477.20^PLAT^PLAT/LH2 domain^36-153^E:3.4e-13	0	1,271	0	3,529	0	4,594	0	4,592	0,027	0,856	.	.	.	.	.	.
SRR1271859_TR18405_c0_g2_i1_len=2878	MYC4_ARATH	Q:565-2382,H:60-585	52.81%ID	E:1e-162	Transcription factor MYC4	PF14215.3^bHLH-MYC_N^bHLH-MYC and R2R3-MYB transcription factors N-terminal^1-81^E:3.1e-22`PF00010.23^HLH^Helix-loop-helix DNA-binding domain^327-372^E:3e-10	0	1,963	0	2,492	0	1,849	0	1,91	0,204	0,546	MYC4_ARATH	Transcription factor MYC4 (AtMYC4) (Basic helix-loop-helix protein 4) (AtbHLH4) (bHLH 4) (Transcription factor EN 37) (bHLH transcription factor bHLH004)	MYC4 BHLH4 EN37 At4g17880 T6K21.60	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; DNA-binding; Nucleus; Reference proteome; Transcription; Transcription regulation
SRR1271859_TR23354_c0_g2_i1_len=1562	NA	NA	NA	NA	NA	PF00257.16^Dehydrin^Dehydrin^10-178^E:2e-43	0	2,197	0	4,675	0	5,109	0	2,946	0	-2,756	.	.	.	.	.	.
SRR1271859_TR31628_c0_g1_i1_len=1321	SAMT_CLABR	Q:1258-167,H:1-357	56.56%ID	E:4e-146	Salicylate carboxymethyltransferase	PF03492.12^Methyltransf_7^SAM dependent carboxyl methyltransferase^39-363^E:1.9e-125	0	4,081	0	4,677	0	3,384	0	3,664	1	2,67	SAMT_CLABR	Salicylate carboxymethyltransferase (EC 2.1.1.274) (S-adenosyl-L-methionine:salicylate acid carboxylmethyltransferase) (CbSAMT) (Salicylate O-methyltransferase)	SAMT	Clarkia breweri (Fairy fans) (Eucharidium breweri)		3D-structure; Magnesium; Metal-binding; Methyltransferase; S-adenosyl-L-methionine; Transferase
SRR1271859_TR33815_c0_g1_i1_len=1249	SRG1_ARATH	Q:474-1040,H:168-356	39.15%ID	E:2e-40	Protein SRG1	PF03171.17^2OG-FeII_Oxy^2OG-Fe(II) oxygenase superfamily^26-124^E:1.6e-27	0	8,413	0	11,646	0	4,389	0	3,139	1	0,872	SRG1_ARATH	Protein SRG1 (AtSRG1) (Protein SENESCENCE-RELATED GENE 1)	SRG1 At1g17020 F20D23.28 F6I1.30	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Iron; Metal-binding; Oxidoreductase; Reference proteome
SRR1271859_TR38939_c0_g1_i1_len=3435	NA	NA	NA	NA	NA	PF13419.3^HAD_2^Haloacid dehalogenase-like hydrolase^130-310^E:1.2e-20`PF00702.23^Hydrolase^haloacid dehalogenase-like hydrolase^213-303^E:4.5e-08`PF13242.3^Hydrolase_like^HAD-hyrolase-like^265-312^E:3.9e-06	0	3,072	0	4,499	0	1,952	0	2,396	1	1,04	.	.	.	.	.	.
SRR1271859_TR43882_c2_g5_i7_len=2157	PTR53_ARATH	Q:2016-256,H:27-615	54.9%ID	E:0	Protein NRT1/ PTR FAMILY 2.11	PF00854.18^PTR2^POT family^95-527^E:1e-80	0,001	1,247	0	3,435	0	5,118	0	4,948	1	0,036	PTR53_ARATH	Protein NRT1/ PTR FAMILY 2.11 (AtNPF2.11) (Nitrate transporter 1.10) (Protein GLUCOSINOLATE TRANSPORTER-2)	NPF2.11 GTR2 NRT1.10 At5g62680 MRG21.10	Arabidopsis thaliana (Mouse-ear cress)		Cell membrane; Complete proteome; Membrane; Reference proteome; Transmembrane; Transmembrane helix; Transport
SRR1271859_TR44431_c0_g1_i3_len=1795	ARGE_ARATH	Q:185-1495,H:1-438	67.57%ID	E:0	Acetylornithine deacetylase	PF01546.25^Peptidase_M20^Peptidase family M20/M25/M40^95-434^E:5.3e-29`PF07687.11^M20_dimer^Peptidase dimerisation domain^203-317^E:6.6e-13	0	2,937	0	5,461	0	5,453	0	4,171	1	1,453	ARGE_ARATH	Acetylornithine deacetylase (EC 3.5.1.16) (N-acetylornithinase) (AO) (Acetylornithinase) (NAO)	At4g17830 dl4945w T6K21	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Amino-acid biosynthesis; L-arginine biosynthesis; L-ornithine from N(2)-acetyl-L-ornithine (linear): step 1/1.	Alternative splicing; Amino-acid biosynthesis; Arginine biosynthesis; Cobalt; Complete proteome; Hydrolase; Metal-binding; Reference proteome; Zinc
SRR342017_TR1488_c0_g1_i1_len=1558	NA	NA	NA	NA	NA	PF17181.1^EPF^Epidermal patterning factor proteins^96-146^E:7.6e-20	0	1,667	0	2,297	0	1,755	0	1,431	0,618	0,264	.	.	.	.	.	.
SRR342017_TR6175_c1_g1_i6_len=2137	SERC_ARATH	Q:205-1083,H:1-294	70.41%ID	E:2e-141	Phosphoserine phosphatase, chloroplastic	PF00702.23^Hydrolase^haloacid dehalogenase-like hydrolase^83-257^E:1.1e-16`PF12710.4^HAD^haloacid dehalogenase-like hydrolase^86-254^E:2.4e-12	0,001	1,165	0	2,133	0	1,739	0	1,848	0,73	0,14	SERC_ARATH	Phosphoserine phosphatase, chloroplastic (PSP) (PSPase) (EC 3.1.3.3) (O-phosphoserine phosphohydrolase)	PSP PSP1 At1g18640 F26I16.2	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Amino-acid biosynthesis; L-serine biosynthesis; L-serine from 3-phospho-D-glycerate: step 3/3.	Amino-acid biosynthesis; Chloroplast; Complete proteome; Hydrolase; Magnesium; Metal-binding; Phosphoprotein; Plastid; Reference proteome; Serine biosynthesis; Transit peptide
SRR342019_TR769_c0_g1_i1_len=1320	NA	NA	NA	NA	NA	PF04193.11^PQ-loop^PQ loop repeat^37-93^E:1.4e-18`PF04193.11^PQ-loop^PQ loop repeat^256-313^E:5.5e-16	0	4,108	0	5,354	0	3,59	0	2,81	0,003	1,368	.	.	.	.	.	.
SRR342019_TR1484_c0_g1_i1_len=1241	NA	NA	NA	NA	NA	PF03350.13^UPF0114^Uncharacterized protein family, UPF0114^106-244^E:1.2e-37	0	1,113	0	1,904	0	1,881	0	1,958	0,596	0,17	.	.	.	.	.	.
SRR342019_TR3321_c0_g1_i2_len=676	SUMO2_ARATH	Q:148-414,H:6-93	89.89%ID	E:3e-49	Small ubiquitin-related modifier 2	PF11976.5^Rad60-SLD^Ubiquitin-2 like Rad60 SUMO-like^26-96^E:4e-25`PF00240.20^ubiquitin^Ubiquitin family^28-98^E:4.9e-14	0,001	1,133	0	1,386	0	1,584	0	1,511	0,862	-0,102	SUMO2_ARATH	Small ubiquitin-related modifier 2 (AtSUMO2)	SUMO2 SUM2 At5g55160 MCO15.11	Arabidopsis thaliana (Mouse-ear cress)		Alternative splicing; Complete proteome; Cytoplasm; Isopeptide bond; Nucleus; Reference proteome; Ubl conjugation pathway
SRR342019_TR3921_c0_g1_i1_len=1395	CSE_ARATH	Q:1127-309,H:50-323	35.4%ID	E:2e-49	Caffeoylshikimate esterase	PF12146.5^Hydrolase_4^Serine aminopeptidase, S33^34-272^E:3.2e-67`PF00561.17^Abhydrolase_1^alpha/beta hydrolase fold^39-148^E:1.1e-08`PF12697.4^Abhydrolase_6^Alpha/beta hydrolase family^39-270^E:9.2e-10	0	2,195	0	3,874	0	6,303	0	6,75	0,381	-0,785	CSE_ARATH	Caffeoylshikimate esterase (EC 3.1.1.-) (Lysophospholipase 2) (LysoPL2)	CSE At1g52760 F14G24.3	Arabidopsis thaliana (Mouse-ear cress)		Cell membrane; Complete proteome; Hydrolase; Lignin biosynthesis; Membrane; Reference proteome
SRR342019_TR4458_c0_g1_i1_len=1942	MYRS_QUEIL	Q:1692-466,H:38-414	53.55%ID	E:1e-134	Myrcene synthase, chloroplastic	PF01397.18^Terpene_synth^Terpene synthase, N-terminal domain^67-170^E:1.7e-24	0	4,335	0	9,243	0	9,985	0	9,901	1	0,755	MYRS_QUEIL	Myrcene synthase, chloroplastic (EC 4.2.3.15)		Quercus ilex (Holly oak)		Chloroplast; Lyase; Magnesium; Manganese; Metal-binding; Plastid; Transit peptide
SRR342019_TR5666_c0_g6_i1_len=1927	FACR5_ARATH	Q:228-1703,H:3-494	50.91%ID	E:6e-171	Probable fatty acyl-CoA reductase 5	PF07993.9^NAD_binding_4^Male sterility protein^18-325^E:2.4e-76`PF03015.16^Sterile^Male sterility protein^400-496^E:3.2e-12	0	2,205	0	6,764	0	5,096	0	6,562	0,356	1,327	FACR5_ARATH	Probable fatty acyl-CoA reductase 5 (EC 1.2.1.n2)	FAR5 At3g44550 F14L2.100	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Lipid biosynthesis; Lipid metabolism; NADP; Oxidoreductase; Reference proteome
SRR342019_TR5968_c2_g4_i3_len=1281	B2_DAUCA	Q:675-220,H:54-205	80.92%ID	E:9e-91	B2 protein	PF10539.6^Dev_Cell_Death^Development and cell death domain^168-294^E:1.7e-41	0	0,871	0	2,49	0	1,277	0	1,511	0,312	0,763	B2_DAUCA	B2 protein		Daucus carota (Wild carrot)		
SRR342019_TR16670_c0_g1_i1_len=578	NA	NA	NA	NA	NA	.	0	3,334	0	4,758	0	4,035	0	3,638	0,014	2,973	.	.	.	.	.	.
SRR342019_TR21154_c0_g1_i1_len=5234	AB4C_ARATH	Q:4828-365,H:23-1516	67.95%ID	E:0	ABC transporter C family member 4	PF00664.20^ABC_membrane^ABC transporter transmembrane region^331-597^E:9.8e-29`PF00005.24^ABC_tran^ABC transporter^663-795^E:1.7e-19`PF00664.20^ABC_membrane^ABC transporter transmembrane region^982-1202^E:5.3e-29`PF00005.24^ABC_tran^ABC transporter^1283-1431^E:4.3e-28	0	2,332	0	3,748	0	2,24	0	1,666	1	-0,186	AB4C_ARATH	ABC transporter C family member 4 (ABC transporter ABCC.4) (AtABCC4) (EC 3.6.3.44) (ATP-energized glutathione S-conjugate pump 4) (Glutathione S-conjugate-transporting ATPase 4) (Multidrug resistance-associated protein 4)	ABCC4 EST3 MRP4 At2g47800 F17A22.19	Arabidopsis thaliana (Mouse-ear cress)		ATP-binding; Cell membrane; Complete proteome; Hydrolase; Membrane; Nucleotide-binding; Reference proteome; Repeat; Transmembrane; Transmembrane helix; Transport; Vacuole
SRR342019_TR22681_c0_g4_i3_len=1765	C74B2_ARATH	Q:1591-197,H:38-492	56.32%ID	E:1e-178	Linolenate hydroperoxide lyase, chloroplastic {ECO:0000305|PubMed:9701595}	PF00067.19^p450^Cytochrome P450^146-495^E:1.1e-24	0	1,326	0	1,076	0	0,998	0	0,916	1	0,375	C74B2_ARATH	Linolenate hydroperoxide lyase, chloroplastic (EC 4.2.99.-) (Cytochrome P450 74B2) (Hydroperoxide lyase 1)	CYP74B2 HPL1	Arabidopsis thaliana (Mouse-ear cress)		Chloroplast; Heme; Iron; Lyase; Metal-binding; Plastid; Transit peptide
SRR342019_TR27753_c0_g2_i1_len=774	GASAE_ARATH	Q:277-83,H:211-275	76.92%ID	E:2e-26	Gibberellin-regulated protein 14	PF02704.11^GASA^Gibberellin regulated protein^170-230^E:1e-18	0	1,452	0	4,741	0	4,934	0	5,266	0,643	-0,587	GASAE_ARATH	Gibberellin-regulated protein 14 (GAST1 protein homolog 14)	GASA14 At5g14920 F2G14.40	Arabidopsis thaliana (Mouse-ear cress)		Alternative splicing; Complete proteome; Disulfide bond; Gibberellin signaling pathway; Reference proteome; Secreted; Signal
SRR342019_TR28505_c2_g4_i4_len=1446	GCL1_ARATH	Q:3-1160,H:82-433	63.99%ID	E:5e-173	LanC-like protein GCL1	PF05147.10^LANC_like^Lanthionine synthetase C-like protein^2-242^E:1.1e-56	0	3,334	0	2,88	0	7,358	0,001	6,639	0,034	5,561	GCL1_ARATH	LanC-like protein GCL1 (G protein-coupled receptor 2-like protein 1) (Protein GCR2-like 1)	GCL1 At5g65280 MQN23.23	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Reference proteome
SRR342019_TR28505_c2_g4_i6_len=2638	GCL1_ARATH	Q:1414-2352,H:126-433	69.97%ID	E:3e-150	LanC-like protein GCL1	PF05147.10^LANC_like^Lanthionine synthetase C-like protein^2-256^E:1.2e-65	0	3,522	0	4,913	0	4,656	0	4,893	0,189	1,712	GCL1_ARATH	LanC-like protein GCL1 (G protein-coupled receptor 2-like protein 1) (Protein GCR2-like 1)	GCL1 At5g65280 MQN23.23	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Reference proteome
SRR342019_TR35584_c0_g2_i1_len=2436	ACOX1_ARATH	Q:255-2243,H:1-663	78.88%ID	E:0	Peroxisomal acyl-coenzyme A oxidase 1	PF14749.3^Acyl-CoA_ox_N^Acyl-coenzyme A oxidase N-terminal^17-132^E:1.4e-31`PF02770.16^Acyl-CoA_dh_M^Acyl-CoA dehydrogenase, middle domain^134-246^E:4.5e-12`PF01756.16^ACOX^Acyl-CoA oxidase^479-656^E:4.1e-46	0,001	1,066	0	2,473	0	2,64	0	2,703	0,255	0,591	ACOX1_ARATH	Peroxisomal acyl-coenzyme A oxidase 1 (AOX 1) (EC 1.3.3.6) (Long-chain acyl-CoA oxidase) (AtCX1)	ACX1 At4g16760 dl4405c FCAALL.119	Arabidopsis thaliana (Mouse-ear cress)		3D-structure; Alternative splicing; Complete proteome; Disulfide bond; FAD; Fatty acid metabolism; Flavoprotein; Lipid metabolism; Oxidoreductase; Peroxisome; Reference proteome
SRR342019_TR37278_c0_g1_i3_len=2454	LAL5_ARATH	Q:290-1687,H:8-464	59.87%ID	E:1e-166	.	PF01554.15^MatE^MatE^57-216^E:1.4e-29`PF01554.15^MatE^MatE^278-439^E:1.1e-25	0	1,538	0	3,871	0	2,082	0	2,148	0,528	-0,245	DTX18_ARATH	Protein DETOXIFICATION 18 (AtDTX18) (Multidrug and toxic compound extrusion protein 18) (MATE protein 18) (Protein LIKE ALF5)	DTX18 LAL5 At3g23550 MDB19.3	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Membrane; Reference proteome; Transmembrane; Transmembrane helix; Transport
SRR342019_TR38071_c4_g2_i10_len=1933	ARGE_ARATH	Q:260-1570,H:1-438	67.8%ID	E:0	Acetylornithine deacetylase	PF01546.25^Peptidase_M20^Peptidase family M20/M25/M40^95-434^E:5.3e-29`PF07687.11^M20_dimer^Peptidase dimerisation domain^203-317^E:2.3e-12	0	3,436	0	4,858	0	5,05	0	4,711	0,058	0,816	ARGE_ARATH	Acetylornithine deacetylase (EC 3.5.1.16) (N-acetylornithinase) (AO) (Acetylornithinase) (NAO)	At4g17830 dl4945w T6K21	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Amino-acid biosynthesis; L-arginine biosynthesis; L-ornithine from N(2)-acetyl-L-ornithine (linear): step 1/1.	Alternative splicing; Amino-acid biosynthesis; Arginine biosynthesis; Cobalt; Complete proteome; Hydrolase; Metal-binding; Reference proteome; Zinc
SRR342019_TR38071_c4_g2_i17_len=1977	ARGE_ARATH	Q:260-1570,H:1-438	67.8%ID	E:0	Acetylornithine deacetylase	PF01546.25^Peptidase_M20^Peptidase family M20/M25/M40^95-434^E:5.3e-29`PF07687.11^M20_dimer^Peptidase dimerisation domain^203-317^E:2.3e-12	0	3,085	0	5,935	0	6,318	0	4,301	1	0	ARGE_ARATH	Acetylornithine deacetylase (EC 3.5.1.16) (N-acetylornithinase) (AO) (Acetylornithinase) (NAO)	At4g17830 dl4945w T6K21	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Amino-acid biosynthesis; L-arginine biosynthesis; L-ornithine from N(2)-acetyl-L-ornithine (linear): step 1/1.	Alternative splicing; Amino-acid biosynthesis; Arginine biosynthesis; Cobalt; Complete proteome; Hydrolase; Metal-binding; Reference proteome; Zinc
SRR342022_TR137_c3_g1_i6_len=1264	EGS1_OCIBA	Q:119-1045,H:7-314	66.99%ID	E:3e-143	Eugenol synthase 1	PF05368.10^NmrA^NmrA-like family^8-231^E:3.3e-55`PF01370.18^Epimerase^NAD dependent epimerase/dehydratase family^8-86^E:1e-05`PF01073.16^3Beta_HSD^3-beta hydroxysteroid dehydrogenase/isomerase family^9-98^E:2.5e-05`PF13460.3^NAD_binding_10^NAD(P)H-binding^12-149^E:4e-12	0	1,77	0	3,318	0	5,065	0	5,922	1	0,082	EGS1_OCIBA	Eugenol synthase 1 (EC 1.1.1.318)	EGS1	Ocimum basilicum (Sweet basil)	PATHWAY: Aromatic compound metabolism; phenylpropanoid biosynthesis.	3D-structure; NADP; Oxidoreductase; Phenylpropanoid metabolism
SRR342022_TR4918_c0_g2_i1_len=1468	STSY_CATRO	Q:106-1170,H:1-352	96.34%ID	E:0	Strictosidine synthase	PF08450.9^SGL^SMP-30/Gluconolaconase/LRE-like region^169-344^E:4.4e-07`PF03088.13^Str_synth^Strictosidine synthase^194-282^E:6.6e-24	0	1,154	0	3,375	0	3,022	0	2,148	1	0,724	STSY_CATRO	Strictosidine synthase (EC 4.3.3.2)	STR1 SSS	Catharanthus roseus (Madagascar periwinkle) (Vinca rosea)	PATHWAY: Alkaloid biosynthesis; 3alpha(S)-strictosidine biosynthesis; 3alpha(S)-strictosidine from secologanin and tryptamine: step 1/1.	Alkaloid metabolism; Direct protein sequencing; Glycoprotein; Lyase; Signal; Vacuole
SRR342022_TR5922_c0_g2_i1_len=2130	ICS_CATRO	Q:1950-376,H:43-579	62.27%ID	E:0	Isochorismate synthase, chloroplastic	PF00425.15^Chorismate_bind^chorismate binding enzyme^316-570^E:5.9e-55	0	1,974	0	2,848	0	3,154	0	2,978	1	0,393	ICS_CATRO	Isochorismate synthase, chloroplastic (EC 5.4.4.2)		Catharanthus roseus (Madagascar periwinkle) (Vinca rosea)		Chloroplast; Direct protein sequencing; Isomerase; Magnesium; Plant defense; Plastid; Transit peptide
SRR342022_TR7495_c0_g2_i1_len=1876	C83B1_ARATH	Q:198-1571,H:41-499	45.12%ID	E:2e-139	Cytochrome P450 83B1	PF00067.19^p450^Cytochrome P450^55-512^E:1.8e-103	0	3,911	0	6,176	0	9,752	0	10,653	1	2,541	C83B1_ARATH	Cytochrome P450 83B1 (EC 1.14.-.-) (Protein ALTERED TRYPTOPHAN REGULATION 4) (Protein RED ELONGATED 1) (Protein SUPERROOT 2)	CYP83B1 ATR4 RED1 RNT1 RUNT1 SUR2 At4g31500 F3L17.70	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Growth regulation; Heme; Iron; Membrane; Metal-binding; Monooxygenase; Oxidoreductase; Reference proteome; Transmembrane; Transmembrane helix
SRR342022_TR9756_c0_g1_i4_len=2081	VINSY_RAUSE	Q:423-1793,H:5-407	34.91%ID	E:5e-77	Vinorine synthase	PF02458.12^Transferase^Transferase family^4-309^E:8.5e-68`PF02458.12^Transferase^Transferase family^336-459^E:2.4e-13	0,001	2,232	0	6,36	0	2,946	0	3,026	1	1,326	VINSY_RAUSE	Vinorine synthase (EC 2.3.1.160)	ACT	Rauvolfia serpentina (Serpentine wood) (Ophioxylon serpentinum)		3D-structure; Acyltransferase; Alkaloid metabolism; Direct protein sequencing; Transferase
SRR342022_TR13452_c0_g2_i1_len=703	HQGT_RAUSE	Q:703-311,H:342-470	80.92%ID	E:1e-64	Hydroquinone glucosyltransferase	PF00201.15^UDPGT^UDP-glucoronosyl and UDP-glucosyl transferase^1-91^E:7.5e-19	0	1,94	0	4,522	0	2,952	0	2,846	1	1,879	HQGT_RAUSE	Hydroquinone glucosyltransferase (EC 2.4.1.218) (Arbutin synthase)	AS	Rauvolfia serpentina (Serpentine wood) (Ophioxylon serpentinum)		Direct protein sequencing; Glycosyltransferase; Transferase
SRR342022_TR15270_c3_g3_i1_len=737	CYB5_BRAOB	Q:130-528,H:2-134	60.9%ID	E:1e-40	Cytochrome b5	PF00173.25^Cyt-b5^Cytochrome b5-like Heme/Steroid binding domain^10-81^E:7.1e-27	0	0,824	0	2,758	0	1,437	0	1,315	1	-1,134	CYB5_BRAOB	Cytochrome b5	CYB5	Brassica oleracea var. botrytis (Cauliflower)		Direct protein sequencing; Electron transport; Endoplasmic reticulum; Heme; Iron; Membrane; Metal-binding; Microsome; Transmembrane; Transmembrane helix; Transport
SRR342022_TR17158_c1_g3_i7_len=3511	GCL1_ARATH	Q:2315-3226,H:164-433	63.82%ID	E:2e-123	LanC-like protein GCL1	PF05147.10^LANC_like^Lanthionine synthetase C-like protein^2-142^E:2.4e-36	0	3,544	0	4,593	0	4,405	0	4,74	0,005	6,199	GCL1_ARATH	LanC-like protein GCL1 (G protein-coupled receptor 2-like protein 1) (Protein GCR2-like 1)	GCL1 At5g65280 MQN23.23	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Reference proteome
SRR342022_TR21854_c3_g4_i2_len=4472	LOX21_SOLTU	Q:3797-1440,H:106-894	71.39%ID	E:0	Linoleate 13S-lipoxygenase 2-1, chloroplastic	PF00305.16^Lipoxygenase^Lipoxygenase^50-717^E:0	0	2,369	0	5,021	0	6,397	0	6,552	0,564	-0,489	LOX21_SOLTU	Linoleate 13S-lipoxygenase 2-1, chloroplastic (EC 1.13.11.12) (Lipoxygenase 2-1)	LOX2.1 LOX-H1	Solanum tuberosum (Potato)	PATHWAY: Lipid metabolism; oxylipin biosynthesis. {ECO:0000255|PROSITE-ProRule:PRU00726}.	Chloroplast; Complete proteome; Dioxygenase; Fatty acid biosynthesis; Fatty acid metabolism; Iron; Lipid biosynthesis; Lipid metabolism; Metal-binding; Oxidoreductase; Oxylipin biosynthesis; Plastid; Reference proteome; Thylakoid; Transit peptide
SRR342022_TR23185_c0_g3_i9_len=2204	MYRS_QUEIL	Q:1938-244,H:36-594	58.23%ID	E:0	Myrcene synthase, chloroplastic	PF01397.18^Terpene_synth^Terpene synthase, N-terminal domain^67-243^E:6.3e-44`PF03936.13^Terpene_synth_C^Terpene synthase family, metal binding domain^275-542^E:6.6e-100	0	5,107	0	9,293	0	7,739	0	7,656	1	0	MYRS_QUEIL	Myrcene synthase, chloroplastic (EC 4.2.3.15)		Quercus ilex (Holly oak)		Chloroplast; Lyase; Magnesium; Manganese; Metal-binding; Plastid; Transit peptide
SRR342022_TR27021_c0_g3_i2_len=1339	TAR4_ARATH	Q:97-1332,H:33-449	53.94%ID	E:2e-157	Tryptophan aminotransferase-related protein 4	PF04864.10^Alliinase_C^Allinase^1-341^E:1.4e-134`PF00155.18^Aminotran_1_2^Aminotransferase class I and II^27-322^E:3.2e-06	0	2,793	0	3,051	0	3,571	0	3,114	0,042	2,175	TAR4_ARATH	Tryptophan aminotransferase-related protein 4 (EC 2.6.1.-)	TAR4 At1g34060 F12G12.12 F12G12.150	Arabidopsis thaliana (Mouse-ear cress)		Aminotransferase; Complete proteome; Membrane; Pyridoxal phosphate; Reference proteome; Transferase; Transmembrane; Transmembrane helix
SRR342022_TR30684_c1_g2_i4_len=1695	FAD3E_TOBAC	Q:326-1420,H:12-374	76.16%ID	E:0	Omega-3 fatty acid desaturase, endoplasmic reticulum	PF11960.5^DUF3474^Domain of unknown function (DUF3474)^6-62^E:7.5e-26`PF00487.21^FA_desaturase^Fatty acid desaturase^77-328^E:4.4e-33	0	4,303	0	6,848	0	8,141	0	9,016	0,034	3,49	FAD3E_TOBAC	Omega-3 fatty acid desaturase, endoplasmic reticulum (EC 1.14.19.-)	FAD3	Nicotiana tabacum (Common tobacco)	PATHWAY: Lipid metabolism; polyunsaturated fatty acid biosynthesis.	Endoplasmic reticulum; Fatty acid biosynthesis; Fatty acid metabolism; Lipid biosynthesis; Lipid metabolism; Membrane; Oxidoreductase; Transmembrane; Transmembrane helix
SRR342022_TR30684_c1_g2_i9_len=1634	FAD3E_TOBAC	Q:265-1359,H:12-374	76.16%ID	E:0	Omega-3 fatty acid desaturase, endoplasmic reticulum	PF11960.5^DUF3474^Domain of unknown function (DUF3474)^6-62^E:7.5e-26`PF00487.21^FA_desaturase^Fatty acid desaturase^77-328^E:4.4e-33	0,001	2,741	0	6,66	0	4,86	0	5,723	1	-0,186	FAD3E_TOBAC	Omega-3 fatty acid desaturase, endoplasmic reticulum (EC 1.14.19.-)	FAD3	Nicotiana tabacum (Common tobacco)	PATHWAY: Lipid metabolism; polyunsaturated fatty acid biosynthesis.	Endoplasmic reticulum; Fatty acid biosynthesis; Fatty acid metabolism; Lipid biosynthesis; Lipid metabolism; Membrane; Oxidoreductase; Transmembrane; Transmembrane helix
SRR342022_TR31491_c0_g1_i2_len=1495	LDOX_MALDO	Q:367-1347,H:10-341	39.34%ID	E:3e-75	Leucoanthocyanidin dioxygenase	PF14226.3^DIOX_N^non-haem dioxygenase in morphine synthesis N-terminal^52-163^E:2e-27`PF03171.17^2OG-FeII_Oxy^2OG-Fe(II) oxygenase superfamily^212-310^E:1.5e-27	0	3,522	0	6,325	0	2,878	0	2,887	0,629	0,944	LDOX_MALDO	Leucoanthocyanidin dioxygenase (LDOX) (Leucocyanidin oxygenase) (EC 1.14.11.19) (Anthocyanidin synthase) (Leucoanthocyanidin hydroxylase)	ANS	Malus domestica (Apple) (Pyrus malus)	PATHWAY: Pigment biosynthesis; anthocyanin biosynthesis.	Dioxygenase; Flavonoid biosynthesis; Iron; Metal-binding; Oxidoreductase; Vitamin C
SRR342023_TR2068_c2_g6_i2_len=3638	PAO2_ARATH	Q:1961-501,H:1-490	80.41%ID	E:0	Probable polyamine oxidase 2	PF00890.21^FAD_binding_2^FAD binding domain^27-70^E:1.9e-06`PF13450.3^NAD_binding_8^NAD(P)-binding Rossmann-like domain^29-83^E:2.2e-13`PF01593.21^Amino_oxidase^Flavin containing amine oxidoreductase^34-453^E:9.6e-94	0	1,521	0	3,976	0	2,916	0	3,721	0,811	0,44	PAO2_ARATH	Probable polyamine oxidase 2 (AtPAO2) (EC 1.5.3.-) (Amine oxidase 1)	PAO2 At2g43020 MFL8.12	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; FAD; Flavoprotein; Oxidoreductase; Peroxisome; Reference proteome
SRR342023_TR2263_c2_g2_i14_len=1134	ARGE_ARATH	Q:2-1018,H:58-394	71.47%ID	E:9e-178	Acetylornithine deacetylase	PF01546.25^Peptidase_M20^Peptidase family M20/M25/M40^41-330^E:2.4e-22`PF07687.11^M20_dimer^Peptidase dimerisation domain^149-263^E:7.2e-12	0	2,497	0	4,748	0	4,424	0	3,258	0,282	1,123	ARGE_ARATH	Acetylornithine deacetylase (EC 3.5.1.16) (N-acetylornithinase) (AO) (Acetylornithinase) (NAO)	At4g17830 dl4945w T6K21	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Amino-acid biosynthesis; L-arginine biosynthesis; L-ornithine from N(2)-acetyl-L-ornithine (linear): step 1/1.	Alternative splicing; Amino-acid biosynthesis; Arginine biosynthesis; Cobalt; Complete proteome; Hydrolase; Metal-binding; Reference proteome; Zinc
SRR342023_TR2555_c4_g2_i1_len=2165	NA	NA	NA	NA	NA	PF06200.11^tify^tify domain^65-96^E:1.4e-16`PF09425.7^CCT_2^Divergent CCT motif^203-223^E:4.2e-09	0,001	2,769	0	3,094	0	2,853	0	2,889	1	0,511	.	.	.	.	.	.
SRR342023_TR4584_c1_g4_i3_len=2527	HQGT_RAUSE	Q:1478-2527,H:27-364	78.29%ID	E:0	Hydroquinone glucosyltransferase	PF03360.13^Glyco_transf_43^Glycosyltransferase family 43^114-321^E:4.4e-72	0	1,578	0	4,475	0	2,445	0	2,588	1	0,791	HQGT_RAUSE	Hydroquinone glucosyltransferase (EC 2.4.1.218) (Arbutin synthase)	AS	Rauvolfia serpentina (Serpentine wood) (Ophioxylon serpentinum)		Direct protein sequencing; Glycosyltransferase; Transferase
SRR342023_TR8541_c0_g2_i1_len=637	RL112_ARATH	Q:133-636,H:1-168	95.83%ID	E:2e-106	60S ribosomal protein L11-2	PF00281.16^Ribosomal_L5^Ribosomal protein L5^9-62^E:8.3e-21`PF00673.18^Ribosomal_L5_C^ribosomal L5P family C-terminus^66-164^E:6.9e-21	0	8,634	0	1,321	0	1,433	0	1,389	0,691	-0,103	RL112_ARATH	60S ribosomal protein L11-2 (L16)	RPL11B At3g58700 T20N10_50; RPL11C RPL16B At4g18730 F28A21.140; RPL11D At5g45775 MRA19.26 MRA19_21	Arabidopsis thaliana (Mouse-ear cress)		Alternative splicing; Complete proteome; Cytoplasm; RNA-binding; Reference proteome; Ribonucleoprotein; Ribosomal protein; rRNA-binding
SRR342023_TR21501_c0_g2_i4_len=3046	PTR45_ARATH	Q:1876-2943,H:217-576	59.72%ID	E:1e-146	Protein NRT1/ PTR FAMILY 5.7	PF03283.10^PAE^Pectinacetylesterase^54-402^E:1e-163	0	3,423	0	5,07	0	2,714	0	2,053	1	-0,36	PTR45_ARATH	Protein NRT1/ PTR FAMILY 5.7 (AtNPF5.7)	NPF5.7 At3g53960 F5K20.260	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Membrane; Phosphoprotein; Reference proteome; Transmembrane; Transmembrane helix; Transport
SRR342023_TR23966_c0_g4_i2_len=997	TAR4_ARATH	Q:888-421,H:296-449	48.72%ID	E:9e-50	Tryptophan aminotransferase-related protein 4	PF04864.10^Alliinase_C^Allinase^1-144^E:2.1e-46	0	2,91	0	2,155	0	4,419	0	3,364	1	2,747	TAR4_ARATH	Tryptophan aminotransferase-related protein 4 (EC 2.6.1.-)	TAR4 At1g34060 F12G12.12 F12G12.150	Arabidopsis thaliana (Mouse-ear cress)		Aminotransferase; Complete proteome; Membrane; Pyridoxal phosphate; Reference proteome; Transferase; Transmembrane; Transmembrane helix
SRR342023_TR25610_c0_g4_i1_len=1629	CLH2_ARATH	Q:1489-644,H:5-299	42.47%ID	E:6e-55	Chlorophyllase-2, chloroplastic	PF07224.8^Chlorophyllase^Chlorophyllase^2-295^E:4e-90`PF12740.4^Chlorophyllase2^Chlorophyllase enzyme^31-279^E:2.9e-87`PF03403.10^PAF-AH_p_II^Platelet-activating factor acetylhydrolase, isoform II^39-77^E:2.5e-06	0	2,221	0	4,248	0	4,126	0	4,111	0,788	0,104	CLH2_ARATH	Chlorophyllase-2, chloroplastic (AtCLH2) (EC 3.1.1.14) (Chlorophyll-chlorophyllido hydrolase 2) (Chlase 2)	CLH2 At5g43860 MQD19.22	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Porphyrin-containing compound metabolism; chlorophyll degradation.	Chlorophyll catabolism; Chloroplast; Complete proteome; Hydrolase; Membrane; Plastid; Reference proteome; Transit peptide
SRR342023_TR26627_c0_g2_i1_len=1613	TPSGD_VITVI	Q:1496-147,H:19-460	53.33%ID	E:9e-164	(-)-germacrene D synthase	PF01397.18^Terpene_synth^Terpene synthase, N-terminal domain^19-199^E:1.8e-51`PF03936.13^Terpene_synth_C^Terpene synthase family, metal binding domain^230-456^E:1e-83	0	1,415	0	1,833	0	1,743	0	1,526	0,505	0,526	TPSGD_VITVI	(-)-germacrene D synthase (EC 4.2.3.22) (EC 4.2.3.75)	VIT_19s0014g04930 VIT_00014569001 VITISV_013313 VITISV_030783 Vv19s0014g04930	Vitis vinifera (Grape)	PATHWAY: Secondary metabolite biosynthesis; terpenoid biosynthesis.	Complete proteome; Cytoplasm; Lyase; Magnesium; Metal-binding; Reference proteome
SRR342023_TR28680_c0_g1_i1_len=1756	C71DC_CATRO	Q:1614-139,H:1-493	67.61%ID	E:0	Tabersonine 16-hydroxylase	PF00067.19^p450^Cytochrome P450^35-482^E:1.7e-100	0	1,005	0	2,356	0	2,329	0	2,247	0,008	0,742	C71DC_CATRO	Tabersonine 16-hydroxylase (EC 1.14.13.73) (Cytochrome P450 71D12) (Fragment)	CYP71D12	Catharanthus roseus (Madagascar periwinkle) (Vinca rosea)	PATHWAY: Alkaloid biosynthesis; vindoline biosynthesis; vindoline from tabersonine: step 1/6.	Endoplasmic reticulum; Heme; Iron; Metal-binding; Monooxygenase; NADP; Oxidoreductase
SRR342023_TR30099_c0_g1_i2_len=1398	CXE1_ACTER	Q:184-1128,H:21-333	45.6%ID	E:3e-97	Carboxylesterase 1	PF10340.6^DUF2424^Protein of unknown function (DUF2424)^67-184^E:2.3e-05`PF07859.10^Abhydrolase_3^alpha/beta hydrolase fold^82-301^E:1.6e-45	0	2,583	0	3,967	0	3,497	0	3,466	0,643	0,494	CXE1_ACTER	Carboxylesterase 1 (AeCXE1) (EC 3.1.1.1)	CXE1	Actinidia eriantha (Velvet vine) (Actinidia fulvicoma var. lanata)		3D-structure; Hydrolase; Serine esterase
SRR342023_TR30617_c3_g3_i4_len=672	C72A1_CATRO	Q:31-399,H:402-524	95.93%ID	E:2e-78	Secologanin synthase	PF00067.19^p450^Cytochrome P450^2-77^E:1.4e-22	0	1,353	0	2,779	0	2,7	0	2,21	0,542	0,17	C72A1_CATRO	Secologanin synthase (SLS) (EC 1.3.3.9) (CYPLXXII) (Cytochrome P450 72A1)	CYP72A1 CYP72 P450CR3	Catharanthus roseus (Madagascar periwinkle) (Vinca rosea)	PATHWAY: Alkaloid biosynthesis; secologanin biosynthesis.	Alkaloid metabolism; Heme; Iron; Membrane; Metal-binding; Monooxygenase; NADP; Oxidoreductase; Transmembrane; Transmembrane helix; Vacuole
SRR342023_TR31426_c4_g1_i1_len=2080	TT12_ARATH	Q:2006-438,H:1-504	46.29%ID	E:1e-139	.	PF01554.15^MatE^MatE^104-264^E:1.5e-34`PF01554.15^MatE^MatE^326-486^E:5.2e-30	0	0,964	0	2,758	0	1,506	0	1,131	1	0	DTX41_ARATH	Protein DETOXIFICATION 41 (AtDTX41) (Multidrug and toxic compound extrusion protein 41) (MATE protein 41) (Protein TANNIN-DEFICIENT SEED 3) (Protein TRANSPARENT TESTA 12)	DTX41 TDS3 TT12 At3g59030 F17J16_80	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Secondary metabolite biosynthesis; flavonoid biosynthesis.	Antiport; Complete proteome; Flavonoid biosynthesis; Membrane; Reference proteome; Transmembrane; Transmembrane helix; Transport; Vacuole
SRR646596_TR1791_c0_g1_i1_len=791	NA	NA	NA	NA	NA	.	0	1,706	0	3,065	0	3,158	0	2,284	0,517	0,885	.	.	.	.	.	.
SRR646596_TR1932_c0_g1_i5_len=3832	MATE3_ARATH	Q:3363-1954,H:60-557	60.04%ID	E:5e-174	.	PF01554.15^MatE^MatE^122-289^E:6.2e-11`PF14667.3^Polysacc_synt_C^Polysaccharide biosynthesis C-terminal domain^247-338^E:8.8e-07`PF01554.15^MatE^MatE^361-491^E:7.6e-12	0	5,496	0	7,627	0	3,574	0	3,831	1	0,865	DTX45_ARATH	Protein DETOXIFICATION 45, chloroplastic (AtDTX45) (Multidrug and toxic compound extrusion protein 45) (MATE protein 45)	DTX45 At4g38380 F22I13.150	Arabidopsis thaliana (Mouse-ear cress)		Chloroplast; Complete proteome; Membrane; Plastid; Reference proteome; Transit peptide; Transmembrane; Transmembrane helix; Transport
SRR646596_TR8324_c0_g1_i1_len=1006	NA	NA	NA	NA	NA	PF14364.3^DUF4408^Domain of unknown function (DUF4408)^91-115^E:4.6e-08	0	1,919	0	3,1	0	1,691	0	1,693	0,381	1,787	.	.	.	.	.	.
SRR646596_TR12573_c1_g2_i3_len=1235	STSY_CATRO	Q:459-905,H:182-332	41.83%ID	E:1e-30	Strictosidine synthase	.	0	3,744	0	5,097	0	4,268	0	3,737	0,025	3,483	STSY_CATRO	Strictosidine synthase (EC 4.3.3.2)	STR1 SSS	Catharanthus roseus (Madagascar periwinkle) (Vinca rosea)	PATHWAY: Alkaloid biosynthesis; 3alpha(S)-strictosidine biosynthesis; 3alpha(S)-strictosidine from secologanin and tryptamine: step 1/1.	Alkaloid metabolism; Direct protein sequencing; Glycoprotein; Lyase; Signal; Vacuole
SRR646596_TR12743_c2_g4_i10_len=986	ARGE_ARATH	Q:631-353,H:346-438	55.91%ID	E:5e-29	Acetylornithine deacetylase	PF01546.25^Peptidase_M20^Peptidase family M20/M25/M40^5-96^E:5.4e-08	0	1,953	0	2,145	0	5,815	0	5,892	0,319	1,074	ARGE_ARATH	Acetylornithine deacetylase (EC 3.5.1.16) (N-acetylornithinase) (AO) (Acetylornithinase) (NAO)	At4g17830 dl4945w T6K21	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Amino-acid biosynthesis; L-arginine biosynthesis; L-ornithine from N(2)-acetyl-L-ornithine (linear): step 1/1.	Alternative splicing; Amino-acid biosynthesis; Arginine biosynthesis; Cobalt; Complete proteome; Hydrolase; Metal-binding; Reference proteome; Zinc
SRR646596_TR12743_c2_g4_i13_len=877	ARGE_ARATH	Q:743-330,H:301-438	57.25%ID	E:5e-50	Acetylornithine deacetylase	.	0	1,814	0	2,795	0	5,061	0	5,647	0,392	-0,331	ARGE_ARATH	Acetylornithine deacetylase (EC 3.5.1.16) (N-acetylornithinase) (AO) (Acetylornithinase) (NAO)	At4g17830 dl4945w T6K21	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Amino-acid biosynthesis; L-arginine biosynthesis; L-ornithine from N(2)-acetyl-L-ornithine (linear): step 1/1.	Alternative splicing; Amino-acid biosynthesis; Arginine biosynthesis; Cobalt; Complete proteome; Hydrolase; Metal-binding; Reference proteome; Zinc
SRR646596_TR12950_c0_g1_i3_len=1711	OPR3_SOLLC	Q:425-1573,H:9-390	79.37%ID	E:0	12-oxophytodienoate reductase 3	PF00724.17^Oxidored_FMN^NADH:flavin oxidoreductase / NADH oxidase family^10-359^E:4.7e-87	0	3,302	0	2,955	0	7,537	0	8,356	0,629	1,127	OPR3_SOLLC	12-oxophytodienoate reductase 3 (EC 1.3.1.42) (12-oxophytodienoate-10,11-reductase 3) (OPDA-reductase 3) (LeOPR3)	OPR3	Solanum lycopersicum (Tomato) (Lycopersicon esculentum)	PATHWAY: Lipid metabolism; oxylipin biosynthesis.	3D-structure; Complete proteome; FMN; Fatty acid biosynthesis; Fatty acid metabolism; Flavoprotein; Lipid biosynthesis; Lipid metabolism; NADP; Oxidoreductase; Oxylipin biosynthesis; Peroxisome; Reference proteome
SRR646596_TR18664_c0_g1_i1_len=2473	CBP1_ORYSJ	Q:1943-486,H:14-510	66.4%ID	E:0	Serine carboxypeptidase 1	PF00450.19^Peptidase_S10^Serine carboxypeptidase^36-493^E:5e-143	0	1,904	0	2,736	0	2,223	0	2,302	1	0,429	CBP1_ORYSJ	Serine carboxypeptidase 1 (EC 3.4.16.5) (Carboxypeptidase C) (Serine carboxypeptidase I) [Cleaved into: Serine carboxypeptidase 1 chain A (Serine carboxypeptidase I chain A); Serine carboxypeptidase 1 chain B (Serine carboxypeptidase I chain B)]	CBP1 Os12g0257000 LOC_Os12g15470	Oryza sativa subsp. japonica (Rice)		Carboxypeptidase; Complete proteome; Disulfide bond; Glycoprotein; Hydrolase; Protease; Reference proteome; Signal; Zymogen
SRR646596_TR18779_c1_g1_i1_len=852	PNAE_RAUSE	Q:85-564,H:9-171	48.47%ID	E:2e-40	Polyneuridine-aldehyde esterase	PF12146.5^Hydrolase_4^Serine aminopeptidase, S33^6-111^E:7.5e-08`PF00561.17^Abhydrolase_1^alpha/beta hydrolase fold^9-158^E:3.4e-13`PF12697.4^Abhydrolase_6^Alpha/beta hydrolase family^10-120^E:5.5e-10	0	4,549	0	6,574	0	4,482	0	4,866	0,132	3,003	PNAE_RAUSE	Polyneuridine-aldehyde esterase (EC 3.1.1.78) (Polyneuridine aldehyde esterase)	PNAE	Rauvolfia serpentina (Serpentine wood) (Ophioxylon serpentinum)	PATHWAY: Alkaloid biosynthesis; ajmaline biosynthesis.	3D-structure; Alkaloid metabolism; Direct protein sequencing; Hydrolase; Serine esterase
SRR646596_TR18779_c1_g1_i3_len=1079	SABP2_TOBAC	Q:91-852,H:5-260	44.19%ID	E:7e-57	Salicylic acid-binding protein 2	PF12146.5^Hydrolase_4^Serine aminopeptidase, S33^6-111^E:1.9e-07`PF00561.17^Abhydrolase_1^alpha/beta hydrolase fold^9-245^E:1.3e-13`PF12697.4^Abhydrolase_6^Alpha/beta hydrolase family^10-246^E:1.1e-12	0	4,454	0	4,446	0	4,607	0	4,939	0,003	1,973	SABP2_TOBAC	Salicylic acid-binding protein 2 (NtSABP2) (EC 3.1.1.-) (Methyl salicylate esterase)	SABP2	Nicotiana tabacum (Common tobacco)		3D-structure; Hydrolase; Immunity; Innate immunity; Plant defense
SRR646596_TR21402_c1_g1_i2_len=3911	Y3475_ARATH	Q:826-3738,H:21-1007	42.71%ID	E:0	Probable LRR receptor-like serine/threonine-protein kinase At3g47570	PF08263.9^LRRNT_2^Leucine rich repeat N-terminal domain^38-76^E:5.1e-09`PF13855.3^LRR_8^Leucine rich repeat^400-459^E:3.6e-08`PF00560.30^LRR_1^Leucine Rich Repeat^400-422^E:0.68`PF13855.3^LRR_8^Leucine rich repeat^423-483^E:3e-07`PF13855.3^LRR_8^Leucine rich repeat^521-579^E:4.8e-09`PF13516.3^LRR_6^Leucine Rich repeat^568-582^E:2`PF00069.22^Pkinase^Protein kinase domain^694-909^E:5e-36`PF07714.14^Pkinase_Tyr^Protein tyrosine kinase^694-911^E:1.8e-34`PF08263.9^LRRNT_2^Leucine rich repeat N-terminal domain^772-779^E:2900	0	2,266	0	5,234	0	4,43	0	4,736	1	1,138	Y3475_ARATH	Probable LRR receptor-like serine/threonine-protein kinase At3g47570 (EC 2.7.11.1)	At3g47570 F1P2.120	Arabidopsis thaliana (Mouse-ear cress)		ATP-binding; Cell membrane; Complete proteome; Glycoprotein; Kinase; Leucine-rich repeat; Membrane; Nucleotide-binding; Phosphoprotein; Receptor; Reference proteome; Repeat; Serine/threonine-protein kinase; Signal; Transferase; Transmembrane; Transmembrane helix
SRR646596_TR31742_c0_g1_i7_len=2326	DCE_SOLLC	Q:2207-1212,H:1-336	84.52%ID	E:0	Glutamate decarboxylase	PF00282.16^Pyridoxal_deC^Pyridoxal-dependent decarboxylase conserved domain^37-331^E:4.9e-88	0	3,434	0	2,215	0	2,377	0	2,055	0,407	0,797	DCE_SOLLC	Glutamate decarboxylase (GAD) (EC 4.1.1.15) (ERT D1)		Solanum lycopersicum (Tomato) (Lycopersicon esculentum)		Calmodulin-binding; Complete proteome; Decarboxylase; Lyase; Pyridoxal phosphate; Reference proteome
SRR646596_TR31742_c0_g1_i8_len=2832	DCE_SOLLC	Q:2044-650,H:28-502	79.37%ID	E:0	Glutamate decarboxylase	PF00282.16^Pyridoxal_deC^Pyridoxal-dependent decarboxylase conserved domain^14-358^E:2.2e-104	0	3,284	0	4,408	0	2,446	0	2,379	0,204	0,566	DCE_SOLLC	Glutamate decarboxylase (GAD) (EC 4.1.1.15) (ERT D1)		Solanum lycopersicum (Tomato) (Lycopersicon esculentum)		Calmodulin-binding; Complete proteome; Decarboxylase; Lyase; Pyridoxal phosphate; Reference proteome
SRR646596_TR31742_c0_g1_i10_len=2345	DCE_SOLLC	Q:1633-650,H:165-502	76.92%ID	E:0	Glutamate decarboxylase	PF00282.16^Pyridoxal_deC^Pyridoxal-dependent decarboxylase conserved domain^10-228^E:3.7e-66	0	3,335	0	2,43	0	2,589	0	2,396	0,067	0,625	DCE_SOLLC	Glutamate decarboxylase (GAD) (EC 4.1.1.15) (ERT D1)		Solanum lycopersicum (Tomato) (Lycopersicon esculentum)		Calmodulin-binding; Complete proteome; Decarboxylase; Lyase; Pyridoxal phosphate; Reference proteome
SRR646596_TR33896_c0_g4_i1_len=2624	DXS2_ORYSJ	Q:2171-213,H:59-712	78.44%ID	E:0	Probable 1-deoxy-D-xylulose-5-phosphate synthase 2, chloroplastic	PF13292.3^DXP_synthase_N^1-deoxy-D-xylulose-5-phosphate synthase^164-448^E:8.6e-109`PF00676.17^E1_dh^Dehydrogenase E1 component^276-335^E:9.1e-06`PF02779.21^Transket_pyr^Transketolase, pyrimidine binding domain^486-646^E:2.3e-41`PF02780.17^Transketolase_C^Transketolase, C-terminal domain^664-787^E:1.7e-34	0	1,605	0	4,372	0	3,228	0	4,001	1	0,027	DXS2_ORYSJ	Probable 1-deoxy-D-xylulose-5-phosphate synthase 2, chloroplastic (1-deoxyxylulose-5-phosphate synthase) (DXP synthase) (DXPS) (EC 2.2.1.7)	Os07g0190000 LOC_Os07g09190 OsJ_23394 OSJNBb0002L09.31 OSJNBb0003E08.7	Oryza sativa subsp. japonica (Rice)	PATHWAY: Metabolic intermediate biosynthesis; 1-deoxy-D-xylulose 5-phosphate biosynthesis; 1-deoxy-D-xylulose 5-phosphate from D-glyceraldehyde 3-phosphate and pyruvate: step 1/1.	Chloroplast; Complete proteome; Isoprene biosynthesis; Magnesium; Metal-binding; Plastid; Reference proteome; Thiamine biosynthesis; Thiamine pyrophosphate; Transferase; Transit peptide
SRR646604_TR1194_c0_g4_i4_len=1853	ARGE_ARATH	Q:235-1545,H:1-438	68.48%ID	E:0	Acetylornithine deacetylase	PF01546.25^Peptidase_M20^Peptidase family M20/M25/M40^95-434^E:5.5e-29`PF07687.11^M20_dimer^Peptidase dimerisation domain^203-317^E:3.3e-12	0	2,904	0	4,421	0	5,227	0	4,046	0,082	0,879	ARGE_ARATH	Acetylornithine deacetylase (EC 3.5.1.16) (N-acetylornithinase) (AO) (Acetylornithinase) (NAO)	At4g17830 dl4945w T6K21	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Amino-acid biosynthesis; L-arginine biosynthesis; L-ornithine from N(2)-acetyl-L-ornithine (linear): step 1/1.	Alternative splicing; Amino-acid biosynthesis; Arginine biosynthesis; Cobalt; Complete proteome; Hydrolase; Metal-binding; Reference proteome; Zinc
SRR646604_TR1194_c0_g4_i14_len=1268	ARGE_ARATH	Q:268-1266,H:1-336	73%ID	E:4e-179	Acetylornithine deacetylase	PF01546.25^Peptidase_M20^Peptidase family M20/M25/M40^95-258^E:6.5e-20`PF07687.11^M20_dimer^Peptidase dimerisation domain^203-317^E:1.9e-12	0	1,82	0	3,406	0	4,266	0	5,023	0,002	2,52	ARGE_ARATH	Acetylornithine deacetylase (EC 3.5.1.16) (N-acetylornithinase) (AO) (Acetylornithinase) (NAO)	At4g17830 dl4945w T6K21	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Amino-acid biosynthesis; L-arginine biosynthesis; L-ornithine from N(2)-acetyl-L-ornithine (linear): step 1/1.	Alternative splicing; Amino-acid biosynthesis; Arginine biosynthesis; Cobalt; Complete proteome; Hydrolase; Metal-binding; Reference proteome; Zinc
SRR646604_TR2878_c0_g1_i2_len=1076	NA	NA	NA	NA	NA	.	0	3,25	0	4,839	0	4,169	0	4,538	1	1,859	.	.	.	.	.	.
SRR646604_TR8057_c0_g1_i6_len=5066	LOX21_SOLTU	Q:115-2826,H:1-894	66.78%ID	E:0	Linoleate 13S-lipoxygenase 2-1, chloroplastic	PF01477.20^PLAT^PLAT/LH2 domain^144-212^E:6.2e-07`PF00305.16^Lipoxygenase^Lipoxygenase^225-892^E:0	0	2,447	0	5,449	0	6,736	0	7,329	1	0,136	LOX21_SOLTU	Linoleate 13S-lipoxygenase 2-1, chloroplastic (EC 1.13.11.12) (Lipoxygenase 2-1)	LOX2.1 LOX-H1	Solanum tuberosum (Potato)	PATHWAY: Lipid metabolism; oxylipin biosynthesis. {ECO:0000255|PROSITE-ProRule:PRU00726}.	Chloroplast; Complete proteome; Dioxygenase; Fatty acid biosynthesis; Fatty acid metabolism; Iron; Lipid biosynthesis; Lipid metabolism; Metal-binding; Oxidoreductase; Oxylipin biosynthesis; Plastid; Reference proteome; Thylakoid; Transit peptide
SRR646604_TR9752_c0_g1_i1_len=864	NA	NA	NA	NA	NA	.	0,001	6,563	0	6,677	0	3,025	0	3,12	1	2,348	.	.	.	.	.	.
SRR646604_TR22073_c0_g2_i6_len=3429	DRL29_ARATH	Q:264-2741,H:1-816	52.96%ID	E:0	Probable disease resistance protein At4g33300	PF05659.8^RPW8^Arabidopsis broad-spectrum mildew resistance protein RPW8^9-135^E:2.4e-13`PF00931.19^NB-ARC^NB-ARC domain^192-454^E:1.7e-38	0,001	2,395	0	3,727	0	4,916	0	5,249	0,517	0,827	DRL29_ARATH	Probable disease resistance protein At4g33300	At4g33300 F17M5.60	Arabidopsis thaliana (Mouse-ear cress)		ATP-binding; Coiled coil; Complete proteome; Leucine-rich repeat; Nucleotide-binding; Plant defense; Reference proteome; Repeat
SRR646604_TR29352_c0_g1_i4_len=1502	ACCO_ACTDE	Q:1329-382,H:3-319	84.54%ID	E:0	1-aminocyclopropane-1-carboxylate oxidase	PF14226.3^DIOX_N^non-haem dioxygenase in morphine synthesis N-terminal^60-150^E:5.3e-12`PF03171.17^2OG-FeII_Oxy^2OG-Fe(II) oxygenase superfamily^214-308^E:2.5e-28	0,001	0,749	0	3,171	0	2,486	0	2,109	0,039	0,492	ACCO_ACTDE	1-aminocyclopropane-1-carboxylate oxidase (ACC oxidase) (EC 1.14.17.4) (Ethylene-forming enzyme) (EFE)	ACO	Actinidia deliciosa (Kiwi)	PATHWAY: Alkene biosynthesis; ethylene biosynthesis via S-adenosyl-L-methionine; ethylene from S-adenosyl-L-methionine: step 2/2.	Ethylene biosynthesis; Fruit ripening; Iron; Metal-binding; Oxidoreductase; Vitamin C
SRR646604_TR32431_c0_g1_i1_len=1417	M2K9_ARATH	Q:1328-360,H:1-308	62.65%ID	E:1e-121	Mitogen-activated protein kinase kinase 9	PF00069.22^Pkinase^Protein kinase domain^57-321^E:8.3e-66`PF07714.14^Pkinase_Tyr^Protein tyrosine kinase^57-316^E:8.5e-39	0,001	1,271	0,001	1,441	0	3,055	0	3,093	0,046	-0,892	M2K9_ARATH	Mitogen-activated protein kinase kinase 9 (AtMKK9) (MAP kinase kinase 9) (EC 2.7.12.2)	MKK9 MAP2K9 At1g73500 T9L24.32	Arabidopsis thaliana (Mouse-ear cress)		ATP-binding; Complete proteome; Cytoplasm; Ethylene biosynthesis; Kinase; Nucleotide-binding; Nucleus; Phosphoprotein; Reference proteome; Serine/threonine-protein kinase; Stress response; Transferase
SRR646604_TR34700_c1_g2_i5_len=2039	C72A1_CATRO	Q:937-1776,H:245-524	95.71%ID	E:0	Secologanin synthase	PF00067.19^p450^Cytochrome P450^93-235^E:2.5e-16	0	1,192	0	3,316	0	1,996	0	1,648	0,002	1,077	C72A1_CATRO	Secologanin synthase (SLS) (EC 1.3.3.9) (CYPLXXII) (Cytochrome P450 72A1)	CYP72A1 CYP72 P450CR3	Catharanthus roseus (Madagascar periwinkle) (Vinca rosea)	PATHWAY: Alkaloid biosynthesis; secologanin biosynthesis.	Alkaloid metabolism; Heme; Iron; Membrane; Metal-binding; Monooxygenase; NADP; Oxidoreductase; Transmembrane; Transmembrane helix; Vacuole
SRR648705_TR27980_c0_g1_i1_len=4205	CBP1_ORYSJ	Q:497-1954,H:14-510	66.6%ID	E:0	Serine carboxypeptidase 1	PF00450.19^Peptidase_S10^Serine carboxypeptidase^36-493^E:4.5e-143	0	1,848	0	2,145	0	2,426	0	2,344	0,296	0,319	CBP1_ORYSJ	Serine carboxypeptidase 1 (EC 3.4.16.5) (Carboxypeptidase C) (Serine carboxypeptidase I) [Cleaved into: Serine carboxypeptidase 1 chain A (Serine carboxypeptidase I chain A); Serine carboxypeptidase 1 chain B (Serine carboxypeptidase I chain B)]	CBP1 Os12g0257000 LOC_Os12g15470	Oryza sativa subsp. japonica (Rice)		Carboxypeptidase; Complete proteome; Disulfide bond; Glycoprotein; Hydrolase; Protease; Reference proteome; Signal; Zymogen
SRR648705_TR41935_c0_g1_i2_len=2197	LPAAT_ARATH	Q:1700-600,H:48-415	79.62%ID	E:0	1-acylglycerol-3-phosphate O-acyltransferase	PF12740.4^Chlorophyllase2^Chlorophyllase enzyme^112-222^E:4.4e-07`PF00561.17^Abhydrolase_1^alpha/beta hydrolase fold^116-230^E:2.3e-19`PF12146.5^Hydrolase_4^Serine aminopeptidase, S33^116-224^E:2.8e-18`PF12697.4^Abhydrolase_6^Alpha/beta hydrolase family^118-384^E:1.1e-16`PF03096.11^Ndr^Ndr family^184-223^E:2e-05	0	1,339	0	3,362	0	1,917	0	2,304	1	-0,075	LPAAT_ARATH	1-acylglycerol-3-phosphate O-acyltransferase (EC 2.3.1.51) (Lipid droplet-binding protein CGI-58 homolog)	At4g24160 T19F6.4	Arabidopsis thaliana (Mouse-ear cress)		Acyltransferase; Alternative splicing; Complete proteome; Cytoplasm; Lipid biosynthesis; Lipid metabolism; Phospholipid biosynthesis; Phospholipid metabolism; Reference proteome; Transferase
SRR648707_TR2690_c0_g1_i3_len=2788	MYRS_QUEIL	Q:1901-2590,H:368-594	61.74%ID	E:7e-113	Myrcene synthase, chloroplastic	PF01397.18^Terpene_synth^Terpene synthase, N-terminal domain^67-243^E:1.2e-44	0	4,859	0	6,502	0	8,007	0	7,986	1	0,655	MYRS_QUEIL	Myrcene synthase, chloroplastic (EC 4.2.3.15)		Quercus ilex (Holly oak)		Chloroplast; Lyase; Magnesium; Manganese; Metal-binding; Plastid; Transit peptide
SRR648707_TR9308_c0_g1_i1_len=1181	MYB4_ORYSJ	Q:1016-669,H:1-116	87.93%ID	E:5e-69	Myb-related protein Myb4	PF00249.28^Myb_DNA-binding^Myb-like DNA-binding domain^14-61^E:5.9e-16`PF13921.3^Myb_DNA-bind_6^Myb-like DNA-binding domain^17-76^E:9.2e-13`PF00249.28^Myb_DNA-binding^Myb-like DNA-binding domain^67-112^E:2.4e-15`PF13921.3^Myb_DNA-bind_6^Myb-like DNA-binding domain^70-118^E:2.7e-06	0	1,776	0	2,594	0	3,04	0	2,509	0,024	1,327	MYB4_ORYSJ	Myb-related protein Myb4 (OsMyb4) (Transcription factor RLTR1)	MYB4 LTR1 Os04g0517100 LOC_Os04g43680 OSJNBa0073E02.6	Oryza sativa subsp. japonica (Rice)		Complete proteome; DNA-binding; Nucleus; Reference proteome; Repeat; Stress response; Transcription; Transcription regulation
SRR648707_TR13926_c0_g1_i3_len=4096	FAO2_LOTJA	Q:336-2456,H:31-748	60.5%ID	E:0	Long-chain-alcohol oxidase FAO2	PF00732.16^GMC_oxred_N^GMC oxidoreductase^246-508^E:4.1e-69`PF05199.10^GMC_oxred_C^GMC oxidoreductase^597-730^E:1.8e-19	0	4,249	0	2,008	0	2,802	0	2,911	0,195	-0,567	FAO2_LOTJA	Long-chain-alcohol oxidase FAO2 (EC 1.1.3.20) (Long-chain fatty alcohol oxidase 2)	FAO2	Lotus japonicus (Lotus corniculatus var. japonicus)		FAD; Flavoprotein; Membrane; Oxidoreductase; Transmembrane; Transmembrane helix
SRR648707_TR19558_c0_g2_i4_len=2022	C72A1_CATRO	Q:1888-317,H:1-524	99.43%ID	E:0	Secologanin synthase	PF00067.19^p450^Cytochrome P450^93-497^E:2e-87	0	1,248	0	3,931	0	2,416	0	1,945	0,038	0,612	C72A1_CATRO	Secologanin synthase (SLS) (EC 1.3.3.9) (CYPLXXII) (Cytochrome P450 72A1)	CYP72A1 CYP72 P450CR3	Catharanthus roseus (Madagascar periwinkle) (Vinca rosea)	PATHWAY: Alkaloid biosynthesis; secologanin biosynthesis.	Alkaloid metabolism; Heme; Iron; Membrane; Metal-binding; Monooxygenase; NADP; Oxidoreductase; Transmembrane; Transmembrane helix; Vacuole
SRR648707_TR19558_c0_g2_i12_len=1119	C72A1_CATRO	Q:797-315,H:373-524	91.3%ID	E:5e-95	Secologanin synthase	PF00067.19^p450^Cytochrome P450^1-114^E:1.3e-37	0	1,693	0	2,535	0	2,828	0	2,328	1	0,06	C72A1_CATRO	Secologanin synthase (SLS) (EC 1.3.3.9) (CYPLXXII) (Cytochrome P450 72A1)	CYP72A1 CYP72 P450CR3	Catharanthus roseus (Madagascar periwinkle) (Vinca rosea)	PATHWAY: Alkaloid biosynthesis; secologanin biosynthesis.	Alkaloid metabolism; Heme; Iron; Membrane; Metal-binding; Monooxygenase; NADP; Oxidoreductase; Transmembrane; Transmembrane helix; Vacuole
SRR648707_TR23313_c0_g1_i2_len=1386	CHIX_PEA	Q:1206-253,H:3-317	67.3%ID	E:5e-146	Endochitinase	PF00187.16^Chitin_bind_1^Chitin recognition protein^21-58^E:6.1e-15`PF00182.16^Glyco_hydro_19^Chitinase class I^81-312^E:4.5e-121	0,001	1,406	0	2,685	0	2	0	1,591	1	0,138	CHIX_PEA	Endochitinase (EC 3.2.1.14)		Pisum sativum (Garden pea)		Carbohydrate metabolism; Chitin degradation; Chitin-binding; Disulfide bond; Glycosidase; Hydrolase; Plant defense; Polysaccharide degradation; Signal
SRR648707_TR24142_c0_g2_i2_len=1738	ASB1_ARATH	Q:1229-	81.65%ID	E:3e-127	Anthranilate synthase beta subunit 1,	PF00117.25^GATase^Glutamine amidotransferase class-I^76-264^E:1.2e-	0	1,293	0	3,533	0	3,355	0	2,974	0,574	0,269	ASB1_ARATH	Anthranilate synthase beta subunit 1, chloroplastic (EC 4.1.3.27) (Anthranilate synthase component 2-1)	ASB1 TRP4 WEI7 At1g25220 F4F7.39	Arabidopsis thaliana (Mouse-ear	PATHWAY: Amino-acid biosynthesis; L-tryptophan biosynthesis; L-tryptophan from chorismate:	Alternative splicing; Amino-acid biosynthesis; Aromatic amino acid biosynthesis;

[illegible]	ASB1_ARATH	576,H:59-273	[illegible]	[illegible]	chloroplastic	47`PF07722.10^Peptidase_C26^Peptidase C26^144-249^E:3.4e-10	0	[illegible]	0	[illegible]	0	[illegible]	0	[illegible]	[illegible]	[illegible]	ASB1_ARATH	BIOSYNTHESIS 4) (Protein WEAK ETHYLENE INSENSITIVE 7)	[illegible]	cress)	step 1/5.	proteome; Transit peptide; Tryptophan biosynthesis
SRR648707_TR28936_c0_g1_i1_len=1053	FACR3_ARATH	Q:856-230,H:285-493	43.6%ID	E:2e-54	Fatty acyl-CoA reductase 3	PF03015.16^Sterile^Male sterility protein^121-217^E:6.3e-13	0	3,079	0	6,235	0	4,721	0	6,157	1	1,785	FACR3_ARATH	Fatty acyl-CoA reductase 3 (EC 1.2.1.n2) (Protein ECERIFERUM 4)	FAR3 CER4 At4g33790 T16L1.280	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Endoplasmic reticulum; Lipid biosynthesis; Lipid metabolism; NADP; Oxidoreductase; Reference proteome
SRR648707_TR29295_c0_g1_i1_len=1842	U91A1_ARATH	Q:1691-309,H:9-466	56.77%ID	E:0	UDP-glycosyltransferase 91A1	PF00201.15^UDPGT^UDP-glucoronosyl and UDP-glucosyl transferase^275-444^E:2.7e-17	0	2,025	0	4,773	0	4,692	0	5,367	0,129	3,74	U91A1_ARATH	UDP-glycosyltransferase 91A1 (EC 2.4.1.-)	UGT91A1 At2g22590 T9I22.3	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Glycosyltransferase; Reference proteome; Transferase
SRR648707_TR29907_c0_g1_i1_len=2033	PTR18_ARATH	Q:1955-237,H:12-590	74.18%ID	E:0	Protein NRT1/ PTR FAMILY 3.1	PF00854.18^PTR2^POT family^88-512^E:1.1e-101	0	1,926	0	4,91	0	1,34	0	0,906	1	-0,041	PTR18_ARATH	Protein NRT1/ PTR FAMILY 3.1 (AtNPF3.1)	NPF3.1 NITR At1g68570 F24J5.19	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Membrane; Nitrate assimilation; Reference proteome; Transmembrane; Transmembrane helix; Transport
SRR924147_TR5199_c0_g1_i1_len=1978	WRK40_ARATH	Q:1610-600,H:6-302	47.93%ID	E:3e-84	Probable WRKY transcription factor 40	PF03106.12^WRKY^WRKY DNA -binding domain^181-239^E:3.3e-24	0	3,451	0	5,478	0	3,135	0	3,888	1	-0,336	WRK40_ARATH	Probable WRKY transcription factor 40 (WRKY DNA-binding protein 40)	WRKY40 At1g80840 F23A5.19	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; DNA-binding; Nucleus; Reference proteome; Transcription; Transcription regulation
SRR924147_TR15039_c0_g1_i1_len=3661	MATE3_ARATH	Q:3139-1730,H:60-557	60.04%ID	E:1e-174	.	PF01554.15^MatE^MatE^122-289^E:6.2e-11`PF14667.3^Polysacc_synt_C^Polysaccharide biosynthesis C-terminal domain^247-338^E:8.8e-07`PF01554.15^MatE^MatE^361-491^E:7.6e-12	0	1,809	0	3,862	0	1,821	0	2,35	1	0	DTX45_ARATH	Protein DETOXIFICATION 45, chloroplastic (AtDTX45) (Multidrug and toxic compound extrusion protein 45) (MATE protein 45)	DTX45 At4g38380 F22I13.150	Arabidopsis thaliana (Mouse-ear cress)		Chloroplast; Complete proteome; Membrane; Plastid; Reference proteome; Transit peptide; Transmembrane; Transmembrane helix; Transport
SRR924147_TR30716_c0_g1_i1_len=798	NA	NA	NA	NA	NA	.	0	2,33	0	4,244	0	6,032	0	3,779	0,904	-0,113	.	.	.	.	.	.
SRR924147_TR31524_c0_g1_i1_len=1812	AAT3_ARATH	Q:160-1470,H:13-449	82.61%ID	E:0	Aspartate aminotransferase 3, chloroplastic	PF00155.18^Aminotran_1_2^Aminotransferase class I and II^77-443^E:2.9e-97	0	2,721	0	6,191	0	5,396	0	5,012	1	-0,36	AAT3_ARATH	Aspartate aminotransferase 3, chloroplastic (EC 2.6.1.1) (Protein YELLOW-LEAF-SPECIFIC GENE 4) (Transaminase A)	ASP3 YLS4 At5g11520 F15N18.110	Arabidopsis thaliana (Mouse-ear cress)		Aminotransferase; Chloroplast; Complete proteome; Plastid; Pyridoxal phosphate; Reference proteome; Transferase; Transit peptide
SRR924148_TR30094_c0_g2_i2_len=1350	YL126_YEAST	Q:972-391,H:1-205	31.43%ID	E:3e-21	Putative glutamine amidotransferase YLR126C	PF00117.25^GATase^Glutamine amidotransferase class-I^55-192^E:3.7e-15`PF04204.13^HTS^Homoserine O-succinyltransferase^57-215^E:6.2e-05`PF07722.10^Peptidase_C26^Peptidase C26^84-189^E:1.1e-05	0	1,391	0	2,229	0	2,523	0	2,678	0,184	-0,362	YL126_YEAST	Putative glutamine amidotransferase YLR126C (EC 2.4.2.-)	YLR126C L3105	Saccharomyces cerevisiae (strain ATCC 204508 / S288c) (Baker's yeast)		Complete proteome; Cytoplasm; Glutamine amidotransferase; Reference proteome; Transferase
SRR342017_TR25892_c2_g4_i6_len=4889	POLX_TOBAC	Q:4888-3482,H:858-1323	55.65%ID	E:1e-150	Retrovirus-related Pol polyprotein from transposon TNT 1-94	PF14223.3^Retrotran_gag_2^gag-polypeptide of LTR copia-type^59-187^E:7e-34`PF00098.20^zf-CCHC^Zinc knuckle^227-242^E:0.00034`PF13976.3^gag_pre-integrs^GAG-pre-integrase domain^397-464^E:1.3e-14`PF00665.23^rve^Integrase core domain^480-594^E:2.5e-26	0	4,536	0	-1,503	0	1,941	0	1,869	0	3,153	POLX_TOBAC	Retrovirus-related Pol polyprotein from transposon TNT 1-94 [Includes: Protease (EC 3.4.23.-); Reverse transcriptase (EC 2.7.7.49); Endonuclease]		Nicotiana tabacum (Common tobacco)		Aspartyl protease; Endonuclease; Hydrolase; Metal-binding; Nuclease; Nucleotidyltransferase; Protease; RNA-directed DNA polymerase; Transferase; Transposable element; Zinc; Zinc-finger
SRR342022_TR3089_c3_g3_i9_len=1204	RNLX_SOLLC	Q:850-248,H:30-230	64.85%ID	E:9e-91	Intracellular ribonuclease LX	PF00445.15^Ribonuclease_T2^Ribonuclease T2 family^1-114^E:6.3e-34	0	0,87	0,276	0,306	0	1,692	0	1,175	0	1,479	RNLX_SOLLC	Intracellular ribonuclease LX (RNase LX) (EC 3.1.27.1)	RNALX	Solanum lycopersicum (Tomato) (Lycopersicon esculentum)		Complete proteome; Cytoplasm; Direct protein sequencing; Disulfide bond; Endonuclease; Hydrolase; Nuclease; Reference proteome; Stress response; Zymogen
SRR122238_TR12534_c1_g6_i3_len=2122	HSP7C_PETHY	Q:119-1972,H:1-618	96.12%ID	E:0	Heat shock cognate 70 kDa protein	PF00012.17^HSP70^Hsp70 protein^9-618^E:3.4e-267`PF06723.10^MreB_Mbl^MreB/Mbl protein^127-380^E:5.6e-14	0,129	0,886	0	4,682	0	1,021	0,001	0,838	0	1,606	HSP7C_PETHY	Heat shock cognate 70 kDa protein	HSP70	Petunia hybrida (Petunia)		ATP-binding; Nucleotide-binding; Stress response
SRR122238_TR12756_c0_g1_i1_len=1660	ACCH1_ARATH	Q:307-1347,H:20-365	48.29%ID	E:1e-114	1-aminocyclopropane-1-carboxylate oxidase homolog 1	PF14226.3^DIOX_N^non-haem dioxygenase in morphine synthesis N-terminal^110-209^E:8.6e-18`PF03171.17^2OG-FeII_Oxy^2OG-Fe(II) oxygenase superfamily^270-362^E:1.4e-21	0,377	0,187	0	0,849	0	2,105	0	2,748	0	1,025	ACCH1_ARATH	1-aminocyclopropane-1-carboxylate oxidase homolog 1	At1g06620 F12K11.24 F12K11.6	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Iron; Metal-binding; Oxidoreductase; Reference proteome
SRR342017_TR9688_c1_g2_i3_len=830	NA	NA	NA	NA	NA	PF00168.27^C2^C2 domain^56-162^E:3.9e-08	0,287	0,302	0	1,777	0	1,886	0	2,04	0	9,28	.	.	.	.	.	.
SRR342017_TR30366_c0_g1_i1_len=668	NA	NA	NA	NA	NA	.	0,158	1,412	0	2,791	0	1,863	0	1,74	0	2,509	.	.	.	.	.	.
SRR342019_TR16142_c0_g1_i2_len=862	NA	NA	NA	NA	NA	PF04570.11^zf-FLZ^zinc-finger of the FCS-type, C2-C2^113-161^E:3.1e-24	0,326	0,324	0	1,506	0	1,481	0	1,705	0	2,147	.	.	.	.	.	.
SRR342022_TR17840_c0_g1_i1_len=2707	NA	NA	NA	NA	NA	.	0,124	0,416	0	1,258	0	1,561	0	1,644	0	3,714	.	.	.	.	.	.
SRR646596_TR12743_c2_g5_i3_len=1246	ARGE_ARATH	Q:268-1242,H:1-303	68.09%ID	E:4e-156	Acetylornithine deacetylase	PF07687.11^M20_dimer^Peptidase dimerisation domain^62-158^E:1.8e-08	0,001	1,635	0	3,75	0	4,697	0	5,127	0	1,751	ARGE_ARATH	Acetylornithine deacetylase (EC 3.5.1.16) (N-acetylornithinase) (AO) (Acetylornithinase) (NAO)	At4g17830 dl4945w T6K21	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Amino-acid biosynthesis; L-arginine biosynthesis; L-ornithine from N(2)-acetyl-L-ornithine (linear): step 1/1.	Alternative splicing; Amino-acid biosynthesis; Arginine biosynthesis; Cobalt; Complete proteome; Hydrolase; Metal-binding; Reference proteome; Zinc
SRR646596_TR30289_c1_g1_i1_len=758	NLTP_HELAN	Q:135-485,H:1-116	52.54%ID	E:7e-27	Non-specific lipid-transfer protein	PF14368.3^LTP_2^Probable lipid transfer^15-105^E:1.4e-05`PF00234.19^Tryp_alpha_amyl^Protease inhibitor/seed storage/LTP family^30-113^E:1e-07	0,032	0,463	0	1,451	0	2,064	0	1,023	0	0,967	NLTP_HELAN	Non-specific lipid-transfer protein (LTP) (NsLTP) (SDI-9)		Helianthus annuus (Common sunflower)		Disulfide bond; Lipid-binding; Signal; Transport
SRR648705_TR41316_c0_g1_i3_len=1005	NA	NA	NA	NA	NA	PF06232.8^ATS3^Embryo-specific protein 3, (ATS3)^30-132^E:4.1e-07`PF01477.20^PLAT^PLAT/LH2 domain^36-153^E:2.2e-14	0,008	0,67	0	3,561	0	4,273	0	3,751	0	1,721	.	.	.	.	.	.
SRR1144634_TR26877_c0_g2_i1_len=505	NA	NA	NA	NA	NA	PF14226.3^DIOX_N^non-haem dioxygenase in morphine synthesis N-terminal^61-124^E:5.8e-17	0	1,565	0	4,074	0	2,211	0	2,107	0	2,281	.	.	.	.	.	.
SRR122238_TR14259_c0_g1_i1_len=1837	TAR4_ARATH	Q:1756-437,H:6-449	52.8%ID	E:4e-159	Tryptophan aminotransferase-related protein 4	PF04863.10^EGF_alliinase^Alliinase EGF-like domain^40-94^E:2.4e-27`PF04864.10^Alliinase_C^Allinase^96-451^E:9.5e-143`PF00155.18^Aminotran_1_2^Aminotransferase class I and II^137-432^E:1.3e-06	0	5,486	0	7,047	0	7,695	0	7,198	0	1,352	TAR4_ARATH	Tryptophan aminotransferase-related protein 4 (EC 2.6.1.-)	TAR4 At1g34060 F12G12.12 F12G12.150	Arabidopsis thaliana (Mouse-ear cress)		Aminotransferase; Complete proteome; Membrane; Pyridoxal phosphate; Reference proteome; Transferase; Transmembrane; Transmembrane helix
SRR122238_TR47400_c1_g1_i7_len=865	C72A1_CATRO	Q:103-846,H:1-248	97.98%ID	E:2e-178	Secologanin synthase	PF00067.19^p450^Cytochrome P450^93-236^E:2e-16	0	1,102	0	4,02	0	2,387	0	2,422	0	2,967	C72A1_CATRO	Secologanin synthase (SLS) (EC 1.3.3.9) (CYPLXXII) (Cytochrome P450 72A1)	CYP72A1 CYP72 P450CR3	Catharanthus roseus (Madagascar periwinkle) (Vinca rosea)	PATHWAY: Alkaloid biosynthesis; secologanin biosynthesis.	Alkaloid metabolism; Heme; Iron; Membrane; Metal-binding; Monooxygenase; NADP; Oxidoreductase; Transmembrane; Transmembrane helix; Vacuole
SRR122238_TR59774_c0_g1_i2_len=1287	STSY_RAUSE	Q:229-1095,H:37-324	43.34%ID	E:3e-75	Strictosidine synthase	PF08450.9^SGL^SMP-30/Gluconolaconase/LRE-like region^122-313^E:1.6e-06`PF03088.13^Str_synth^Strictosidine synthase^144-231^E:4.6e-25	0	2,435	0	3,284	0	3,742	0	2,723	0	2,506	STSY_RAUSE	Strictosidine synthase (EC 4.3.3.2)	STR1	Rauvolfia serpentina (Serpentine wood) (Ophioxylon serpentinum)	PATHWAY: Alkaloid biosynthesis; 3alpha(S)-strictosidine biosynthesis; 3alpha(S)-strictosidine from secologanin and tryptamine: step 1/1.	3D-structure; Alkaloid metabolism; Direct protein sequencing; Glycoprotein; Lyase; Signal; Vacuole
SRR122238_TR61939_c0_g1_i8_len=3198	NES1_FRAAN	Q:2896-1379,H:14-515	53.95%ID	E:3e-168	(3S,6E)-nerolidol synthase 1	PF01397.18^Terpene_synth^Terpene synthase, N-terminal domain^67-224^E:3.5e-42`PF03936.13^Terpene_synth_C^Terpene synthase family, metal binding domain^258-522^E:8.5e-76	0	3,04	0	4,257	0	2,385	0	2,974	0	2,351	NES1_FRAAN	(3S,6E)-nerolidol synthase 1 (FaNES1) (EC 4.2.3.48)		Fragaria ananassa (Strawberry)	PATHWAY: Secondary metabolite biosynthesis; terpenoid biosynthesis.	Cytoplasm; Lyase; Magnesium; Manganese; Metal-binding
SRR1271857_TR24914_c0_g2_i15_len=2512	DCE_PETHY	Q:142-1137,H:1-335	89.25%ID	E:0	Glutamate decarboxylase	PF00282.16^Pyridoxal_deC^Pyridoxal-dependent decarboxylase conserved domain^37-331^E:1.8e-92	0	2,48	0	2,012	0	2,402	0	2,212	0	0,797	DCE_PETHY	Glutamate decarboxylase (GAD) (EC 4.1.1.15)	GAD	Petunia hybrida (Petunia)		3D-structure; Calmodulin-binding; Decarboxylase; Lyase; Pyridoxal phosphate
SRR1271859_TR4959_c0_g1_i6_len=2049	CBP1_ORYSJ	Q:860-1852,H:136-469	65.87%ID	E:4e-179	Serine carboxypeptidase 1	PF00450.19^Peptidase_S10^Serine carboxypeptidase^2-320^E:9.6e-76	0	2,169	0	3,34	0	2,614	0	2,554	0	2,131	CBP1_ORYSJ	Serine carboxypeptidase 1 (EC 3.4.16.5) (Carboxypeptidase C) (Serine carboxypeptidase I) [Cleaved into: Serine carboxypeptidase 1 chain A (Serine carboxypeptidase I chain A); Serine carboxypeptidase 1 chain B (Serine carboxypeptidase I chain B)]	CBP1 Os12g0257000 LOC_Os12g15470	Oryza sativa subsp. japonica (Rice)		Carboxypeptidase; Complete proteome; Disulfide bond; Glycoprotein; Hydrolase; Protease; Reference proteome; Signal; Zymogen
SRR342019_TR29234_c2_g1_i5_len=927	C72A1_CATRO	Q:156-926,H:1-257	98.44%ID	E:0	Secologanin synthase	PF00067.19^p450^Cytochrome P450^93-238^E:8.5e-17	0	1,041	0	5,643	0	1,943	0	1,745	0	1,607	C72A1_CATRO	Secologanin synthase (SLS) (EC 1.3.3.9) (CYPLXXII) (Cytochrome P450 72A1)	CYP72A1 CYP72 P450CR3	Catharanthus roseus (Madagascar periwinkle) (Vinca rosea)	PATHWAY: Alkaloid biosynthesis; secologanin biosynthesis.	Alkaloid metabolism; Heme; Iron; Membrane; Metal-binding; Monooxygenase; NADP; Oxidoreductase; Transmembrane; Transmembrane helix; Vacuole
SRR342019_TR38836_c2_g1_i2_len=540	DCE_SOLLC	Q:116-538,H:1-142	83.1%ID	E:3e-69	Glutamate decarboxylase	PF00282.16^Pyridoxal_deC^Pyridoxal-dependent decarboxylase conserved domain^37-141^E:5.5e-26	0	2,65	0	6,769	0	3,135	0	3,703	0	1,973	DCE_SOLLC	Glutamate decarboxylase (GAD) (EC 4.1.1.15) (ERT D1)		Solanum lycopersicum (Tomato) (Lycopersicon esculentum)		Calmodulin-binding; Complete proteome; Decarboxylase; Lyase; Pyridoxal phosphate; Reference proteome
SRR342022_TR17158_c1_g3_i4_len=1780	GCL1_ARATH	Q:212-1495,H:1-433	63.64%ID	E:0	LanC-like protein GCL1	PF05147.10^LANC_like^Lanthionine synthetase C-like protein^71-427^E:2.4e-86	0	2,748	0	4,475	0	2,795	0	3,51	0	7,916	GCL1_ARATH	LanC-like protein GCL1 (G protein-coupled receptor 2-like protein 1) (Protein GCR2-like 1)	GCL1 At5g65280 MQN23.23	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Reference proteome
SRR342022_TR26103_c2_g5_i3_len=1741	FLS_PETCR	Q:1472-630,H:44-328	38.06%ID	E:2e-53	Flavonol synthase/flavanone 3-hydroxylase	PF14226.3^DIOX_N^non-haem dioxygenase in morphine synthesis N-terminal^3-70^E:1.2e-10`PF03171.17^2OG-FeII_Oxy^2OG-Fe(II) oxygenase superfamily^119-211^E:2e-23	0	1,533	0	2,226	0	2,711	0	2,365	0	1,324	FLS_PETCR	Flavonol synthase/flavanone 3-hydroxylase (EC 1.14.11.23) (EC 1.14.11.9)	FLS	Petroselinum crispum (Parsley) (Petroselinum hortense)	PATHWAY: Secondary metabolite biosynthesis; flavonoid biosynthesis.	Dioxygenase; Flavonoid biosynthesis; Iron; Metal-binding; Oxidoreductase; Vitamin C
SRR342022_TR27013_c0_g6_i2_len=1057	SABP2_TOBAC	Q:799-38,H:5-260	44.19%ID	E:5e-57	Salicylic acid-binding protein 2	PF12146.5^Hydrolase_4^Serine aminopeptidase, S33^6-111^E:1.9e-07`PF00561.17^Abhydrolase_1^alpha/beta hydrolase fold^9-245^E:1.3e-13`PF12697.4^Abhydrolase_6^Alpha/beta hydrolase family^10-246^E:1.1e-12	0	3,473	0	5,298	0	5,147	0	5,337	0	2,625	SABP2_TOBAC	Salicylic acid-binding protein 2 (NtSABP2) (EC 3.1.1.-) (Methyl salicylate esterase)	SABP2	Nicotiana tabacum (Common tobacco)		3D-structure; Hydrolase; Immunity; Innate immunity; Plant defense
SRR342022_TR28792_c1_g1_i8_len=2262	PTR21_ARATH	Q:171-1892,H:45-617	53.9%ID	E:0	Protein NRT1/ PTR FAMILY 2.13	PF07690.13^MFS_1^Major Facilitator Superfamily^82-547^E:3e-10`PF00854.18^PTR2^POT family^137-568^E:2.2e-82	0	1,341	0	2,924	0	1,864	0	1,751	0,001	1,37	PTR21_ARATH	Protein NRT1/ PTR FAMILY 2.13 (AtNPF2.13) (Nitrate transporter 1.7)	NPF2.13 NRT1.7 At1g69870 T17F3.10	Arabidopsis thaliana (Mouse-ear cress)		Cell membrane; Complete proteome; Membrane; Nitrate assimilation; Reference proteome; Symport; Transmembrane; Transmembrane helix; Transport
SRR342023_TR7070_c5_g1_i3_len=551	ACCO_PEA	Q:128-487,H:144-261	43.8%ID	E:3e-27	1-aminocyclopropane-1-carboxylate oxidase	.	0	1,747	0	2,378	0	2,662	0	2,471	0	1,362	ACCO_PEA	1-aminocyclopropane-1-carboxylate oxidase (ACC oxidase) (EC 1.14.17.4) (Ethylene-forming enzyme) (EFE)	ACO	Pisum sativum (Garden pea)	PATHWAY: Alkene biosynthesis; ethylene biosynthesis via S-adenosyl-L-methionine; ethylene from S-adenosyl-L-methionine: step 2/2.	Ethylene biosynthesis; Fruit ripening; Iron; Metal-binding; Oxidoreductase; Vitamin C
SRR646596_TR12573_c1_g2_i1_len=1709	STSY_RAUSE	Q:666-1373,H:89-324	42.5%ID	E:5e-56	Strictosidine synthase	PF08450.9^SGL^SMP-30/Gluconolaconase/LRE-like region^31-246^E:6.3e-07`PF03088.13^Str_synth^Strictosidine synthase^77-164^E:2.9e-25	0	3,755	0	5,773	0	4,127	0	3,509	0	3,344	STSY_RAUSE	Strictosidine synthase (EC 4.3.3.2)	STR1	Rauvolfia serpentina (Serpentine wood) (Ophioxylon serpentinum)	PATHWAY: Alkaloid biosynthesis; 3alpha(S)-strictosidine biosynthesis; 3alpha(S)-strictosidine from secologanin and tryptamine: step 1/1.	3D-structure; Alkaloid metabolism; Direct protein sequencing; Glycoprotein; Lyase; Signal; Vacuole
SRR646596_TR26064_c0_g2_i1_len=1017	NA	NA	NA	NA	NA	PF00257.16^Dehydrin^Dehydrin^10-176^E:4.1e-43	0	2,413	0	4,94	0	5,355	0	3,389	0	4,133	.	.	.	.	.	.
SRR646596_TR31742_c0_g1_i6_len=2241	DCE_SOLLC	Q:2122-650,H:1-502	79.08%ID	E:0	Glutamate decarboxylase	PF00282.16^Pyridoxal_deC^Pyridoxal-dependent decarboxylase conserved domain^37-381^E:2.1e-104	0	2,48	0	2,982	0	2,709	0	2,648	0	2,967	DCE_SOLLC	Glutamate decarboxylase (GAD) (EC 4.1.1.15) (ERT D1)		Solanum lycopersicum (Tomato) (Lycopersicon esculentum)		Calmodulin-binding; Complete proteome; Decarboxylase; Lyase; Pyridoxal phosphate; Reference proteome
SRR646604_TR34700_c1_g2_i4_len=1523	C72A1_CATRO	Q:108-1259,H:1-384	98.96%ID	E:0	Secologanin synthase	PF00067.19^p450^Cytochrome P450^90-382^E:9e-43	0	1,288	0	4,215	0	2,46	0	2,042	0	1,323	C72A1_CATRO	Secologanin synthase (SLS) (EC 1.3.3.9) (CYPLXXII) (Cytochrome P450 72A1)	CYP72A1 CYP72 P450CR3	Catharanthus roseus (Madagascar periwinkle) (Vinca rosea)	PATHWAY: Alkaloid biosynthesis; secologanin biosynthesis.	Alkaloid metabolism; Heme; Iron; Membrane; Metal-binding; Monooxygenase; NADP; Oxidoreductase; Transmembrane; Transmembrane helix; Vacuole
SRR924147_TR18297_c0_g1_i13_len=1440	C72A1_CATRO	Q:120-1265,H:1-382	99.48%ID	E:0	Secologanin synthase	PF00067.19^p450^Cytochrome P450^93-382^E:1.7e-42	0	1,083	0	4,882	0	2,152	0	1,771	0	1,126	C72A1_CATRO	Secologanin synthase (SLS) (EC 1.3.3.9) (CYPLXXII) (Cytochrome P450 72A1)	CYP72A1 CYP72 P450CR3	Catharanthus roseus (Madagascar periwinkle) (Vinca rosea)	PATHWAY: Alkaloid biosynthesis; secologanin biosynthesis.	Alkaloid metabolism; Heme; Iron; Membrane; Metal-binding; Monooxygenase; NADP; Oxidoreductase; Transmembrane; Transmembrane helix; Vacuole
SRR924148_TR15471_c0_g2_i2_len=1833	DIOX3_PAPSO	Q:1505-477,H:18-360	33.43%ID	E:2e-55	Codeine O-demethylase	PF14226.3^DIOX_N^non-haem dioxygenase in morphine synthesis N-terminal^61-165^E:1.6e-22`PF03171.17^2OG-FeII_Oxy^2OG-Fe(II) oxygenase superfamily^214-306^E:3.7e-23	0	2,023	0	2,558	0	2,711	0	2,411	0	1,708	DIOX3_PAPSO	Codeine O-demethylase (EC 1.14.11.32)	CODM DIOX3	Papaver somniferum (Opium poppy)	PATHWAY: Alkaloid biosynthesis; morphine biosynthesis.	Alkaloid metabolism; Dioxygenase; Iron; Metal-binding; Methyltransferase; Oxidoreductase; Transferase
SRR1144633_TR19640_c0_g2_i1_len=920	RPBAL_ARATH	Q:84-290,H:1-69	91.3%ID	E:4e-39	DNA-directed RNA polymerase subunit 10-like protein {ECO:0000303|PubMed:19110459}	.	0	7,498	0	6,832	0	-7,425	0	-5,851	1	0,028	RPBAL_ARATH	DNA-directed RNA polymerase subunit 10-like protein (ABC10) (DNA-directed RNA polymerase III subunit L) (DNA-directed RNA polymerases I, II, and III subunit RPABC5) (RNA polymerases I, II, and III subunit ABC5) (RPB10 homolog)	NRPB10L At1g61700 T13M11.6	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; DNA-directed RNA polymerase; Metal-binding; Nucleus; Reference proteome; Transcription; Zinc
SRR1144633_TR29660_c0_g1_i3_len=1731	NA	NA	NA	NA	NA	.	0	1,512	0	1,371	0	-0,782	0,011	-0,53	0,484	-0,42	.	.	.	.	.	.
SRR1144633_TR33857_c0_g1_i1_len=1899	GGPPS_CATRO	Q:1436-372,H:1-357	96.92%ID	E:0	Geranylgeranyl pyrophosphate synthase, chloroplastic	PF00348.14^polyprenyl_synt^Polyprenyl synthetase^117-351^E:1.8e-57	0,001	1,025	0	1,71	0,002	0,934	0,39	0,3	0,821	0,109	GGPPS_CATRO	Geranylgeranyl pyrophosphate synthase, chloroplastic (GGPP synthase) (GGPS) (EC 2.5.1.-) ((2E,6E)-farnesyl diphosphate synthase) (Dimethylallyltranstransferase) (EC 2.5.1.1) (Farnesyl diphosphate synthase) (Farnesyltranstransferase) (EC 2.5.1.29) (Geranyltranstransferase) (EC 2.5.1.10)	GGPS1 GGC1	Catharanthus roseus (Madagascar periwinkle) (Vinca rosea)	PATHWAY: Isoprenoid biosynthesis; farnesyl diphosphate biosynthesis; farnesyl diphosphate from geranyl diphosphate and isopentenyl diphosphate: step 1/1.; PATHWAY: Isoprenoid biosynthesis; geranyl diphosphate biosynthesis; geranyl diphosphate from dimethylallyl diphosphate and isopentenyl diphosphate: step 1/1.; PATHWAY: Isoprenoid biosynthesis; geranylgeranyl diphosphate biosynthesis; geranylgeranyl diphosphate from farnesyl diphosphate and isopentenyl diphosphate: step 1/1.	Carotenoid biosynthesis; Chloroplast; Isoprene biosynthesis; Magnesium; Metal-binding; Plastid; Transferase; Transit peptide
SRR1144633_TR37464_c0_g3_i1_len=269	NA	NA	NA	NA	NA	.	0	1,318	0	2,312	0,255	0,444	0,223	0,476	1	-0,006	.	.	.	.	.	.
SRR1144634_TR19041_c0_g2_i1_len=1676	GOLS1_AJURE	Q:1466-669,H:1-261	84.96%ID	E:3e-163	Galactinol synthase 1	PF01501.17^Glyco_transf_8^Glycosyl transferase family 8^32-265^E:9.3e-40	0	1,176	0	1,661	0,083	0,367	0,063	0,392	1	1,721	GOLS1_AJURE	Galactinol synthase 1 (ArGolS1) (GolS-1) (EC 2.4.1.123)	GOLS1	Ajuga reptans (Bugle)		Carbohydrate metabolism; Cytoplasm; Galactose metabolism; Glycosyltransferase; Manganese; Metal-binding; Transferase
SRR1144634_TR23505_c0_g1_i1_len=660	NA	NA	NA	NA	NA	PF00810.15^ER_lumen_recept^ER lumen protein retaining receptor^1-49^E:2.2e-18	0	7,836	0	7,051	0,129	-3,245	0,129	-4,862	1	0	.	.	.	.	.	.
SRR1144634_TR39096_c0_g1_i1_len=869	NA	NA	NA	NA	NA	PF02466.16^Tim17^Tim17/Tim22/Tim23/Pmp24 family^35-127^E:1e-09	0	8,686	0	7,332	0	-6,345	0	-6,968	1	0	.	.	.	.	.	.
SRR122238_TR4557_c0_g1_i1_len=503	NA	NA	NA	NA	NA	.	0	1,135	0	1,335	0,503	0,167	0,017	0,568	0,053	-0,586	.	.	.	.	.	.
SRR122238_TR20218_c1_g1_i2_len=629	NA	NA	NA	NA	NA	PF13499.3^EF-hand_7^EF-hand domain pair^24-98^E:7.4e-10`PF13202.3^EF-hand_5^EF hand^26-47^E:0.00024`PF13202.3^EF-hand_5^EF hand^75-96^E:0.0013	0	1,048	0	1,07	0,005	0,693	0,223	0,313	0,894	0,051	.	.	.	.	.	.
SRR122238_TR58145_c0_g1_i1_len=868	NA	NA	NA	NA	NA	.	0	3,359	0	5,823	0,228	1,252	1	-0,282	1	0,304	.	.	.	.	.	.
SRR1271857_TR38410_c0_g1_i1_len=573	NA	NA	NA	NA	NA	.	0	1,544	0	0,791	0,145	-0,322	0,473	0,16	0,223	0,268	.	.	.	.	.	.
SRR1271859_TR2696_c0_g1_i1_len=1190	21KD_DAUCA	Q:353-841,H:27-191	46.67%ID	E:4e-46	21 kDa protein	PF04043.12^PMEI^Plant invertase/pectin methylesterase inhibitor^48-201^E:1.1e-34	0	1,414	0	2,46	0,088	-1,549	0,16	-1,217	0,402	-1,159	21KD_DAUCA	21 kDa protein (1.2 protein)		Daucus carota (Wild carrot)		Signal
SRR1271859_TR7367_c0_g1_i2_len=912	RBS_MALSP	Q:673-173,H:17-183	85.03%ID	E:7e-104	Ribulose bisphosphate carboxylase small chain, chloroplastic	PF12338.5^RbcS^Ribulose-1,5-bisphosphate carboxylase small subunit^4-44^E:4.4e-23`PF00101.17^RuBisCO_small^Ribulose bisphosphate carboxylase, small chain^71-179^E:1.3e-39	0	1,039	0,001	0,716	0	-1,471	0	-1,312	0,006	-0,585	RBS_MALSP	Ribulose bisphosphate carboxylase small chain, chloroplastic (RuBisCO small subunit) (EC 4.1.1.39)	RBCS	Malus sp. (Crab apple)		Calvin cycle; Carbon dioxide fixation; Chloroplast; Lyase; Monooxygenase; Oxidoreductase; Photorespiration; Photosynthesis; Plastid; Transit peptide
SRR1271859_TR17834_c0_g1_i1_len=512	NA	NA	NA	NA	NA	.	0	1,376	0	8,288	0,066	5,219	1	2,21	0	-2,11	.	.	.	.	.	.
SRR1271859_TR29215_c0_g2_i1_len=1507	BT1_ARATH	Q:1292-354,H:14-335	66.77%ID	E:3e-139	BTB/POZ and TAZ domain-containing protein 1	PF00651.28^BTB^BTB/POZ domain^84-178^E:6.7e-12`PF02135.13^zf-TAZ^TAZ zinc finger^267-353^E:1.7e-12	0	1,235	0	2,734	0,822	0,292	0,094	1,128	0,51	-0,319	BT1_ARATH	BTB/POZ and TAZ domain-containing protein 1 (BTB and TAZ domain protein 1)	BT1 At5g63160 MDC12.13	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Protein modification; protein ubiquitination.	Complete proteome; Cytoplasm; Metal-binding; Nucleus; Reference proteome; Ubl conjugation pathway; Zinc; Zinc-finger
SRR342017_TR8859_c1_g4_i2_len=1411	GEDH1_OCIBA	Q:1273-218,H:3-358	62.29%ID	E:5e-128	Geraniol dehydrogenase 1	PF08240.9^ADH_N^Alcohol dehydrogenase GroES-like domain^82-190^E:9.2e-22`PF00107.23^ADH_zinc_N^Zinc-binding dehydrogenase^234-357^E:1.8e-13	0	2,234	0	2,524	0,286	0,953	0,56	-0,686	0,094	1,196	GEDH1_OCIBA	Geraniol dehydrogenase 1 (ObaGEDH1) (EC 1.1.1.183)	GEDH1	Ocimum basilicum (Sweet basil)		Metal-binding; NADP; Oxidoreductase; Zinc
SRR342017_TR12325_c0_g3_i2_len=1007	NA	NA	NA	NA	NA	.	0,001	2,117	0	6,212	0,254	4,604	1	3,646	0,56	0,738	.	.	.	.	.	.
SRR342017_TR22430_c1_g1_i8_len=3110	PP226_ARATH	Q:2639-1662,H:54-379	44.48%ID	E:2e-84	Pentatricopeptide repeat-containing protein At3g13160, mitochondrial	PF01535.17^PPR^PPR repeat^160-185^E:0.00039`PF17177.1^PPR_long^Pentacotripeptide-repeat region of PROPR^167-276^E:1.1e-07`PF13812.3^PPR_3^Pentatricopeptide repeat domain^175-233^E:2.8e-09`PF01535.17^PPR^PPR repeat^191-217^E:0.09`PF12854.4^PPR_1^PPR repeat^221-252^E:1.8e-12`PF13041.3^PPR_2^PPR repeat family^223-270^E:4.9e-16`PF01535.17^PPR^PPR repeat^226-256^E:6e-07`PF13812.3^PPR_3^Pentatricopeptide repeat domain^247-302^E:1.8e-07`PF12854.4^PPR_1^PPR repeat^255-287^E:8.9e-06`PF13041.3^PPR_2^PPR repeat family^258-305^E:8.8e-08`PF01535.17^PPR^PPR repeat^261-290^E:0.0007`PF13041.3^PPR_2^PPR repeat family^294-340^E:9.6e-11`PF01535.17^PPR^PPR repeat^297-326^E:0.0036`PF13812.3^PPR_3^Pentatricopeptide repeat domain^317-371^E:4e-11`PF13041.3^PPR_2^PPR repeat family^329-373^E:3.9e-11`PF01535.17^PPR^PPR repeat^331-361^E:1.8e-06	0	7,679	0	3,02	1	-0,048	0,732	0,732	0,025	1,259	PP226_ARATH	Pentatricopeptide repeat-containing protein At3g13160, mitochondrial	At3g13160 MJG19.11	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Mitochondrion; Reference proteome; Repeat; Transit peptide
SRR342017_TR22466_c1_g1_i1_len=760	NA	NA	NA	NA	NA	PF00564.21^PB1^PB1 domain^5-85^E:9.4e-11	0	6,981	0	6,713	0,57	0,351	0,281	0,576	0,005	6,235	.	.	.	.	.	.
SRR342019_TR6910_c0_g1_i1_len=1531	WTR41_ARATH	Q:1415-822,H:14-216	51.18%ID	E:8e-87	WAT1-related protein At5g40230	PF00892.17^EamA^EamA-like transporter family^30-156^E:5.3e-12	0	2,099	0	2,449	0,017	2,123	0,517	0,847	1	-0,358	WTR41_ARATH	WAT1-related protein At5g40230	At5g40230 MSN9.130	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Membrane; Reference proteome; Repeat; Transmembrane; Transmembrane helix
SRR342019_TR7099_c4_g2_i9_len=1574	MTDH_FRAAN	Q:441-1292,H:70-353	63.38%ID	E:2e-96	Probable mannitol dehydrogenase	PF08240.9^ADH_N^Alcohol dehydrogenase GroES-like domain^4-82^E:1.2e-14`PF02826.16^2-Hacid_dh_C^D-isomer specific 2-hydroxyacid dehydrogenase, NAD binding domain^105-156^E:8e-07`PF00107.23^ADH_zinc_N^Zinc-binding dehydrogenase^126-249^E:1.8e-19	0	1,204	0	1,396	0,41	0,351	0,328	-0,442	0,183	0,653	MTDH_FRAAN	Probable mannitol dehydrogenase (EC 1.1.1.255) (NAD-dependent mannitol dehydrogenase)	CAD	Fragaria ananassa (Strawberry)		Metal-binding; NAD; Oxidoreductase; Zinc
SRR342022_TR3169_c4_g14_i1_len=1681	HST_TOBAC	Q:385-1515,H:57-430	26.02%ID	E:2e-30	Shikimate O-hydroxycinnamoyltransferase	PF02458.12^Transferase^Transferase family^7-445^E:2.7e-93	0	1,949	0	2,853	1	1,362	1	1,966	0,211	0,791	HST_TOBAC	Shikimate O-hydroxycinnamoyltransferase (EC 2.3.1.133) (Hydroxycinnamoyl transferase) (Hydroxycinnamoyl-Coenzyme A shikimate/quinate hydroxycinnamoyltransferase)	HST HCT	Nicotiana tabacum (Common tobacco)		Acyltransferase; Direct protein sequencing; Transferase
SRR342022_TR13627_c2_g2_i6_len=1731	FAR_SIMCH	Q:1029-97,H:181-492	48.09%ID	E:2e-94	Alcohol-forming fatty acyl-CoA reductase	PF07993.9^NAD_binding_4^Male sterility protein^35-148^E:1e-26`PF03015.16^Sterile^Male sterility protein^223-319^E:1.4e-12	0	1,968	0	5,551	0,014	3,01	0,025	2,902	1	2,136	FAR_SIMCH	Alcohol-forming fatty acyl-CoA reductase (EC 1.2.1.84)		Simmondsia chinensis (Jojoba) (Buxus chinensis)		Lipid biosynthesis; Lipid metabolism; NADP; Oxidoreductase
SRR342023_TR1546_c4_g3_i1_len=2664	DCAM_IPONI	Q:1332-244,H:1-361	72.45%ID	E:0	S-adenosylmethionine decarboxylase proenzyme	PF01536.13^SAM_decarbox^Adenosylmethionine decarboxylase^9-332^E:9.8e-108	0,001	1,4	0	2,45	0,237	0,326	0,155	0,384	1	-0,1	DCAM_IPONI	S-adenosylmethionine decarboxylase proenzyme (AdoMetDC) (SAMDC) (EC 4.1.1.50) [Cleaved into: S-adenosylmethionine decarboxylase alpha chain; S-adenosylmethionine decarboxylase beta chain]	SAMDC SDCG1	Ipomoea nil (Japanese morning glory) (Pharbitis nil)	PATHWAY: Amine and polyamine biosynthesis; S-adenosylmethioninamine biosynthesis; S-adenosylmethioninamine from S-adenosyl-L-methionine: step 1/1.	Autocatalytic cleavage; Decarboxylase; Lyase; Polyamine biosynthesis; Pyruvate; S-adenosyl-L-methionine; Schiff base; Spermidine biosynthesis; Zymogen
SRR342023_TR8498_c0_g1_i2_len=923	NA	NA	NA	NA	NA	.	0	1,636	0	1,335	0,009	0,554	0,004	0,603	1	0,109	.	.	.	.	.	.
SRR342023_TR18599_c2_g5_i8_len=3489	DGAT2_ARATH	Q:518-1456,H:2-314	67.2%ID	E:2e-149	Diacylglycerol O-acyltransferase 2	PF03547.15^Mem_trans^Membrane transport protein^11-405^E:7.7e-65	0	2,336	0,001	1,482	0,732	0,569	0,629	-0,988	0,357	0,689	DGAT2_ARATH	Diacylglycerol O-acyltransferase 2 (EC 2.3.1.20)	DGAT2 At3g51520 F26O13.160	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Glycerolipid metabolism; triacylglycerol biosynthesis.	Acyltransferase; Complete proteome; Endoplasmic reticulum; Glycerol metabolism; Glycoprotein; Lipid biosynthesis; Lipid metabolism; Membrane; Reference proteome; Transferase; Transmembrane; Transmembrane helix
SRR342023_TR19146_c0_g4_i3_len=1968	WTR7_ARATH	Q:595-1623,H:2-340	53.64%ID	E:4e-103	WAT1-related protein At1g43650	PF00892.17^EamA^EamA-like transporter family^15-150^E:1.1e-16`PF00892.17^EamA^EamA-like transporter family^188-325^E:2.5e-14	0	2,258	0	1,894	0,294	0,525	1	-0,1	0,239	1,297	WTR7_ARATH	WAT1-related protein At1g43650	At1g43650 F2J6.1	Arabidopsis thaliana (Mouse-ear cress)		Alternative splicing; Complete proteome; Membrane; Reference proteome; Repeat; Transmembrane; Transmembrane helix
SRR646572_TR18061_c3_g2_i4_len=1750	WTR41_ARATH	Q:1632-730,H:14-319	51.91%ID	E:1e-99	WAT1-related protein At5g40230	PF00892.17^EamA^EamA-like transporter family^31-156^E:1.2e-11`PF00892.17^EamA^EamA-like transporter family^190-308^E:1.3e-06	0	1,642	0	2,771	0,043	2,576	0,629	1,315	1	0,994	WTR41_ARATH	WAT1-related protein At5g40230	At5g40230 MSN9.130	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Membrane; Reference proteome; Repeat; Transmembrane; Transmembrane helix
SRR646572_TR22346_c0_g1_i3_len=7946	PSBB_TOBAC	Q:313-1833,H:1-507	99.61%ID	E:0	Photosystem II CP47 reaction center protein {ECO:0000255|HAMAP-Rule:MF_01495}	PF00421.16^PSII^Photosystem II protein^1-500^E:5.6e-264	0	1,912	0	1,778	0,028	-0,893	0,117	-0,604	1	-0,094	PSBB_TOBAC	Photosystem II CP47 reaction center protein (PSII 47 kDa protein) (Protein CP-47)	psbB	Nicotiana tabacum (Common tobacco)		Chlorophyll; Chloroplast; Chromophore; Membrane; Photosynthesis; Photosystem II; Plastid; Thylakoid; Transmembrane; Transmembrane helix
SRR646596_TR1473_c0_g1_i14_len=1038	ASA2_ORYSJ	Q:310-801,H:442-605	85.98%ID	E:1e-81	Anthranilate synthase alpha subunit 2, chloroplastic	PF00425.15^Chorismate_bind^chorismate binding enzyme^1-133^E:5.5e-37	0	2,657	0	4,437	0,002	2,617	0,118	1,663	0,593	-0,807	ASA2_ORYSJ	Anthranilate synthase alpha subunit 2, chloroplastic (OsASA2) (EC 4.1.3.27)	OsASA2 OASA2 Os03g0264400 LOC_Os03g15780	Oryza sativa subsp. japonica (Rice)	PATHWAY: Amino-acid biosynthesis; L-tryptophan biosynthesis; L-tryptophan from chorismate: step 1/5.	Amino-acid biosynthesis; Aromatic amino acid biosynthesis; Chloroplast; Complete proteome; Lyase; Plastid; Reference proteome; Transit peptide; Tryptophan biosynthesis
SRR646596_TR10462_c0_g1_i1_len=1056	NA	NA	NA	NA	NA	.	0	1,691	0	1,703	0,855	0,043	0,318	-0,231	0,226	0,416	.	.	.	.	.	.
SRR648705_TR5576_c0_g1_i3_len=4219	TRPX_ARATH	Q:2949-1891,H:255-607	80.45%ID	E:9e-175	Anthranilate synthase alpha subunit 2, chloroplastic	PF00425.15^Chorismate_bind^chorismate binding enzyme^42-313^E:6.8e-86	0	2,037	0	3,272	0,009	1,582	0,028	1,439	1	-1,048	TRPX_ARATH	Anthranilate synthase alpha subunit 2, chloroplastic (EC 4.1.3.27) (Anthranilate synthase component 1-2) (Anthranilate synthase component I-2)	ASA2 At2g29690 T27A16.21	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Amino-acid biosynthesis; L-tryptophan biosynthesis; L-tryptophan from chorismate: step 1/5.	Amino-acid biosynthesis; Aromatic amino acid biosynthesis; Chloroplast; Complete proteome; Lyase; Plastid; Reference proteome; Transit peptide; Tryptophan biosynthesis
SRR648705_TR18740_c1_g1_i1_len=785	LSM5_ARATH	Q:658-401,H:1-85	93.02%ID	E:1e-47	Sm-like protein LSM5 {ECO:0000305}	.	0	6,618	0	7,238	0,823	0,106	1	-0,056	0,008	0,764	LSM5_ARATH	Sm-like protein LSM5 (AtLSM5) (Protein SUPERSENSITIVE TO ABA AND DROUGHT 1) (AtSAD1) (U6 snRNA-associated Sm-like protein LSM5)	LSM5 SAD1 At5g48870 K24G6.21	Arabidopsis thaliana (Mouse-ear cress)		Acetylation; Complete proteome; Cytoplasm; Nucleus; RNA-binding; Reference proteome; Ribonucleoprotein; Spliceosome; Stress response; mRNA processing; mRNA splicing
SRR648705_TR18759_c0_g2_i3_len=2884	TRPB_CAMAC	Q:1301-588,H:229-466	94.54%ID	E:2e-153	Tryptophan synthase beta chain 2, chloroplastic	PF00291.22^PALP^Pyridoxal-phosphate dependent enzyme^126-235^E:2.6e-21	0	1,216	0	2,275	0,636	0,151	0,34	-0,288	0,767	0,123	TRPB_CAMAC	Tryptophan synthase beta chain 2, chloroplastic (EC 4.2.1.20)	TSB	Camptotheca acuminata (Happy tree)	PATHWAY: Amino-acid biosynthesis; L-tryptophan biosynthesis; L-tryptophan from chorismate: step 5/5.	Amino-acid biosynthesis; Aromatic amino acid biosynthesis; Chloroplast; Lyase; Plastid; Pyridoxal phosphate; Transit peptide; Tryptophan biosynthesis
SRR648707_TR1596_c0_g2_i1_len=2070	NA	NA	NA	NA	NA	PF01925.16^TauE^Sulfite exporter TauE/SafE^74-191^E:7.8e-12`PF01925.16^TauE^Sulfite exporter TauE/SafE^249-434^E:8.9e-15	0	1,811	0	3,9	0,008	0,768	0,027	0,659	0,518	0,361	.	.	.	.	.	.
SRR648707_TR15318_c0_g4_i3_len=2226	TRPB_CAMAC	Q:2050-641,H:1-466	83.86%ID	E:0	Tryptophan synthase beta chain 2, chloroplastic	PF00291.22^PALP^Pyridoxal-phosphate dependent enzyme^126-455^E:4e-49	0	1,24	0	2,338	0,479	-0,222	0,067	-0,588	1	0	TRPB_CAMAC	Tryptophan synthase beta chain 2, chloroplastic (EC 4.2.1.20)	TSB	Camptotheca acuminata (Happy tree)	PATHWAY: Amino-acid biosynthesis; L-tryptophan biosynthesis; L-tryptophan from chorismate: step 5/5.	Amino-acid biosynthesis; Aromatic amino acid biosynthesis; Chloroplast; Lyase; Plastid; Pyridoxal phosphate; Transit peptide; Tryptophan biosynthesis
SRR648707_TR26086_c0_g1_i14_len=2158	TRPD_ARATH	Q:1089-1946,H:157-442	79.72%ID	E:3e-149	Anthranilate phosphoribosyltransferase, chloroplastic	PF00591.18^Glycos_transf_3^Glycosyl transferase family, a/b domain^13-261^E:7.8e-99	0	1,39	0	2,585	0,006	1,086	0,138	0,658	0,203	0,486	TRPD_ARATH	Anthranilate phosphoribosyltransferase, chloroplastic (EC 2.4.2.18)	PAT1 At5g17990 MCM23.6	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Amino-acid biosynthesis; L-tryptophan biosynthesis; L-tryptophan from chorismate: step 2/5.	Amino-acid biosynthesis; Aromatic amino acid biosynthesis; Chloroplast; Complete proteome; Glycosyltransferase; Plastid; Reference proteome; Transferase; Transit peptide; Tryptophan biosynthesis
SRR648707_TR29014_c0_g1_i2_len=2273	BT1_ARATH	Q:229-1077,H:14-304	69.07%ID	E:2e-125	BTB/POZ and TAZ domain-containing protein 1	PF00651.28^BTB^BTB/POZ domain^89-183^E:5.1e-12`PF02135.13^zf-TAZ^TAZ zinc finger^272-358^E:1.4e-12	0	1,8	0,001	1,218	1	0,035	0,692	0,7	0,364	0,287	BT1_ARATH	BTB/POZ and TAZ domain-containing protein 1 (BTB and TAZ domain protein 1)	BT1 At5g63160 MDC12.13	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Protein modification; protein ubiquitination.	Complete proteome; Cytoplasm; Metal-binding; Nucleus; Reference proteome; Ubl conjugation pathway; Zinc; Zinc-finger
SRR648707_TR33272_c1_g1_i13_len=1712	TRPX_ARATH	Q:250-1488,H:26-446	71.02%ID	E:0	Anthranilate synthase alpha subunit 2, chloroplastic	PF04715.10^Anth_synt_I_N^Anthranilate synthase component I, N terminal region^104-258^E:1e-30`PF00425.15^Chorismate_bind^chorismate binding enzyme^319-451^E:3.2e-37	0	1,791	0	6,814	0,068	1,207	0,524	0,561	0,692	0,828	TRPX_ARATH	Anthranilate synthase alpha subunit 2, chloroplastic (EC 4.1.3.27) (Anthranilate synthase component 1-2) (Anthranilate synthase component I-2)	ASA2 At2g29690 T27A16.21	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Amino-acid biosynthesis; L-tryptophan biosynthesis; L-tryptophan from chorismate: step 1/5.	Amino-acid biosynthesis; Aromatic amino acid biosynthesis; Chloroplast; Complete proteome; Lyase; Plastid; Reference proteome; Transit peptide; Tryptophan biosynthesis
SRR924147_TR20336_c0_g1_i3_len=2526	MTHR2_ARATH	Q:2140-359,H:1-594	82.15%ID	E:0	Methylenetetrahydrofolate reductase 2	PF02219.14^MTHFR^Methylenetetrahydrofolate reductase^6-301^E:1.7e-126	0	0,932	0	4,094	0,403	0,249	0,377	0,257	0,732	0,778	MTHR2_ARATH	Methylenetetrahydrofolate reductase 2 (AtMTHFR2) (EC 1.5.1.20)	MTHFR2 At2g44160 F6E13.29	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: One-carbon metabolism; tetrahydrofolate interconversion.	Complete proteome; FAD; Flavoprotein; NAD; Oxidoreductase; Reference proteome
SRR924148_TR20412_c0_g1_i1_len=2557	AFC2_ARATH	Q:2417-1575,H:1-206	61.57%ID	E:7e-102	Serine/threonine-protein kinase AFC2	PF00069.22^Pkinase^Protein kinase domain^106-161^E:2.1e-07	0	2,767	0	2,754	0,016	-1,313	0	-2,853	1	0	AFC2_ARATH	Serine/threonine-protein kinase AFC2 (EC 2.7.12.1)	AFC2 At4g24740 F22K18.60	Arabidopsis thaliana (Mouse-ear cress)		ATP-binding; Alternative splicing; Complete proteome; Kinase; Nucleotide-binding; Reference proteome; Serine/threonine-protein kinase; Transferase
SRR924148_TR35240_c0_g1_i2_len=1597	BT1_ARATH	Q:1166-321,H:45-335	69.07%ID	E:3e-127	BTB/POZ and TAZ domain-containing protein 1	PF02135.13^zf-TAZ^TAZ zinc finger^115-201^E:7.4e-13	0	2,388	0	1,227	0,299	1,647	0,189	1,837	1	0,41	BT1_ARATH	BTB/POZ and TAZ domain-containing protein 1 (BTB and TAZ domain protein 1)	BT1 At5g63160 MDC12.13	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Protein modification; protein ubiquitination.	Complete proteome; Cytoplasm; Metal-binding; Nucleus; Reference proteome; Ubl conjugation pathway; Zinc; Zinc-finger
SRR924148_TR37769_c0_g1_i4_len=2268	AGT23_ARATH	Q:228-1616,H:20-481	75.59%ID	E:0	Alanine--glyoxylate aminotransferase 2 homolog 3, mitochondrial	PF00202.18^Aminotran_3^Aminotransferase class-III^89-483^E:5.3e-98	0	3,335	0	6,415	0,009	6,043	0,034	5,611	0,042	1,836	AGT23_ARATH	Alanine--glyoxylate aminotransferase 2 homolog 3, mitochondrial (EC 2.6.1.44) (Beta-alanine-pyruvate aminotransferase 3)	At3g08860 T16O11.21	Arabidopsis thaliana (Mouse-ear cress)		Aminotransferase; Complete proteome; Mitochondrion; Photorespiration; Pyridoxal phosphate; Reference proteome; Transferase; Transit peptide
SRR924148_TR38387_c0_g1_i1_len=1972	METK2_CATRO	Q:268-1446,H:1-393	100%ID	E:0	S-adenosylmethionine synthase 2	PF00438.17^S-AdoMet_synt_N^S-adenosylmethionine synthetase, N-terminal domain^4-101^E:6.5e-43`PF02772.13^S-AdoMet_synt_M^S-adenosylmethionine synthetase, central domain^117-238^E:4.5e-46`PF02773.13^S-AdoMet_synt_C^S-adenosylmethionine synthetase, C-terminal domain^240-381^E:1.3e-62	0	0,814	0	3,263	0,759	-0,076	0,127	-0,373	0,27	0,243	METK2_CATRO	S-adenosylmethionine synthase 2 (AdoMet synthase 2) (EC 2.5.1.6) (Methionine adenosyltransferase 2) (MAT 2)	SAMS2	Catharanthus roseus (Madagascar periwinkle) (Vinca rosea)	PATHWAY: Amino-acid biosynthesis; S-adenosyl-L-methionine biosynthesis; S-adenosyl-L-methionine from L-methionine: step 1/1.	ATP-binding; Cobalt; Cytoplasm; Magnesium; Manganese; Metal-binding; Nucleotide-binding; One-carbon metabolism; Potassium; Transferase

Ms1wk

Transcript (CDF97)	Uniprot homolog	BLASTX Position	BLASTX %Identity	BLASTX evalue	Uniprot descr	Pfam	PValue_Ms6h	logFC_Ms6h	PValue_Ms8h	logFC_Ms8h	PValue_MsDamaged24h	logFC_MsDamaged24h	PValue_MsIntact24h	logFC_MsIntact24h	PValue_Ms1wk	logFC_Ms1wk	Entry.name	Protein names	Gene names	Organism	Pathway	Keywords
SRR1144633_TR659_c0_g1_i1_len=807	PLY22_ARATH	Q:616-2,H:50-253	83.9%ID	E:3e-125	Probable pectate lyase 22	.	1	0,024	1	0,143	0	-1,773	0,002	-0,911	0	7,306	PLY22_ARATH	Probable pectate lyase 22 (EC 4.2.2.2)	At5g63180 MDC12_15	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Glycan metabolism; pectin degradation; 2-dehydro-3-deoxy-D-gluconate from pectin: step 2/5.	Calcium; Complete proteome; Glycoprotein; Lyase; Metal-binding; Reference proteome; Signal
SRR1144633_TR6803_c0_g2_i1_len=593	NLTP_VIGUN	Q:146-385,H:20-99	52.5%ID	E:1e-22	Probable non-specific lipid-transfer protein AKCS9	PF14368.3^LTP_2^Probable lipid transfer^48-126^E:3.3e-07	0,396	-0,257	0,581	-0,412	0,004	1,691	0,037	1,296	0	2,095	NLTP_VIGUN	Probable non-specific lipid-transfer protein AKCS9 (LTP)		Vigna unguiculata (Cowpea)		Disulfide bond; Lipid-binding; Signal; Transport
SRR1144633_TR8670_c0_g1_i1_len=1161	HIDM_GLYEC	Q:150-1070,H:16-327	45.57%ID	E:4e-91	2-hydroxyisoflavanone dehydratase	PF00135.25^COesterase^Carboxylesterase family^63-119^E:3.6e-06`PF07859.10^Abhydrolase_3^alpha/beta hydrolase fold^77-285^E:2.9e-34	0,732	0,886	1	0,866	0,254	4,424	1	0	0	2,279	HIDM_GLYEC	2-hydroxyisoflavanone dehydratase (EC 3.1.1.1) (EC 4.2.1.105) (Carboxylesterase HIDM)	HIDM	Glycyrrhiza echinata (Licorice)	PATHWAY: Secondary metabolite biosynthesis; flavonoid biosynthesis.	Flavonoid biosynthesis; Hydrolase; Lyase
SRR1144633_TR8670_c0_g1_i2_len=805	HIDM_GLYEC	Q:150-731,H:16-207	50.76%ID	E:1e-58	2-hydroxyisoflavanone dehydratase	PF00135.25^COesterase^Carboxylesterase family^63-119^E:2e-06`PF07859.10^Abhydrolase_3^alpha/beta hydrolase fold^77-217^E:1.7e-31	0,593	-0,591	0,226	3,041	1	0,145	1	-0,29	0	1,63	HIDM_GLYEC	2-hydroxyisoflavanone dehydratase (EC 3.1.1.1) (EC 4.2.1.105) (Carboxylesterase HIDM)	HIDM	Glycyrrhiza echinata (Licorice)	PATHWAY: Secondary metabolite biosynthesis; flavonoid biosynthesis.	Flavonoid biosynthesis; Hydrolase; Lyase
SRR1144633_TR8670_c0_g1_i7_len=1285	HIDM_GLYEC	Q:262-1194,H:16-327	46.08%ID	E:3e-94	2-hydroxyisoflavanone dehydratase	PF00135.25^COesterase^Carboxylesterase family^62-122^E:3e-05`PF07859.10^Abhydrolase_3^alpha/beta hydrolase fold^80-288^E:3.4e-37	0,517	1,273	0,692	-0,843	0,452	-0,535	0,094	-1,259	0	1,954	HIDM_GLYEC	2-hydroxyisoflavanone dehydratase (EC 3.1.1.1) (EC 4.2.1.105) (Carboxylesterase HIDM)	HIDM	Glycyrrhiza echinata (Licorice)	PATHWAY: Secondary metabolite biosynthesis; flavonoid biosynthesis.	Flavonoid biosynthesis; Hydrolase; Lyase
SRR1144633_TR8696_c0_g1_i1_len=917	NDUB8_ARATH	Q:735-361,H:1-125	82.4%ID	E:1e-50	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8, mitochondrial	.	0,927	0,048	0,568	-0,187	0,121	0,473	0,352	0,286	0	5,776	NDUB8_ARATH	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8, mitochondrial	At5g47570 MNJ7.16	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Electron transport; Membrane; Mitochondrion; Mitochondrion inner membrane; Reference proteome; Respiratory chain; Transit peptide; Transmembrane; Transmembrane helix; Transport
SRR1144633_TR11410_c0_g1_i3_len=1613	GALE2_CYATE	Q:1361-339,H:6-346	83.87%ID	E:0	UDP-glucose 4-epimerase GEPI48	PF04321.14^RmlD_sub_bind^RmlD substrate binding domain^5-165^E:6.2e-11`PF01370.18^Epimerase^NAD dependent epimerase/dehydratase family^7-269^E:9.1e-53`PF02719.12^Polysacc_synt_2^Polysaccharide biosynthesis protein^7-189^E:1.3e-13`PF16363.2^GDP_Man_Dehyd^GDP-mannose 4,6 dehydratase^8-331^E:1.3e-61`PF01073.16^3Beta_HSD^3-beta hydroxysteroid dehydrogenase/isomerase family^8-163^E:6.3e-13	0,606	0,141	0,003	0,761	0,304	-0,251	0,001	-0,808	0	4,244	GALE2_CYATE	UDP-glucose 4-epimerase GEPI48 (EC 5.1.3.2) (Galactowaldenase) (UDP-galactose 4-epimerase)		Cyamopsis tetragonoloba (Guar) (Cluster bean)	PATHWAY: Carbohydrate metabolism; galactose metabolism.	Carbohydrate metabolism; Galactose metabolism; Isomerase; NAD
SRR1144633_TR22705_c0_g1_i1_len=1281	CB22_TOBAC	Q:181-975,H:1-265	93.96%ID	E:0	Chlorophyll a-b binding protein 21, chloroplastic	PF00504.18^Chloroa_b-bind^Chlorophyll A-B binding protein^65-231^E:1.6e-50	0	-0,975	0,048	0,654	0,004	-0,781	0,172	-0,364	0	1,654	CB22_TOBAC	Chlorophyll a-b binding protein 21, chloroplastic (LHCII type I CAB-21) (LHCP)	CAB21	Nicotiana tabacum (Common tobacco)		Acetylation; Chlorophyll; Chloroplast; Chromophore; Magnesium; Membrane; Metal-binding; Phosphoprotein; Photosynthesis; Photosystem I; Photosystem II; Plastid; Thylakoid; Transit peptide; Transmembrane; Transmembrane helix
SRR1144633_TR27825_c0_g4_i1_len=5279	POLX_TOBAC	Q:1725-5252,H:1-1161	40.27%ID	E:0	Retrovirus-related Pol polyprotein from transposon TNT 1-94	PF14223.3^Retrotran_gag_2^gag-polypeptide of LTR copia-type^59-187^E:1.8e-33`PF00098.20^zf-CCHC^Zinc knuckle^227-242^E:0.00069`PF13976.3^gag_pre-integrs^GAG-pre-integrase domain^397-464^E:2.9e-14`PF00665.23^rve^Integrase core domain^480-594^E:6.3e-26`PF07727.11^RVT_2^Reverse transcriptase (RNA-dependent DNA polymerase)^854-1101^E:1.2e-91	0,014	0,761	0,777	0,226	0,329	-0,403	0,241	-0,467	0	2,392	POLX_TOBAC	Retrovirus-related Pol polyprotein from transposon TNT 1-94 [Includes: Protease (EC 3.4.23.-); Reverse transcriptase (EC 2.7.7.49); Endonuclease]		Nicotiana tabacum (Common tobacco)		Aspartyl protease; Endonuclease; Hydrolase; Metal-binding; Nuclease; Nucleotidyltransferase; Protease; RNA-directed DNA polymerase; Transferase; Transposable element; Zinc; Zinc-finger
SRR1144634_TR1138_c1_g1_i1_len=1173	CBSX1_ARATH	Q:419-1012,H:39-236	75.76%ID	E:1e-98	CBS domain-containing protein CBSX1, chloroplastic	PF00571.25^CBS^CBS domain^79-133^E:9.7e-14`PF00571.25^CBS^CBS domain^173-226^E:1.9e-16	0,517	-0,187	0,321	-0,286	0,715	0,142	0,513	0,222	0,001	1,059	CBSX1_ARATH	CBS domain-containing protein CBSX1, chloroplastic (CBS domain-containing protein 2) (AtCDCP2) (Protein LOSS OF THE TIMING OF ET AND JA BIOSYNTHESIS 2) (AtLEJ2)	CBSX1 CDCP2 At4g36910 AP22.61 C7A10.450	Arabidopsis thaliana (Mouse-ear cress)		3D-structure; Acetylation; CBS domain; Chloroplast; Complete proteome; Plastid; Reference proteome; Repeat; Transit peptide
SRR1144634_TR21610_c1_g4_i1_len=593	NA	NA	NA	NA	NA	PF01439.15^Metallothio_2^Metallothionein^40-116^E:4.1e-29	1	-0,001	0	-1,209	0,748	0,082	0,017	-0,592	0	0,989	.	.	.	.	.	.
SRR1144634_TR29100_c0_g1_i1_len=2934	TC159_ARATH	Q:1057-50,H:639-983	63.58%ID	E:4e-103	Translocase of chloroplast 159, chloroplastic	PF04548.13^AIG1^AIG1 family^749-881^E:3.9e-21`PF01926.20^MMR_HSR1^50S ribosome-binding GTPase^750-838^E:1e-07	0,419	-0,375	0,356	1,505	0,56	-0,731	0,643	0,361	0,001	2,165	TC159_ARATH	Translocase of chloroplast 159, chloroplastic (AtToc159) (EC 3.6.5.-) (159 kDa chloroplast outer envelope protein) (Plastid protein import 2) (Translocase of chloroplast 160, chloroplastic) (AtToc160) (Translocase of chloroplast 86, chloroplastic) (AtToc86)	TOC159 PPI2 TOC160 TOC86 At4g02510 T10P11.19 T14P8.24	Arabidopsis thaliana (Mouse-ear cress)		Chloroplast; Coiled coil; Complete proteome; Cytoplasm; GTP-binding; Hydrolase; Magnesium; Membrane; Metal-binding; Nucleotide-binding; Phosphoprotein; Plastid; Plastid outer membrane; Protein transport; Receptor; Reference proteome; Transmembrane; Transmembrane helix; Transport
SRR1144634_TR32664_c0_g1_i1_len=1622	CDSP_ARATH	Q:186-1079,H:1-298	67.76%ID	E:8e-139	Thioredoxin-like protein CDSP32, chloroplastic	PF00085.17^Thioredoxin^Thioredoxin^79-165^E:1.4e-07`PF00085.17^Thioredoxin^Thioredoxin^204-289^E:1.4e-11	0,272	-0,278	0,375	-0,212	0,002	-0,798	0,015	-0,61	0	5,958	CDSP_ARATH	Thioredoxin-like protein CDSP32, chloroplastic (Chloroplastic drought-induced stress protein of 32 KDa) (AtCDSP32)	CDSP32 At1g76080 T23E18.2	Arabidopsis thaliana (Mouse-ear cress)		Chloroplast; Complete proteome; Disulfide bond; Electron transport; Plastid; Redox-active center; Reference proteome; Transit peptide; Transport
SRR122236_TR8892_c0_g1_i1_len=796	GAT22_ARATH	Q:397-750,H:117-230	39.55%ID	E:7e-21	Putative GATA transcription factor 22	PF00320.24^GATA^GATA zinc finger^122-155^E:4.1e-17	0,629	-1,042	1	-0,336	1	0,193	1	-0,399	0,001	2,633	GAT22_ARATH	Putative GATA transcription factor 22	GATA22 At4g26150 F20B18.260	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; DNA-binding; Metal-binding; Nucleus; Reference proteome; Transcription; Transcription regulation; Zinc; Zinc-finger
SRR122236_TR10709_c1_g1_i1_len=904	ARF2B_ARATH	Q:903-373,H:5-181	99.44%ID	E:2e-126	ADP-ribosylation factor 2-B	PF00025.18^Arf^ADP-ribosylation factor family^2-173^E:3.8e-80`PF09439.7^SRPRB^Signal recognition particle receptor beta subunit^12-139^E:7.9e-14`PF08477.10^Roc^Ras of Complex, Roc, domain of DAPkinase^15-125^E:9.9e-14`PF04670.9^Gtr1_RagA^Gtr1/RagA G protein conserved region^15-138^E:2.3e-10`PF01926.20^MMR_HSR1^50S ribosome-binding GTPase^15-118^E:4.4e-05`PF00071.19^Ras^Ras family^16-168^E:9.5e-13	1	0	1	0	1	-0,139	1	-0,301	0	5,784	ARF2B_ARATH	ADP-ribosylation factor 2-B (AtARF2) (ARF1-like protein U5)	ARF2-B ARFA1-D ARFA2-B U5 At1g70490 F20B24.21 F24J13.6	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; ER-Golgi transport; GTP-binding; Golgi apparatus; Lipoprotein; Myristate; Nucleotide-binding; Protein transport; Reference proteome; Transport
SRR122236_TR15235_c0_g1_i2_len=915	RL9_PEA	Q:105-671,H:1-189	87.83%ID	E:2e-116	60S ribosomal protein L9	PF00347.20^Ribosomal_L6^Ribosomal protein L6^12-89^E:8.8e-11`PF00347.20^Ribosomal_L6^Ribosomal protein L6^102-180^E:6.5e-12	0,629	-1,157	0,732	0,545	1	2,251	1	3,332	0	9,92	RL9_PEA	60S ribosomal protein L9 (Gibberellin-regulated protein GA)	RPL9	Pisum sativum (Garden pea)		Ribonucleoprotein; Ribosomal protein
SRR122237_TR3203_c0_g1_i1_len=936	NA	NA	NA	NA	NA	.	1	0	1	0	1	0	1	0	0	5,601	.	.	.	.	.	.

SRR122237_TR6355_c0_g1_i1_len=1105	EXPA8_ARATH	Q:159-848,H:25-253	84.42%ID	E:6e-130	Expansin-A8	PF03330.15^DPBB_1^Lytic transglycolase^93-180^E:1.7e-23`PF01357.18^Pollen_allerg_1^Pollen allergen^191-268^E:5.3e-30	0,464	0,329	0,689	-0,205	0,003	-0,777	0,924	-0,029	0	1,848	EXPA8_ARATH	Expansin-A8 (AtEXPA8) (Alpha-expansin-8) (At-EXP8) (AtEx8) (Ath-ExpAlpha-1.11)	EXPA8 EXP8 At2g40610 T2P4.4	Arabidopsis thaliana (Mouse-ear cress)		Cell wall; Cell wall biogenesis/degradation; Complete proteome; Disulfide bond; Membrane; Reference proteome; Secreted; Signal
SRR122237_TR27637_c0_g1_i1_len=1982	INO1_TOBAC	Q:148-1677,H:1-510	94.12%ID	E:0	Inositol-3-phosphate synthase	PF07994.9^NAD_binding_5^Myo-inositol-1-phosphate synthase^62-494^E:1.7e-142`PF01658.14^Inos-1-P_synth^Myo-inositol-1-phosphate synthase^310-423^E:2.6e-48	0,555	-0,301	0,56	-0,626	1	0	0,001	-0,721	0	1,311	INO1_TOBAC	Inositol-3-phosphate synthase (MIP synthase) (EC 5.5.1.4) (Myo-inositol 1-phosphate synthase) (IPS) (MI-1-P synthase)		Nicotiana tabacum (Common tobacco)	PATHWAY: Polyol metabolism; myo-inositol biosynthesis; myo-inositol from D-glucose 6-phosphate: step 1/2.	Cytoplasm; Inositol biosynthesis; Isomerase; Lipid biosynthesis; Lipid metabolism; NAD; Phospholipid biosynthesis; Phospholipid metabolism
SRR122238_TR9817_c1_g4_i1_len=850	EF4L4_ARATH	Q:534-190,H:1-114	72.17%ID	E:1e-47	Protein ELF4-LIKE 4	PF07011.8^DUF1313^Protein of unknown function (DUF1313)^15-96^E:2e-40	1	0	1	2,638	0,017	-5,92	0,56	-0,762	0	7,173	EF4L4_ARATH	Protein ELF4-LIKE 4	EFL4 ELF4-L4 At1g17455 F1L3.15 F28G4.6	Arabidopsis thaliana (Mouse-ear cress)		Biological rhythms; Complete proteome; Nucleus; Reference proteome
SRR122238_TR12605_c0_g1_i3_len=3130	GCR2_ARATH	Q:293-1516,H:1-410	67.07%ID	E:0	LanC-like protein GCR2	PF08659.7^KR^KR domain^119-211^E:8.8e-09`PF00106.22^adh_short^short chain dehydrogenase^121-263^E:7.3e-21`PF13561.3^adh_short_C2^Enoyl-(Acyl carrier protein) reductase^125-262^E:1.7e-12	0,001	-0,748	0,001	-1,022	0,18	-0,796	0,08	-1,113	0	1,802	GCR2_ARATH	LanC-like protein GCR2 (G-protein coupled receptor 2)	GCR2 GPCR At1g52920 F14G24.19	Arabidopsis thaliana (Mouse-ear cress)		3D-structure; Abscisic acid signaling pathway; Complete proteome; Metal-binding; Reference proteome; Zinc
SRR122238_TR16068_c0_g1_i1_len=1495	DPM1_HUMAN	Q:600-1142,H:81-260	69.06%ID	E:2e-79	Dolichol-phosphate mannosyltransferase subunit 1	PF00535.23^Glycos_transf_2^Glycosyl transferase family 2^17-124^E:1.7e-19`PF13641.3^Glyco_tranf_2_3^Glycosyltransferase like family 2^22-155^E:1.4e-06`PF13506.3^Glyco_transf_21^Glycosyl transferase family 21^29-124^E:3.7e-07	1	0,104	1	0,852	1	1,158	1	1,778	0,001	6,57	DPM1_HUMAN	Dolichol-phosphate mannosyltransferase subunit 1 (EC 2.4.1.83) (Dolichol-phosphate mannose synthase subunit 1) (DPM synthase subunit 1) (Dolichyl-phosphate beta-D-mannosyltransferase subunit 1) (Mannose-P-dolichol synthase subunit 1) (MPD synthase subunit 1)	DPM1	Homo sapiens (Human)	PATHWAY: Protein modification; protein glycosylation.	Acetylation; Complete proteome; Congenital disorder of glycosylation; Congenital muscular dystrophy; Disease mutation; Dystroglycanopathy; Endoplasmic reticulum; Glycosyltransferase; Phosphoprotein; Reference proteome; Transferase
SRR122238_TR24014_c0_g1_i2_len=2256	CATA2_GOSHI	Q:411-1886,H:1-492	89.84%ID	E:0	Catalase isozyme 2	PF00199.16^Catalase^Catalase^18-398^E:1.4e-174`PF06628.9^Catalase-rel^Catalase-related immune-responsive^423-486^E:3.2e-16	0,799	-0,113	0,684	0,183	0,062	-0,396	0,466	-0,154	0	1,895	CATA2_GOSHI	Catalase isozyme 2 (EC 1.11.1.6)	CAT2 SU2	Gossypium hirsutum (Upland cotton) (Gossypium mexicanum)		Heme; Hydrogen peroxide; Iron; Metal-binding; Oxidoreductase; Peroxidase; Peroxisome
SRR122238_TR24095_c0_g1_i2_len=514	PIMT_WHEAT	Q:193-474,H:1-94	65.96%ID	E:2e-36	Protein-L-isoaspartate O-methyltransferase	PF01135.16^PCMT^Protein-L-isoaspartate(D-aspartate) O-methyltransferase (PCMT)^76-157^E:2.7e-27	0,832	-0,3	0,034	5,585	0,472	0,694	0,034	-5,622	0,001	6,568	PIMT_WHEAT	Protein-L-isoaspartate O-methyltransferase (PIMT) (EC 2.1.1.77) (L-isoaspartyl protein carboxyl methyltransferase) (Protein L-isoaspartyl methyltransferase) (Protein-beta-aspartate methyltransferase)	PCM	Triticum aestivum (Wheat)		Complete proteome; Cytoplasm; Direct protein sequencing; Methyltransferase; Reference proteome; S-adenosyl-L-methionine; Transferase
SRR122238_TR28591_c0_g1_i2_len=771	ELOF1_ORYSJ	Q:650-387,H:1-89	92.13%ID	E:1e-41	Transcription elongation factor 1 homolog	.	0,643	0,138	0,395	0,308	0,017	0,636	0,038	-0,605	0	1,59	ELOF1_ORYSJ	Transcription elongation factor 1 homolog	Os07g0631100 LOC_Os07g43730 OsJ_25233 P0519E12.3	Oryza sativa subsp. japonica (Rice)		Complete proteome; Metal-binding; Nucleus; Reference proteome; Transcription; Transcription regulation; Zinc; Zinc-finger
SRR122238_TR32490_c0_g2_i2_len=1707	ANM11_ARATH	Q:195-1325,H:18-390	74.34%ID	E:0	Protein arginine N-methyltransferase 1.1	PF05185.13^PRMT5^PRMT5 arginine-N-methyltransferase^84-355^E:4.3e-07`PF06325.10^PrmA^Ribosomal protein L11 methyltransferase (PrmA)^107-181^E:1.6e-09`PF05175.11^MTS^Methyltransferase small domain^108-180^E:9.2e-05`PF13649.3^Methyltransf_25^Methyltransferase domain^111-185^E:1.5e-08`PF08241.9^Methyltransf_11^Methyltransferase domain^112-197^E:2.8e-07	1	-1,379	1	0	1	0	1	0	0	6,829	ANM11_ARATH	Protein arginine N-methyltransferase 1.1 (AtPRMT11) (EC 2.1.1.-) (EC 2.1.1.125) (Arginine methyltransferase pam1) (Histone-arginine N-methyltransferase PRMT11)	PRMT11 PAM1 PRMT1.1 PRMT1B At4g29510 T16L4.20	Arabidopsis thaliana (Mouse-ear cress)		Chromatin regulator; Complete proteome; Cytoplasm; Methyltransferase; Nucleus; Reference proteome; S-adenosyl-L-methionine; Transcription; Transcription regulation; Transferase
SRR122238_TR39694_c2_g3_i1_len=1361	GGPPS_HEVBR	Q:1181-240,H:52-369	65.41%ID	E:4e-142	Geranylgeranyl pyrophosphate synthase, chloroplastic	PF00348.14^polyprenyl_synt^Polyprenyl synthetase^42-278^E:4.5e-49	1	0,01	1	-0,311	0,245	-0,507	0,108	-0,689	0	2,576	GGPPS_HEVBR	Geranylgeranyl pyrophosphate synthase, chloroplastic (GGPP synthase) (GGPS) (EC 2.5.1.-) ((2E,6E)-farnesyl diphosphate synthase) (Dimethylallyltranstransferase) (EC 2.5.1.1) (Farnesyl diphosphate synthase) (Farnesyltranstransferase) (EC 2.5.1.29) (Geranyltranstransferase) (EC 2.5.1.10)	GGPS GG GGPPS1	Hevea brasiliensis (Para rubber tree) (Siphonia brasiliensis)	PATHWAY: Isoprenoid biosynthesis; farnesyl diphosphate biosynthesis; farnesyl diphosphate from geranyl diphosphate and isopentenyl diphosphate: step 1/1.; PATHWAY: Isoprenoid biosynthesis; geranyl diphosphate biosynthesis; geranyl diphosphate from dimethylallyl diphosphate and isopentenyl diphosphate: step 1/1.; PATHWAY: Isoprenoid biosynthesis; geranylgeranyl diphosphate biosynthesis; geranylgeranyl diphosphate from farnesyl diphosphate and isopentenyl diphosphate: step 1/1.	Carotenoid biosynthesis; Chloroplast; Isoprene biosynthesis; Magnesium; Metal-binding; Plastid; Transferase; Transit peptide
SRR122238_TR45834_c0_g1_i3_len=605	HEM62_ARATH	Q:424-2,H:19-149	58.87%ID	E:5e-39	Coproporphyrinogen-III oxidase 2, chloroplastic	PF01218.15^Coprogen_oxidas^Coproporphyrinogen III oxidase^101-165^E:7.7e-18	1	0,823	1	0,141	1	-0,222	1	-0,24	0	5,503	HEM62_ARATH	Coproporphyrinogen-III oxidase 2, chloroplastic (AtCPO-II) (Coprogen oxidase) (Coproporphyrinogenase) (EC 1.3.3.3)	CPX2 HEMF2 At4g03205 F4C21	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Porphyrin-containing compound metabolism; protoporphyrin-IX biosynthesis; protoporphyrinogen-IX from coproporphyrinogen-III (O2 route): step 1/1.; PATHWAY: Porphyrin-containing compound metabolism; chlorophyll biosynthesis.	Alternative splicing; Chlorophyll biosynthesis; Chloroplast; Complete proteome; Heme biosynthesis; Oxidoreductase; Plastid; Porphyrin biosynthesis; Reference proteome; Transit peptide
SRR122238_TR48850_c1_g1_i1_len=560	NA	NA	NA	NA	NA	.	0,781	-0,573	0,832	0,242	0,44	0,762	0,228	1,079	0	2,512	.	.	.	.	.	.
SRR122238_TR50670_c0_g1_i4_len=505	PPA2_ARATH	Q:502-20,H:124-286	62.58%ID	E:4e-65	Probable inactive purple acid phosphatase 2	PF16656.2^Pur_ac_phosph_N^Purple acid Phosphatase, N-terminal domain^21-123^E:5e-22	0,91	0,09	0,019	1,478	0,154	0,767	0,154	0,759	0,001	2,015	PPA2_ARATH	Probable inactive purple acid phosphatase 2	PAP2 At1g13900 F16A14.11	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Glycoprotein; Iron; Metal-binding; Reference proteome; Secreted; Signal; Zinc
SRR122238_TR50728_c1_g1_i1_len=866	NA	NA	NA	NA	NA	PF00111.24^Fer2^2Fe-2S iron-sulfur cluster binding domain^143-191^E:1.3e-09	0,22	-0,401	0	-1,735	0,002	-1,223	0,013	-0,93	0	2,399	.	.	.	.	.	.
SRR122238_TR50993_c0_g1_i2_len=809	CVIF1_ARATH	Q:167-601,H:26-162	37.24%ID	E:5e-23	Cell wall / vacuolar inhibitor of fructosidase 1	PF04043.12^PMEI^Plant invertase/pectin methylesterase inhibitor^55-199^E:2.4e-14	0,502	3,794	1	-1,588	0,502	3,73	1	1,242	0	2,812	CVIF1_ARATH	Cell wall / vacuolar inhibitor of fructosidase 1 (AtC/VIF1)	C/VIF1 CIF1 VIF1 At1g47960 T2J15.13	Arabidopsis thaliana (Mouse-ear cress)		Alternative splicing; Complete proteome; Disulfide bond; Glycoprotein; Reference proteome; Signal; Vacuole
SRR122238_TR57600_c0_g1_i2_len=849	BAM5_ARATH	Q:720-127,H:12-210	76.88%ID	E:4e-101	Beta-amylase 5	PF01373.14^Glyco_hydro_14^Glycosyl hydrolase family 14^13-208^E:3e-66	0,146	0,49	0,826	0,156	0,001	1,35	0,591	0,282	0	4,665	BAM5_ARATH	Beta-amylase 5 (AtBeta-Amy) (EC 3.2.1.2) (1,4-alpha-D-glucan maltohydrolase) (Protein REDUCED BETA AMYLASE 1)	BAM5 BMY1 RAM1 At4g15210 dl3650c FCAALL.97	Arabidopsis thaliana (Mouse-ear cress)		Alternative splicing; Carbohydrate metabolism; Complete proteome; Cytoplasm; Glycosidase; Hydrolase; Polysaccharide degradation; Reference proteome
SRR122238_TR58493_c0_g1_i3_len=1388	NA	NA	NA	NA	NA	.	1	0	1	0	1	-0,572	1	-0,572	0,001	6,599	.	.	.	.	.	.
SRR122238_TR58493_c0_g1_i6_len=1387	NA	NA	NA	NA	NA	.	1	-0,291	1	-0,425	1	0,397	1	1,597	0,001	4,918	.	.	.	.	.	.
SRR122238_TR59597_c1_g1_i2_len=1706	PMGI_MESCR	Q:275-1405,H:181-557	89.66%ID	E:0	2,3-bisphosphoglycerate-independent phosphoglycerate mutase	PF06415.10^iPGM_N^BPG-independent PGAM N-terminus (iPGM_N)^8-142^E:3.5e-32`PF01676.15^Metalloenzyme^Metalloenzyme superfamily^147-365^E:1.5e-71	0,643	-0,135	0,269	0,294	0,014	0,683	0,032	0,6	0	1,029	PMGI_MESCR	2,3-bisphosphoglycerate-independent phosphoglycerate mutase (BPG-independent PGAM) (Phosphoglyceromutase) (EC 5.4.2.12) (PGAM-I)	PGM1	Mesembryanthemum crystallinum (Common ice plant) (Cryophytum crystallinum)	PATHWAY: Carbohydrate degradation; glycolysis; pyruvate from D-glyceraldehyde 3-phosphate: step 3/5.	Cytoplasm; Glycolysis; Isomerase; Manganese; Metal-binding; Stress response
SRR122238_TR63925_c0_g1_i2_len=1406	CYT12_ORYSJ	Q:1097-483,H:39-244	65.22%ID	E:1e-83	Cysteine proteinase inhibitor 12	PF00031.18^Cystatin^Cystatin domain^48-127^E:5.9e-15`PF16845.2^SQAPI^Aspartic acid proteinase inhibitor^51-127^E:5.3e-21	0,691	0,237	0,018	1,12	0,065	0,716	0,106	0,638	0	1,687	CYT12_ORYSJ	Cysteine proteinase inhibitor 12 (Oryzacystatin XII) (OC-XII) (Oryzacystatin-12)	Os01g0270100 LOC_Os01g16430 P0667A10.20	Oryza sativa subsp. japonica (Rice)		Complete proteome; Plant defense; Protease inhibitor; Reference proteome; Repeat; Secreted; Signal; Thiol protease inhibitor
SRR122238_TR65744_c0_g1_i1_len=916	FK151_ARATH	Q:145-540,H:23-153	82.58%ID	E:6e-73	Peptidyl-prolyl cis-trans isomerase FKBP15-1	PF00254.25^FKBP_C^FKBP-type peptidyl-prolyl cis-trans isomerase^72-163^E:1.1e-35	0,001	-4,462	1	-0,187	0,017	5,795	1	2,619	0	6,884	FK151_ARATH	Peptidyl-prolyl cis-trans isomerase FKBP15-1 (PPIase FKBP15-1) (EC 5.2.1.8) (15 kDa FK506-binding protein) (15 kDa FKBP) (FK506-binding protein 15-1) (AtFKBP15-1) (FK506-binding protein 2-1) (Immunophilin FKBP15-1) (Rotamase)	FKBP15-1 At3g25220 MJL12.17	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Endoplasmic reticulum; Isomerase; Reference proteome; Rotamase; Signal
SRR122238_TR65776_c0_g1_i1_len=664	NA	NA	NA	NA	NA	PF08041.8^PetM^PetM family of cytochrome b6f complex subunit 7^118-145^E:4.1e-11	0,165	-0,315	0,506	0,161	0	-0,923	0,06	-0,408	0	1,194	.	.	.	.	.	.
SRR122238_TR66842_c2_g3_i3_len=1227	BBX19_ARATH	Q:893-351,H:1-154	60.77%ID	E:2e-65	B-box zinc finger protein 19 {ECO:0000303|PubMed:19920209}	PF00643.21^zf-B_box^B-box zinc finger^3-42^E:1e-06`PF00643.21^zf-B_box^B-box zinc finger^54-90^E:3.3e-07	1	0	1	0	1	0	1	0	0	8,055	BBX19_ARATH	B-box zinc finger protein 19 (Protein DOUBLE B-BOX 1B) (Protein SALT TOLERANCE HOMOLOG 5)	BBX19 DBB1B STH5 At4g38960 F19H22.60	Arabidopsis thaliana (Mouse-ear cress)		Alternative splicing; Complete proteome; Metal-binding; Nucleus; Reference proteome; Repeat; Repressor; Transcription; Transcription regulation; Zinc; Zinc-finger
SRR122238_TR68876_c0_g1_i5_len=1248	NA	NA	NA	NA	NA	.	0,299	-1,509	0,226	3,115	1	0	1	0	0	6,548	.	.	.	.	.	.
SRR122238_TR69655_c0_g1_i3_len=765	NA	NA	NA	NA	NA	.	1	0	1	0	1	0	1	0	0	6,861	.	.	.	.	.	.
SRR122238_TR71732_c0_g1_i4_len=1194	GPX4_TOBAC	Q:721-215,H:1-169	84.62%ID	E:7e-102	Probable phospholipid hydroperoxide glutathione peroxidase	PF08534.7^Redoxin^Redoxin^84-237^E:2.1e-07`PF00255.16^GSHPx^Glutathione peroxidase^85-193^E:5.4e-43`PF00578.18^AhpC-TSA^AhpC/TSA family^85-148^E:1.7e-09	1	0	1	2,223	1	0	1	0	0	4,186	GPX4_TOBAC	Probable phospholipid hydroperoxide glutathione peroxidase (PHGPx) (EC 1.11.1.12) (Nt-SubC08)		Nicotiana tabacum (Common tobacco)		Cytoplasm; Oxidoreductase; Peroxidase
SRR122238_TR72015_c0_g1_i6_len=590	CAHC_TOBAC	Q:192-590,H:59-192	67.91%ID	E:2e-59	Carbonic anhydrase, chloroplastic	PF00484.16^Pro_CA^Carbonic anhydrase^152-190^E:5.4e-12	1	-1,349	1	-2,334	1	2,976	1	0	0	8,486	CAHC_TOBAC	Carbonic anhydrase, chloroplastic (EC 4.2.1.1) (Carbonate dehydratase)		Nicotiana tabacum (Common tobacco)		Chloroplast; Lyase; Plastid; Transit peptide; Zinc
SRR122238_TR75687_c0_g1_i4_len=1439	DIOX2_ARATH	Q:1286-297,H:1-332	68.86%ID	E:8e-171	Probable 2-oxoglutarate-dependent dioxygenase At3g49630	PF14226.3^DIOX_N^non-haem dioxygenase in morphine synthesis N-terminal^8-136^E:1.8e-34`PF03171.17^2OG-FeII_Oxy^2OG-Fe(II) oxygenase superfamily^202-289^E:2.2e-22	1	0,039	0,811	-0,336	1	0,137	0,798	0,475	0	4,118	DIOX2_ARATH	Probable 2-oxoglutarate-dependent dioxygenase At3g49630 (EC 1.14.11.-)	At3g50210 F11C1.50	Arabidopsis thaliana (Mouse-ear cress)		Alternative splicing; Complete proteome; Dioxygenase; Iron; Metal-binding; Oxidoreductase; Reference proteome
SRR122238_TR82375_c0_g2_i1_len=1297	XTH32_ARATH	Q:162-944,H:37-297	73.95%ID	E:6e-138	Probable xyloglucan endotransglucosylase/hydrolase protein 32	PF00722.18^Glyco_hydro_16^Glycosyl hydrolases family 16^61-243^E:4.6e-54`PF06955.9^XET_C^Xyloglucan endo-transglycosylase (XET) C-terminus^278-314^E:1.3e-13	0,214	0,866	1	-0,086	1	0,683	1	-1,538	0	1,706	XTH32_ARATH	Probable xyloglucan endotransglucosylase/hydrolase protein 32 (At-XTH32) (XTH-32) (EC 2.4.1.207)	XTH32 At2g36870 T1J8.5	Arabidopsis thaliana (Mouse-ear cress)		Alternative splicing; Apoplast; Cell wall; Cell wall biogenesis/degradation; Complete proteome; Disulfide bond; Glycosidase; Hydrolase; Reference proteome; Secreted; Signal; Transferase
SRR122238_TR87175_c2_g1_i1_len=4037	POLX_TOBAC	Q:4-3333,H:235-1323	44.1%ID	E:0	Retrovirus-related Pol polyprotein from transposon TNT 1-94	PF13976.3^gag_pre-integrs^GAG-pre-integrase domain^168-235^E:1.8e-14`PF00665.23^rve^Integrase core domain^251-365^E:5.9e-26`PF07727.11^RVT_2^Reverse transcriptase (RNA-dependent DNA polymerase)^625-872^E:1.6e-92	0,692	0,544	0,692	-1,208	1	-0,03	1	-0,903	0	3,561	POLX_TOBAC	Retrovirus-related Pol polyprotein from transposon TNT 1-94 [Includes: Protease (EC 3.4.23.-); Reverse transcriptase (EC 2.7.7.49); Endonuclease]		Nicotiana tabacum (Common tobacco)		Aspartyl protease; Endonuclease; Hydrolase; Metal-binding; Nuclease; Nucleotidyltransferase; Protease; RNA-directed DNA polymerase; Transferase; Transposable element; Zinc; Zinc-finger
SRR122238_TR88011_c0_g2_i2_len=598	PGKH_TOBAC	Q:2-316,H:368-472	97.14%ID	E:4e-52	Phosphoglycerate kinase, chloroplastic	PF00162.16^PGK^Phosphoglycerate kinase^1-97^E:2.2e-39	1	1,051	1	1,239	1	1,241	1	1,119	0	10,581	PGKH_TOBAC	Phosphoglycerate kinase, chloroplastic (EC 2.7.2.3)		Nicotiana tabacum (Common tobacco)	PATHWAY: Carbohydrate biosynthesis; Calvin cycle.	ATP-binding; Calvin cycle; Chloroplast; Kinase; Nucleotide-binding; Plastid; Transferase; Transit peptide
SRR122238_TR89375_c0_g1_i7_len=999	ACL5_ARATH	Q:717-115,H:29-229	79.6%ID	E:2e-113	Thermospermine synthase ACAULIS5	PF01564.14^Spermine_synth^Spermine/spermidine synthase^41-228^E:1e-47	0,484	0,426	0,832	-0,26	0,623	0,368	0,52	0,477	0	2,474	ACL5_ARATH	Thermospermine synthase ACAULIS5 (EC 2.5.1.79)	ACL5 TKV At5g19530 T20D1.50	Arabidopsis thaliana (Mouse-ear cress)		Alternative splicing; Complete proteome; Polyamine biosynthesis; Reference proteome; Transferase
SRR1271857_TR2657_c0_g1_i8_len=3347	SYY_MIMIV	Q:1972-3000,H:10-342	45.09%ID	E:2e-86	Tyrosine--tRNA ligase	PF00579.22^tRNA-synt_1b^tRNA synthetases class I (W and Y)^68-357^E:9.8e-67	1	0,741	1	-0,494	1	1,324	0,629	1,714	0	4,581	SYY_MIMIV	Tyrosine--tRNA ligase (EC 6.1.1.1) (Tyrosyl-tRNA synthetase) (TyrRS)	YARS MIMI_L124	Acanthamoeba polyphaga mimivirus (APMV)		3D-structure; ATP-binding; Aminoacyl-tRNA synthetase; Complete proteome; Ligase; Nucleotide-binding; Protein biosynthesis; Reference proteome
SRR1271857_TR4548_c0_g1_i1_len=879	DNJ11_ARATH	Q:332-622,H:65-161	67.35%ID	E:4e-38	Chaperone protein dnaJ 11, chloroplastic	PF00226.28^DnaJ^DnaJ domain^112-175^E:2.2e-21	0,692	1,244	0,006	2,534	1	-0,062	0,76	-0,376	0	2,37	DNJ11_ARATH	Chaperone protein dnaJ 11, chloroplastic (AtDjC11) (AtJ11)	ATJ11 C11 J11 At4g36040 T19K4.170	Arabidopsis thaliana (Mouse-ear cress)		Chaperone; Chloroplast; Complete proteome; Direct protein sequencing; Plastid; Reference proteome; Transit peptide
SRR1271857_TR4645_c1_g1_i1_len=1192	NA	NA	NA	NA	NA	PF13266.3^DUF4057^Protein of unknown function (DUF4057)^3-214^E:3.6e-97	1	0,205	0,692	-1,113	1	1,537	1	2,331	0	3,485	.	.	.	.	.	.
SRR1271857_TR7063_c1_g1_i2_len=3022	SR54C_ARATH	Q:1131-355,H:306-564	86.1%ID	E:5e-150	Signal recognition particle 54 kDa protein, chloroplastic	PF02881.16^SRP54_N^SRP54-type protein, helical bundle domain^91-168^E:5.1e-20`PF06414.9^Zeta_toxin^Zeta toxin^183-292^E:1.7e-06`PF00448.19^SRP54^SRP54-type protein, GTPase domain^186-317^E:6e-50`PF01583.17^APS_kinase^Adenylylsulphate kinase^186-227^E:2.5e-05`PF02374.12^ArsA_ATPase^Anion-transporting ATPase^188-223^E:2.7e-05`PF01656.20^CbiA^CobQ/CobB/MinD/ParA nucleotide binding domain^196-305^E:7.1e-06	1	-0,323	0,066	-3,133	1	-0,572	1	-1,46	0	5,91	SR54C_ARATH	Signal recognition particle 54 kDa protein, chloroplastic (54 chloroplast protein) (54CP) (SRP54) (cpSRP54) (FFC)	FFC CPSRP54 At5g03940 F8F6_150	Arabidopsis thaliana (Mouse-ear cress)		3D-structure; Chloroplast; Complete proteome; GTP-binding; Nucleotide-binding; Plastid; RNA-binding; Reference proteome; Ribonucleoprotein; Signal recognition particle; Transit peptide
SRR1271857_TR7700_c0_g1_i4_len=667	RUXG_ARATH	Q:124-363,H:1-80	90%ID	E:2e-44	Probable small nuclear ribonucleoprotein G	.	1	3,502	1	0	1	1,512	1	0	0	7,911	RUXG_ARATH	Probable small nuclear ribonucleoprotein G (snRNP-G) (Sm protein G) (Sm-G) (SmG)	At2g23930 T29E15.13	Arabidopsis thaliana (Mouse-ear cress)		Alternative splicing; Complete proteome; Nucleus; RNA-binding; Reference proteome; Ribonucleoprotein; Spliceosome; mRNA processing; mRNA splicing
SRR1271857_TR7766_c1_g1_i1_len=1023	HSP80_SOLLC	Q:975-61,H:1-305	94.43%ID	E:2e-172	Heat shock cognate protein 80	PF13589.3^HATPase_c_3^Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase^25-146^E:5.3e-11`PF02518.23^HATPase_c^Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase^27-181^E:1.2e-16`PF00183.15^HSP90^Hsp90 protein^184-305^E:1.8e-43	0,132	-1,872	0,129	3,041	1	-0,641	1	0,373	0	1,45	HSP80_SOLLC	Heat shock cognate protein 80	HSC80	Solanum lycopersicum (Tomato) (Lycopersicon esculentum)		ATP-binding; Chaperone; Complete proteome; Cytoplasm; Nucleotide-binding; Reference proteome; Stress response
SRR1271857_TR9930_c0_g1_i2_len=1657	ENDUB_DANRE	Q:1234-440,H:7-275	41.18%ID	E:3e-57	Poly(U)-specific endoribonuclease-B	PF09412.7^XendoU^Endoribonuclease XendoU^88-352^E:5.1e-98	0,043	0,655	0,021	0,73	0,626	0,274	0,474	0,363	0	3,717	ENDUB_DANRE	Poly(U)-specific endoribonuclease-B (EC 3.1.-.-) (Protein endoU-B) (Uridylate-specific endoribonuclease-B)	endoub zgc:110053	Danio rerio (Zebrafish) (Brachydanio rerio)		Complete proteome; Endonuclease; Hydrolase; Manganese; Metal-binding; Nuclease; RNA-binding; Reference proteome
SRR1271857_TR11664_c0_g1_i4_len=887	BI1L_ARATH	Q:117-791,H:24-251	70.18%ID	E:6e-100	BI1-like protein	PF01027.17^Bax1-I^Inhibitor of apoptosis-promoting Bax1^60-263^E:4.2e-46	0,502	4,108	0,226	2,296	0,502	4,042	1	0	0	8,17	BI1L_ARATH	BI1-like protein	At4g15470 dl3775w FCAALL.58	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Membrane; Reference proteome; Transmembrane; Transmembrane helix
SRR1271857_TR11665_c0_g1_i1_len=593	NA	NA	NA	NA	NA	.	0,005	6,198	1	0,327	0,489	-0,526	0,656	0,303	0	3,502	.	.	.	.	.	.
SRR1271857_TR12243_c0_g1_i3_len=1710	FENR1_TOBAC	Q:158-1105,H:29-343	89.24%ID	E:0	Ferredoxin--NADP reductase, leaf-type isozyme, chloroplastic	PF00970.21^FAD_binding_6^Oxidoreductase FAD-binding domain^140-226^E:0.00017`PF00175.18^NAD_binding_1^Oxidoreductase NAD-binding domain^240-355^E:8.2e-30	1	0,324	0,065	-1,499	0,333	-0,669	0,882	-0,2	0	4,846	FENR1_TOBAC	Ferredoxin--NADP reductase, leaf-type isozyme, chloroplastic (FNR) (EC 1.18.1.2)	PETH	Nicotiana tabacum (Common tobacco)	PATHWAY: Energy metabolism; photosynthesis.	Chloroplast; Electron transport; FAD; Flavoprotein; Membrane; NADP; Oxidoreductase; Photosynthesis; Plastid; Thylakoid; Transit peptide; Transport
SRR1271857_TR15487_c0_g1_i2_len=1173	PPSP1_ARATH	Q:991-338,H:16-236	56.11%ID	E:4e-94	Inorganic pyrophosphatase 1	PF06888.9^Put_Phosphatase^Putative Phosphatase^7-235^E:1.2e-89`PF12710.4^HAD^haloacid dehalogenase-like hydrolase^7-183^E:5.5e-09	1	0,505	1	0	1	0	1	0	0,001	6,543	PPSP1_ARATH	Inorganic pyrophosphatase 1 (AtPPsPase1) (PPi phosphatase 1) (Pyrophosphate-specific phosphatase 1) (EC 3.6.1.1) (Protein PHOSPHATE STARVATION-INDUCED GENE 2) (AtPS2)	PS2 At1g73010 F3N23.21	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Hydrolase; Magnesium; Metal-binding; Reference proteome
SRR1271857_TR17224_c4_g3_i1_len=2093	TBB8_ARATH	Q:177-863,H:1-229	95.2%ID	E:7e-141	Tubulin beta-8 chain	PF00091.22^Tubulin^Tubulin/FtsZ family, GTPase domain^3-211^E:4.8e-69	1	0,071	1	-0,2	1	-0,595	1	-0,926	0	2,727	TBB8_ARATH	Tubulin beta-8 chain (Beta-8-tubulin)	TUBB8 TUB8 At5g23860 MRO11.10	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Cytoplasm; Cytoskeleton; GTP-binding; Microtubule; Nucleotide-binding; Reference proteome
SRR1271857_TR18874_c2_g3_i2_len=1184	PTH2_BOVIN	Q:761-369,H:41-174	43.28%ID	E:8e-29	Peptidyl-tRNA hydrolase 2, mitochondrial	PF01981.13^PTH2^Peptidyl-tRNA hydrolase PTH2^81-194^E:5e-45	0,692	-0,671	1	-0,385	1	0,358	1	0,272	0	3,207	PTH2_BOVIN	Peptidyl-tRNA hydrolase 2, mitochondrial (PTH 2) (EC 3.1.1.29) (Bcl-2 inhibitor of transcription)	PTRH2 BIT1	Bos taurus (Bovine)		Complete proteome; Hydrolase; Isopeptide bond; Mitochondrion; Reference proteome; Transit peptide; Ubl conjugation
SRR1271857_TR19383_c0_g1_i2_len=1452	ATCA1_ARATH	Q:926-216,H:29-265	46.84%ID	E:1e-81	Alpha carbonic anhydrase 1, chloroplastic	PF00194.18^Carb_anhydrase^Eukaryotic-type carbonic anhydrase^35-267^E:5.1e-45	1	-0,529	1	-0,085	1	-0,322	1	-0,411	0	5,436	ATCA1_ARATH	Alpha carbonic anhydrase 1, chloroplastic (AtaCA1) (AtalphaCA1) (EC 4.2.1.1) (Alpha carbonate dehydratase 1)	ACA1 CAH1 At3g52720 F3C22.120	Arabidopsis thaliana (Mouse-ear cress)		Alternative splicing; Chloroplast; Complete proteome; Disulfide bond; Endoplasmic reticulum; Glycoprotein; Lyase; Metal-binding; Plastid; Reference proteome; Signal; Zinc
SRR1271857_TR19998_c0_g2_i1_len=1840	C82G1_ARATH	Q:224-1732,H:15-512	48.73%ID	E:4e-154	Cytochrome P450 82G1	PF00067.19^p450^Cytochrome P450^42-501^E:2.8e-87	0	-4,653	0,35	0,458	0,231	0,579	0,214	-0,913	0	1,514	C82G1_ARATH	Cytochrome P450 82G1 (EC 1.14.-.-)	CYP82G1 At3g25180 MJL12.5	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Secondary metabolite biosynthesis; terpenoid biosynthesis.	Alternative splicing; Complete proteome; Heme; Iron; Membrane; Metal-binding; Monooxygenase; Oxidoreductase; Plant defense; Reference proteome; Transmembrane; Transmembrane helix
SRR1271857_TR20126_c0_g2_i1_len=938	NA	NA	NA	NA	NA	.	1	0,904	1	0	1	0	1	2,235	0,001	4,878	.	.	.	.	.	.
SRR1271857_TR23859_c0_g1_i5_len=1868	TRL11_ARATH	Q:1542-766,H:1-248	57.85%ID	E:3e-77	Thioredoxin-like 1-1, chloroplastic	PF00085.17^Thioredoxin^Thioredoxin^119-186^E:9.3e-13	0,866	-0,108	0,761	0,127	0,183	0,407	0,648	0,151	0	1,72	TRL11_ARATH	Thioredoxin-like 1-1, chloroplastic (Atypical cysteine/histidine-rich thioredoxin 4) (AtACHT4) (Lilium-type thioredoxin 1-1)	At1g08570 F22O13.5	Arabidopsis thaliana (Mouse-ear cress)		Alternative splicing; Chloroplast; Complete proteome; Disulfide bond; Electron transport; Plastid; Redox-active center; Reference proteome; Transit peptide; Transport
SRR1271857_TR26079_c0_g1_i2_len=1866	FDFT_NICBE	Q:345-1574,H:1-410	81.71%ID	E:0	Squalene synthase	PF00494.16^SQS_PSY^Squalene/phytoene synthase^45-315^E:3.9e-45	0,269	0,36	0,423	-0,272	0,781	0,092	0,528	0,185	0	3,456	FDFT_NICBE	Squalene synthase (SQS) (SS) (EC 2.5.1.21) (FPP:FPP farnesyltransferase) (Farnesyl-diphosphate farnesyltransferase)		Nicotiana benthamiana	PATHWAY: Terpene metabolism; lanosterol biosynthesis; lanosterol from farnesyl diphosphate: step 1/3.	Endoplasmic reticulum; Isoprene biosynthesis; Magnesium; Membrane; Multifunctional enzyme; NADP; Oxidoreductase; Transferase; Transmembrane; Transmembrane helix
SRR1271857_TR26079_c0_g1_i4_len=1887	FDFT_NICBE	Q:366-1595,H:1-410	81.71%ID	E:0	Squalene synthase	PF00494.16^SQS_PSY^Squalene/phytoene synthase^45-315^E:3.9e-45	0,608	-0,24	0,004	2,384	0,138	0,531	0,064	0,642	0	7,215	FDFT_NICBE	Squalene synthase (SQS) (SS) (EC 2.5.1.21) (FPP:FPP farnesyltransferase) (Farnesyl-diphosphate farnesyltransferase)		Nicotiana benthamiana	PATHWAY: Terpene metabolism; lanosterol biosynthesis; lanosterol from farnesyl diphosphate: step 1/3.	Endoplasmic reticulum; Isoprene biosynthesis; Magnesium; Membrane; Multifunctional enzyme; NADP; Oxidoreductase; Transferase; Transmembrane; Transmembrane helix
SRR1271857_TR33180_c0_g1_i2_len=1085	RR10_MESCR	Q:478-837,H:78-197	87.5%ID	E:1e-71	30S ribosomal protein S10, chloroplastic	.	0,046	-0,478	0	-1,197	0,124	-0,391	0,467	-0,188	0	7,485	RR10_MESCR	30S ribosomal protein S10, chloroplastic	RPS10	Mesembryanthemum crystallinum (Common ice plant) (Cryophytum crystallinum)		Chloroplast; Plastid; Ribonucleoprotein; Ribosomal protein; Transit peptide
SRR1271857_TR33537_c0_g1_i1_len=1236	R10A3_ARATH	Q:894-244,H:1-217	91.24%ID	E:2e-127	60S ribosomal protein L10a-3	PF00687.18^Ribosomal_L1^Ribosomal protein L1p/L10e family^23-213^E:1.1e-44	1	-1,047	1	-1,791	1	0,797	1	0,284	0	9,276	R10A3_ARATH	60S ribosomal protein L10a-3	RPL10AC At5g22440 MWD9.24	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Reference proteome; Ribonucleoprotein; Ribosomal protein
SRR1271857_TR38014_c0_g1_i13_len=2357	TCPB_ARATH	Q:1545-400,H:146-527	90.05%ID	E:0	T-complex protein 1 subunit beta {ECO:0000303|PubMed:11599560}	PF00118.21^Cpn60_TCP1^TCP-1/cpn60 chaperonin family^2-363^E:3.5e-102	1	-0,007	0,629	0,901	1	0,27	1	0,333	0	5,911	TCPB_ARATH	T-complex protein 1 subunit beta (TCP-1-beta) (CCT-beta) (Chaperonin CCT2)	CCT2 At5g20890 F22D1.60	Arabidopsis thaliana (Mouse-ear cress)		ATP-binding; Chaperone; Complete proteome; Cytoplasm; Nucleotide-binding; Reference proteome
SRR1271857_TR40721_c0_g1_i8_len=976	NA	NA	NA	NA	NA	PF02341.12^RcbX^RbcX protein^112-219^E:7.5e-35	0,256	0,438	0,011	-0,86	1	0	1	0	0	6,89	.	.	.	.	.	.
SRR1271857_TR43439_c0_g4_i3_len=2904	GLYM_SOLTU	Q:2634-1591,H:1-347	93.97%ID	E:0	Serine hydroxymethyltransferase, mitochondrial	PF00464.16^SHMT^Serine hydroxymethyltransferase^58-348^E:1.6e-158	0,875	0,052	0,007	0,771	0	-1,114	0,003	-0,718	0	2,713	GLYM_SOLTU	Serine hydroxymethyltransferase, mitochondrial (SHMT) (EC 2.1.2.1) (Glycine hydroxymethyltransferase) (Serine methylase)		Solanum tuberosum (Potato)	PATHWAY: One-carbon metabolism; tetrahydrofolate interconversion.	Complete proteome; Mitochondrion; One-carbon metabolism; Pyridoxal phosphate; Reference proteome; Transferase; Transit peptide
SRR1271857_TR44327_c0_g1_i1_len=1953	EF1A_TOBAC	Q:1829-522,H:1-436	97.94%ID	E:0	Elongation factor 1-alpha	PF00009.24^GTP_EFTU^Elongation factor Tu GTP binding domain^47-262^E:1.3e-52`PF03144.22^GTP_EFTU_D2^Elongation factor Tu domain 2^289-354^E:8.3e-15`PF03143.14^GTP_EFTU_D3^Elongation factor Tu C-terminal domain^363-470^E:4.5e-38	1	-0,218	0,195	1,51	0,381	1,53	0,381	1,517	0	5,289	EF1A_TOBAC	Elongation factor 1-alpha (EF-1-alpha) (Vitronectin-like adhesion protein 1) (PVN1)		Nicotiana tabacum (Common tobacco)		Cytoplasm; Elongation factor; GTP-binding; Nucleotide-binding; Phosphoprotein; Protein biosynthesis
SRR1271858_TR566_c1_g2_i4_len=1709	NA	NA	NA	NA	NA	PF09598.7^Stm1_N^Stm1^1-76^E:8.9e-23`PF04774.12^HABP4_PAI-RBP1^Hyaluronan / mRNA binding family^155-263^E:3.3e-30	1	0	1	0	1	0	1	0	0	9,639	.	.	.	.	.	.
SRR1271858_TR629_c0_g1_i1_len=2226	NA	NA	NA	NA	NA	PF03031.15^NIF^NLI interacting factor-like phosphatase^318-500^E:1.3e-18	1	-1,922	1	-1,39	1	2,145	1	1,395	0	5,324	.	.	.	.	.	.
SRR1271858_TR2709_c3_g4_i4_len=1972	EF1A_TOBAC	Q:140-1447,H:1-436	97.94%ID	E:0	Elongation factor 1-alpha	PF00009.24^GTP_EFTU^Elongation factor Tu GTP binding domain^52-267^E:1.3e-52`PF03144.22^GTP_EFTU_D2^Elongation factor Tu domain 2^294-359^E:8.4e-15`PF03143.14^GTP_EFTU_D3^Elongation factor Tu C-terminal domain^368-475^E:4.6e-38	0,356	-1,289	1	-0,06	1	-0,641	0,692	-0,816	0	2,236	EF1A_TOBAC	Elongation factor 1-alpha (EF-1-alpha) (Vitronectin-like adhesion protein 1) (PVN1)		Nicotiana tabacum (Common tobacco)		Cytoplasm; Elongation factor; GTP-binding; Nucleotide-binding; Phosphoprotein; Protein biosynthesis
SRR1271858_TR5529_c1_g3_i3_len=1444	NA	NA	NA	NA	NA	.	1	1,206	1	-0,045	1	0	1	1,092	0	7,514	.	.	.	.	.	.
SRR1271858_TR7418_c0_g1_i1_len=2273	CBF5_ARATH	Q:2014-644,H:16-460	82.71%ID	E:0	H/ACA ribonucleoprotein complex subunit 4	PF08068.9^DKCLD^DKCLD (NUC011) domain^50-107^E:5.6e-31`PF01509.15^TruB_N^TruB family pseudouridylate synthase (N terminal domain)^111-227^E:2.1e-19`PF16198.2^TruB_C_2^tRNA pseudouridylate synthase B C-terminal domain^228-294^E:2.8e-22`PF01472.17^PUA^PUA domain^298-370^E:1.8e-21	0,001	-1,109	0,235	0,406	0,235	0,837	1	-0,263	0	3,461	CBF5_ARATH	H/ACA ribonucleoprotein complex subunit 4 (EC 5.4.99.-) (CBF5 homolog) (Dyskerin) (Nopp-140-associated protein of 57 kDa homolog) (AtNAP57) (Nucleolar protein NAP57 homolog)	CBF5 NAP57 At3g57150 F24I3.230	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Isomerase; Nucleus; Phosphoprotein; RNA-binding; Reference proteome; Ribonucleoprotein; Ribosome biogenesis; rRNA processing
SRR1271858_TR15681_c0_g1_i1_len=1365	NA	NA	NA	NA	NA	.	1	0,963	1	-1,183	1	-1,011	1	-2,599	0	5,41	.	.	.	.	.	.
SRR1271858_TR26973_c1_g5_i2_len=2752	CGS1_ARATH	Q:1230-2435,H:163-563	85.82%ID	E:0	Cystathionine gamma-synthase 1, chloroplastic {ECO:0000305}	PF01053.17^Cys_Met_Meta_PP^Cys/Met metabolism PLP-dependent enzyme^159-542^E:2.8e-140	1	1,751	1	0,849	0,502	1,959	1	1,406	0	2,21	CGS1_ARATH	Cystathionine gamma-synthase 1, chloroplastic (AtCGS1) (EC 2.5.1.48) (METHIONINE OVERACCUMULATION 1) (O-succinylhomoserine (thiol)-lyase)	CGS1 CYS1 MTO1 At3g01120 T4P13.19	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Amino-acid biosynthesis; L-methionine biosynthesis via de novo pathway; L-cystathionine from O-succinyl-L-homoserine: step 1/1. {ECO:0000305}.	Amino-acid biosynthesis; Chloroplast; Complete proteome; Direct protein sequencing; Methionine biosynthesis; Plastid; Polymorphism; Pyridoxal phosphate; Reference proteome; Transferase; Transit peptide
SRR1271858_TR34334_c0_g3_i13_len=4289	VIP1_HUMAN	Q:3777-1453,H:68-808	47.18%ID	E:0	Inositol hexakisphosphate and diphosphoinositol-pentakisphosphate kinase 1	PF00328.19^His_Phos_2^Histidine phosphatase superfamily (branch 2)^334-795^E:7.6e-110	1	-0,125	1	-0,906	1	-0,082	1	0,109	0	5,66	VIP1_HUMAN	Inositol hexakisphosphate and diphosphoinositol-pentakisphosphate kinase 1 (EC 2.7.4.21) (EC 2.7.4.24) (Diphosphoinositol pentakisphosphate kinase 1) (Histidine acid phosphatase domain-containing protein 2A) (IP6 kinase) (Inositol pyrophosphate synthase 1) (InsP6 and PP-IP5 kinase 1) (VIP1 homolog) (hsVIP1)	PPIP5K1 HISPPD2A IP6K IPS1 KIAA0377 VIP1	Homo sapiens (Human)		ATP-binding; Alternative splicing; Cell membrane; Complete proteome; Cytoplasm; Kinase; Membrane; Nucleotide-binding; Phosphoprotein; Reference proteome; Transferase
SRR1271858_TR44225_c0_g2_i1_len=659	NLTP_VIGUN	Q:507-265,H:20-99	57.32%ID	E:4e-23	Probable non-specific lipid-transfer protein AKCS9	.	0,15	-0,528	0	-1,224	0,023	0,822	0	-8,349	0	2,598	NLTP_VIGUN	Probable non-specific lipid-transfer protein AKCS9 (LTP)		Vigna unguiculata (Cowpea)		Disulfide bond; Lipid-binding; Signal; Transport
SRR1271858_TR46206_c0_g1_i2_len=3711	ANXD2_ARATH	Q:1301-2176,H:24-316	73.04%ID	E:1e-148	Annexin D2	PF13266.3^DUF4057^Protein of unknown function (DUF4057)^38-220^E:1.9e-92	1	0,765	1	2,474	1	-0,209	1	3,181	0	7,145	ANXD2_ARATH	Annexin D2 (AnnAt2)	ANN2 ANNAT2 At5g65020 MXK3.27	Arabidopsis thaliana (Mouse-ear cress)		Acetylation; Alternative splicing; Annexin; Calcium; Calcium/phospholipid-binding; Complete proteome; Cytoplasm; Membrane; Reference proteome; Repeat
SRR1271858_TR47859_c0_g2_i2_len=1379	EXPA4_ARATH	Q:159-875,H:19-257	90.38%ID	E:4e-159	Expansin-A4	PF03330.15^DPBB_1^Lytic transglycolase^68-155^E:1.3e-21`PF01357.18^Pollen_allerg_1^Pollen allergen^166-243^E:1.6e-24	1	0,044	0,299	-1,58	1	-0,268	1	-1,142	0	1,666	EXPA4_ARATH	Expansin-A4 (AtEXPA4) (Alpha-expansin-4) (At-EXP4) (AtEx4) (Ath-ExpAlpha-1.6)	EXPA4 EXP4 At2g39700 F17A14.7	Arabidopsis thaliana (Mouse-ear cress)		Cell wall; Cell wall biogenesis/degradation; Complete proteome; Direct protein sequencing; Disulfide bond; Membrane; Reference proteome; Secreted; Signal
SRR1271858_TR48117_c0_g1_i2_len=2641	NA	NA	NA	NA	NA	PF01490.15^Aa_trans^Transmembrane amino acid transporter protein^45-262^E:1.2e-31`PF03222.10^Trp_Tyr_perm^Tryptophan/tyrosine permease family^46-269^E:2e-09	1	0,234	1	0	1	0	1	0	0	7,593	.	.	.	.	.	.
SRR1271858_TR48724_c0_g3_i3_len=853	RL4_PRUAR	Q:84-851,H:9-261	83.59%ID	E:1e-147	60S ribosomal protein L4	PF00573.19^Ribosomal_L4^Ribosomal protein L4/L1 family^30-260^E:1.7e-36	1	0	1	0,89	1	0	1	0	0,001	6,574	RL4_PRUAR	60S ribosomal protein L4 (L1)	RPL4	Prunus armeniaca (Apricot) (Armeniaca vulgaris)		Ribonucleoprotein; Ribosomal protein
SRR1271858_TR51167_c0_g2_i3_len=2239	NA	NA	NA	NA	NA	.	1	-1,24	0	-6,624	0,502	3,271	0,502	3,176	0	7,262	.	.	.	.	.	.
SRR1271858_TR53419_c1_g1_i11_len=966	HMGL_IPONI	Q:39-431,H:1-126	71.76%ID	E:1e-44	HMG1/2-like protein	PF09011.7^HMG_box_2^HMG-box domain^49-121^E:2.5e-15`PF00505.16^HMG_box^HMG (high mobility group) box^52-121^E:1.5e-22	0,799	-0,072	0,016	-0,595	0,005	1,118	0,221	0,534	0	1,578	HMGL_IPONI	HMG1/2-like protein		Ipomoea nil (Japanese morning glory) (Pharbitis nil)		DNA-binding; Nucleus
SRR1271858_TR54721_c0_g2_i6_len=1472	GPX1_HELAN	Q:669-1127,H:14-166	78.43%ID	E:3e-71	Glutathione peroxidase 1	PF00255.16^GSHPx^Glutathione peroxidase^2-104^E:1.4e-41`PF00578.18^AhpC-TSA^AhpC/TSA family^2-57^E:6.9e-07`PF08534.7^Redoxin^Redoxin^4-55^E:1.4e-06	0,689	0,202	0,069	1,059	0,016	1,496	0,003	1,763	0	3,75	GPX1_HELAN	Glutathione peroxidase 1 (EC 1.11.1.9)	GPXHA-1	Helianthus annuus (Common sunflower)		Oxidoreductase; Peroxidase
SRR1271858_TR58027_c0_g1_i7_len=2710	SYT1_ARATH	Q:1358-2386,H:197-541	73.04%ID	E:2e-175	Synaptotagmin-1	PF00168.27^C2^C2 domain^170-274^E:8.8e-23`PF00168.27^C2^C2 domain^329-431^E:1.7e-13	1	-0,552	1	0,478	1	0,58	1	-0,212	0	2,821	SYT1_ARATH	Synaptotagmin-1 (NTMC2T1.1) (Synaptotagmin A)	SYT1 SYTA At2g20990 F26H11.25 F5H14.5	Arabidopsis thaliana (Mouse-ear cress)		Alternative splicing; Calcium; Cell membrane; Complete proteome; Endocytosis; Endosome; Host-virus interaction; Lipid-binding; Membrane; Metal-binding; Reference proteome; Repeat; Transmembrane; Transmembrane helix
SRR1271858_TR58106_c0_g1_i1_len=1181	VDAC1_SOLTU	Q:974-450,H:1-175	82.86%ID	E:4e-102	Mitochondrial outer membrane protein porin of 34 kDa	PF01459.19^Porin_3^Eukaryotic porin^5-175^E:3.1e-41	1	0	1	0	1	0	1	0	0	9,402	VDAC1_SOLTU	Mitochondrial outer membrane protein porin of 34 kDa (POM 34) (Voltage-dependent anion-selective channel protein) (VDAC)		Solanum tuberosum (Potato)		Complete proteome; Direct protein sequencing; Ion transport; Membrane; Mitochondrion; Mitochondrion outer membrane; Porin; Reference proteome; Transmembrane; Transmembrane beta strand; Transport
SRR1271858_TR61665_c1_g1_i2_len=4402	PP329_ARATH	Q:383-2662,H:4-761	48.62%ID	E:0	Pentatricopeptide repeat-containing protein At4g20770	PF01535.17^PPR^PPR repeat^74-103^E:2.9e-05`PF01535.17^PPR^PPR repeat^105-131^E:0.00043`PF13041.3^PPR_2^PPR repeat family^203-251^E:3.4e-07`PF01535.17^PPR^PPR repeat^206-235^E:0.00058`PF01535.17^PPR^PPR repeat^293-313^E:0.095`PF13041.3^PPR_2^PPR repeat family^319-364^E:2.1e-07`PF01535.17^PPR^PPR repeat^321-351^E:0.0011`PF01535.17^PPR^PPR repeat^356-382^E:1.3`PF12854.4^PPR_1^PPR repeat^381-413^E:4.6e-07`PF13041.3^PPR_2^PPR repeat family^384-431^E:8.2e-11`PF01535.17^PPR^PPR repeat^388-413^E:7.6e-09`PF01535.17^PPR^PPR repeat^488-517^E:0.056`PF01535.17^PPR^PPR repeat^561-584^E:0.0068`PF13041.3^PPR_2^PPR repeat family^586-634^E:1.2e-11`PF01535.17^PPR^PPR repeat^589-618^E:1.7e-06`PF13812.3^PPR_3^Pentatricopeptide repeat domain^618-670^E:0.0017`PF01535.17^PPR^PPR repeat^625-652^E:0.23`PF01535.17^PPR^PPR repeat^661-683^E:1.3	1	0,052	1	-1,219	1	0,757	1	-0,406	0	4,977	PP329_ARATH	Pentatricopeptide repeat-containing protein At4g20770	PCMP-E35 At4g20770 F21C20.120	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Reference proteome; Repeat
SRR1271858_TR64616_c0_g1_i1_len=821	PRS2_SOLTU	Q:327-773,H:1-152	37.18%ID	E:2e-22	Pathogenesis-related protein STH-2	PF00407.16^Bet_v_1^Pathogenesis-related protein Bet v I family^1-147^E:8.3e-14	1	0	1	0	1	1,279	1	1,249	0	2,399	PRS2_SOLTU	Pathogenesis-related protein STH-2	STH-2	Solanum tuberosum (Potato)		Complete proteome; Pathogenesis-related protein; Plant defense; Reference proteome
SRR1271858_TR64995_c0_g1_i1_len=658	NA	NA	NA	NA	NA	.	0,735	-0,22	0,895	-0,146	0,174	-0,479	0,095	-0,572	0	4,789	.	.	.	.	.	.
SRR1271859_TR1496_c0_g1_i4_len=1473	RZP23_ORYSJ	Q:253-579,H:1-103	79.82%ID	E:8e-45	Serine/arginine-rich splicing factor RSZ23	PF00076.19^RRM_1^RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)^4-61^E:2.5e-17`PF00098.20^zf-CCHC^Zinc knuckle^93-108^E:8.2e-08	0,623	-0,331	1	0	1	0	0,017	5,919	0	6,81	RZP23_ORYSJ	Serine/arginine-rich splicing factor RSZ23 (RS-containing zinc finger protein 23) (Os-RSZ23) (Os-RSZp23)	RSZ23 RSZP23 Os02g0610600 LOC_Os02g39720 OJ1476_F05.20	Oryza sativa subsp. japonica (Rice)		Complete proteome; Metal-binding; Nucleus; Reference proteome; Zinc; Zinc-finger; mRNA processing; mRNA splicing
SRR1271859_TR2244_c0_g4_i3_len=2636	SFH8_ARATH	Q:2320-464,H:1-620	76%ID	E:0	Phosphatidylinositol/phosphatidylcholine transfer protein SFH8	PF03765.12^CRAL_TRIO_N^CRAL/TRIO, N-terminal domain^108-131^E:1.3e-05`PF00650.17^CRAL_TRIO^CRAL/TRIO domain^155-321^E:8e-34	1	0,033	0,502	1,792	1	0,529	1	0,214	0	5,677	SFH8_ARATH	Phosphatidylinositol/phosphatidylcholine transfer protein SFH8 (Protein SEC FOURTEEN HOMOLOGS 8) (AtSFH8)	SFH8 At2g21520 F3K23.28	Arabidopsis thaliana (Mouse-ear cress)		Alternative splicing; Cell membrane; Coiled coil; Complete proteome; Golgi apparatus; Membrane; Protein transport; Reference proteome; Transport
SRR1271859_TR7000_c4_g1_i1_len=1423	UBC2_WHEAT	Q:646-1101,H:1-152	96.05%ID	E:6e-103	Ubiquitin-conjugating enzyme E2 2	PF00179.23^UQ_con^Ubiquitin-conjugating enzyme^8-144^E:1.9e-52	1	0,438	1	0	1	0,557	1	-1,397	0	8,183	UBC2_WHEAT	Ubiquitin-conjugating enzyme E2 2 (EC 2.3.2.23) (E2 ubiquitin-conjugating enzyme 2) (Ubiquitin carrier protein 2) (Ubiquitin-conjugating enzyme E2-16 kDa) (Ubiquitin-protein ligase 2)	UBC2 UBC1	Triticum aestivum (Wheat)	PATHWAY: Protein modification; protein ubiquitination. {ECO:0000255|PROSITE-ProRule:PRU00388}.	ATP-binding; Complete proteome; Nucleotide-binding; Reference proteome; Transferase; Ubl conjugation pathway
SRR1271859_TR7000_c4_g1_i11_len=1085	UBC2_WHEAT	Q:299-754,H:1-152	96.05%ID	E:2e-104	Ubiquitin-conjugating enzyme E2 2	PF00179.23^UQ_con^Ubiquitin-conjugating enzyme^66-202^E:5.4e-52	0,889	-0,166	0,267	0,717	0,129	0,842	0,1	0,919	0	2,154	UBC2_WHEAT	Ubiquitin-conjugating enzyme E2 2 (EC 2.3.2.23) (E2 ubiquitin-conjugating enzyme 2) (Ubiquitin carrier protein 2) (Ubiquitin-conjugating enzyme E2-16 kDa) (Ubiquitin-protein ligase 2)	UBC2 UBC1	Triticum aestivum (Wheat)	PATHWAY: Protein modification; protein ubiquitination. {ECO:0000255|PROSITE-ProRule:PRU00388}.	ATP-binding; Complete proteome; Nucleotide-binding; Reference proteome; Transferase; Ubl conjugation pathway
SRR1271859_TR8788_c0_g1_i2_len=2978	UGDH1_SOYBN	Q:1200-2639,H:1-480	92.29%ID	E:0	UDP-glucose 6-dehydrogenase 1	PF03721.11^UDPG_MGDP_dh_N^UDP-glucose/GDP-mannose dehydrogenase family, NAD binding domain^21-202^E:5.8e-66`PF00984.16^UDPG_MGDP_dh^UDP-glucose/GDP-mannose dehydrogenase family, central domain^228-322^E:7.3e-32`PF03720.12^UDPG_MGDP_dh_C^UDP-glucose/GDP-mannose dehydrogenase family, UDP binding domain^346-469^E:1.5e-37	1	0,613	1	1,912	0,629	-1,563	0,629	-1,422	0	3,196	UGDH1_SOYBN	UDP-glucose 6-dehydrogenase 1 (UDP-Glc dehydrogenase 1) (UDP-GlcDH 1) (UDPGDH 1) (EC 1.1.1.22) (Gm-UGD1)	UGD1	Glycine max (Soybean) (Glycine hispida)	PATHWAY: Nucleotide-sugar biosynthesis; UDP-alpha-D-glucuronate biosynthesis; UDP-alpha-D-glucuronate from UDP-alpha-D-glucose: step 1/1.	Complete proteome; NAD; Oxidoreductase; Phosphoprotein; Reference proteome
SRR1271859_TR10403_c0_g3_i6_len=1649	NA	NA	NA	NA	NA	.	1	-2,32	1	0,627	1	-0,559	1	-0,716	0	4,891	.	.	.	.	.	.
SRR1271859_TR10543_c2_g1_i18_len=968	CYSK_SPIOL	Q:246-968,H:1-241	85.48%ID	E:8e-140	Cysteine synthase	PF00291.22^PALP^Pyridoxal-phosphate dependent enzyme^13-239^E:6.7e-52	1	0,846	1	0,442	1	-0,158	1	-0,488	0	1,109	CYSK_SPIOL	Cysteine synthase (EC 2.5.1.47) (CSase A) (O-acetylserine (thiol)-lyase) (OAS-TL A) (O-acetylserine sulfhydrylase)		Spinacia oleracea (Spinach)	PATHWAY: Amino-acid biosynthesis; L-cysteine biosynthesis; L-cysteine from L-serine: step 2/2.	Amino-acid biosynthesis; Cysteine biosynthesis; Cytoplasm; Direct protein sequencing; Pyridoxal phosphate; Transferase
SRR1271859_TR13163_c0_g2_i3_len=2727	SPX4_ARATH	Q:1347-454,H:1-303	62.06%ID	E:1e-107	SPX domain-containing protein 4	PF03105.16^SPX^SPX domain^9-67^E:3.8e-11`PF03105.16^SPX^SPX domain^78-122^E:3.5e-07`PF03105.16^SPX^SPX domain^139-176^E:7.8e-09	1	0,885	1	-0,486	1	0	1	0	0	6,657	SPX4_ARATH	SPX domain-containing protein 4 (Protein SPX DOMAIN GENE 4) (AtSPX4)	SPX4 At5g15330 F8M21_220	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Reference proteome
SRR1271859_TR13703_c0_g1_i4_len=2267	THO4A_ARATH	Q:258-992,H:4-244	55.65%ID	E:2e-57	THO complex subunit 4A	PF00076.19^RRM_1^RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)^156-224^E:1.3e-15`PF13865.3^FoP_duplication^C-terminal duplication domain of Friend of PRMT1^254-306^E:1.8e-08	1	0,575	1	2,635	1	1,06	1	1,122	0	5,586	THO4A_ARATH	THO complex subunit 4A (ALYREF homolog 1) (AtALY1)	ALY1 THO4A At5g59950 MMN10.26	Arabidopsis thaliana (Mouse-ear cress)		Acetylation; Alternative splicing; Complete proteome; Nucleus; RNA-binding; Reference proteome; Transport; mRNA transport
SRR1271859_TR13950_c0_g1_i3_len=2369	NA	NA	NA	NA	NA	PF09405.7^Btz^CASC3/Barentsz eIF4AIII binding^142-249^E:2.9e-20	0,517	-0,926	1	-0,184	1	0,232	1	0	0	4,942	.	.	.	.	.	.
SRR1271859_TR13962_c2_g2_i1_len=1717	TBB6_MAIZE	Q:144-1433,H:1-430	94.65%ID	E:0	Tubulin beta-6 chain	PF00091.22^Tubulin^Tubulin/FtsZ family, GTPase domain^3-211^E:3.6e-68`PF03953.14^Tubulin_C^Tubulin C-terminal domain^261-381^E:5.5e-41	1	-0,095	1	0,124	1	1,868	1	2,615	0	5,653	TBB6_MAIZE	Tubulin beta-6 chain (Beta-6-tubulin)	TUBB6 TUB6	Zea mays (Maize)		Complete proteome; Cytoplasm; Cytoskeleton; GTP-binding; Microtubule; Nucleotide-binding; Reference proteome
SRR1271859_TR17355_c0_g1_i1_len=1457	FLS_PETHY	Q:1329-307,H:11-348	76.02%ID	E:0	Flavonol synthase/flavanone 3-hydroxylase	PF14226.3^DIOX_N^non-haem dioxygenase in morphine synthesis N-terminal^43-154^E:1.4e-25`PF03171.17^2OG-FeII_Oxy^2OG-Fe(II) oxygenase superfamily^204-300^E:3.3e-27	1	0	1	0	1	0	1	0	0	8,494	FLS_PETHY	Flavonol synthase/flavanone 3-hydroxylase (FLS) (EC 1.14.11.23) (EC 1.14.11.9)	FL	Petunia hybrida (Petunia)	PATHWAY: Secondary metabolite biosynthesis; flavonoid biosynthesis.	Cytoplasm; Dioxygenase; Flavonoid biosynthesis; Iron; Metal-binding; Oxidoreductase; Vitamin C
SRR1271859_TR18461_c0_g1_i6_len=2642	AB7G_ARATH	Q:2248-443,H:65-666	82.23%ID	E:0	ABC transporter G family member 7	PF00005.24^ABC_tran^ABC transporter^87-239^E:2.8e-23`PF01061.21^ABC2_membrane^ABC-2 type transporter^388-599^E:1.2e-41	0,524	-0,223	0,21	-0,529	0,145	-0,658	0,145	-0,628	0,001	1,317	AB7G_ARATH	ABC transporter G family member 7 (ABC transporter ABCG.7) (AtABCG7) (White-brown complex homolog protein 7) (AtWBC7)	ABCG7 WBC7 At2g01320 F10A8.20	Arabidopsis thaliana (Mouse-ear cress)		ATP-binding; Alternative splicing; Complete proteome; Membrane; Nucleotide-binding; Reference proteome; Transmembrane; Transmembrane helix; Transport
SRR1271859_TR19103_c0_g1_i6_len=3375	GLGB_SOLTU	Q:372-2306,H:1-653	77.17%ID	E:0	1,4-alpha-glucan-branching enzyme	PF02922.15^CBM_48^Carbohydrate-binding module 48 (Isoamylase N-terminal domain)^134-217^E:1.6e-20`PF00128.21^Alpha-amylase^Alpha amylase, catalytic domain^298-396^E:6.9e-11	0,211	0,738	0,402	1,128	0,111	1,285	0,593	0,62	0	1,687	GLGB_SOLTU	1,4-alpha-glucan-branching enzyme (EC 2.4.1.18) (Q-enzyme) (Starch-branching enzyme)	SBE1 SBE	Solanum tuberosum (Potato)	PATHWAY: Glycan biosynthesis; starch biosynthesis.	Amyloplast; Chloroplast; Complete proteome; Glycosyltransferase; Plastid; Reference proteome; Starch biosynthesis; Transferase
SRR1271859_TR23830_c0_g1_i2_len=1945	NA	NA	NA	NA	NA	PF04788.9^DUF620^Protein of unknown function (DUF620)^122-378^E:4.2e-121	0,461	1,15	0,158	1,649	0,132	2,172	0,629	1,191	0	6,318	.	.	.	.	.	.
SRR1271859_TR25327_c0_g1_i1_len=622	H4_SOYBN	Q:200-445,H:22-103	100%ID	E:2e-49	Histone H4	.	0,319	0,965	0	-6,689	0,643	-0,429	0,472	-0,672	0	6,755	H4_SOYBN	Histone H4		Glycine max (Soybean) (Glycine hispida)		Acetylation; Chromosome; Complete proteome; DNA-binding; Methylation; Nucleosome core; Nucleus; Reference proteome
SRR1271859_TR26429_c0_g3_i1_len=1023	CRD1_ARATH	Q:427-897,H:1-158	72.96%ID	E:1e-62	Magnesium-protoporphyrin IX monomethyl ester [oxidative] cyclase, chloroplastic	.	0	-1,843	0,009	6,097	0	-5,267	0	-1,996	0	3,481	CRD1_ARATH	Magnesium-protoporphyrin IX monomethyl ester [oxidative] cyclase, chloroplastic (Mg-protoporphyrin IX monomethyl ester oxidative cyclase) (EC 1.14.13.81) (Copper response defect 1 protein) (Dicarboxylate diiron protein) (AtZIP) (MPE-cyclase)	CRD1 ACSF AT103 CHL27 ZIP At3g56940 F24I3.20	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Porphyrin-containing compound metabolism; chlorophyll biosynthesis.	Alternative splicing; Chlorophyll biosynthesis; Chloroplast; Complete proteome; Iron; Membrane; Metal-binding; NADP; Oxidoreductase; Photosynthesis; Plastid; Plastid inner membrane; Reference proteome; Thylakoid; Transit peptide
SRR1271859_TR26434_c0_g1_i1_len=1695	PSMD4_ARATH	Q:143-1306,H:1-368	62.92%ID	E:2e-143	26S proteasome non-ATPase regulatory subunit 4 homolog	PF13519.3^VWA_2^von Willebrand factor type A domain^6-115^E:1.4e-27`PF02809.17^UIM^Ubiquitin interaction motif^224-237^E:0.54`PF02809.17^UIM^Ubiquitin interaction motif^290-305^E:0.069`PF02809.17^UIM^Ubiquitin interaction motif^324-338^E:0.55	1	0	1	1,518	1	0	1	0	0	5,768	PSMD4_ARATH	26S proteasome non-ATPase regulatory subunit 4 homolog (26S proteasome regulatory subunit RPN10) (AtRPN10) (26S proteasome regulatory subunit S5A homolog) (Multiubiquitin chain-binding protein 1) (AtMCB1)	RPN10 MBP1 MCB1 At4g38630 F20M13.190 T9A14.7	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Phosphoprotein; Proteasome; Reference proteome; Repeat
SRR1271859_TR28211_c0_g1_i3_len=934	FER3_ARATH	Q:819-364,H:1-155	56.77%ID	E:6e-57	Ferredoxin-3, chloroplastic	PF00111.24^Fer2^2Fe-2S iron-sulfur cluster binding domain^65-138^E:2.6e-21	1	-1,869	1	1,875	1	1,543	1	0	0	8,315	FER3_ARATH	Ferredoxin-3, chloroplastic (AtFd3)	FD3 At2g27510 F10A12.19	Arabidopsis thaliana (Mouse-ear cress)		2Fe-2S; Acetylation; Chloroplast; Complete proteome; Electron transport; Iron; Iron-sulfur; Metal-binding; Plastid; Reference proteome; Transit peptide; Transport
SRR1271859_TR31741_c0_g1_i3_len=2813	CSC1L_BRAJU	Q:405-2549,H:1-713	65.69%ID	E:0	CSC1-like protein ERD4	PF13967.3^RSN1_TM^Late exocytosis, associated with Golgi transport^5-165^E:5.5e-31`PF14703.3^PHM7_cyt^Cytosolic domain of 10TM putative phosphate transporter^187-354^E:2.3e-33`PF02714.12^RSN1_7TM^Calcium-dependent channel, 7TM region, putative phosphate^365-636^E:8.8e-78	0,373	0,333	0,008	1,377	0,9	-0,093	0,564	0,315	0	2,004	CSC1L_BRAJU	CSC1-like protein ERD4 (Protein EARLY-RESPONSIVE TO DEHYDRATION STRESS 4)	ERD4	Brassica juncea (Indian mustard) (Sinapis juncea)		Calcium; Chloroplast; Ion channel; Ion transport; Membrane; Plastid; Transmembrane; Transmembrane helix; Transport
SRR1271859_TR32580_c0_g3_i19_len=774	SC61A_DICDI	Q:172-753,H:2-247	52.44%ID	E:1e-78	Protein transport protein Sec61 subunit alpha	PF10559.6^Plug_translocon^Plug domain of Sec61p^42-76^E:2.3e-18`PF00344.17^SecY^SecY translocase^77-173^E:5.2e-16	0,44	-1,039	0,129	2,635	1	0,9	1	1,413	0	1,307	SC61A_DICDI	Protein transport protein Sec61 subunit alpha (Secretory 61 complex subunit alpha)	sec61a DDB_G0278885	Dictyostelium discoideum (Slime mold)		Complete proteome; Endoplasmic reticulum; Membrane; Protein transport; Reference proteome; Translocation; Transmembrane; Transmembrane helix; Transport
SRR1271859_TR33166_c3_g2_i3_len=1375	TI201_ARATH	Q:970-158,H:1-274	71.17%ID	E:1e-114	Protein TIC 20-I, chloroplastic {ECO:0000303|PubMed:23372012}	PF16166.2^TIC20^Chloroplast import apparatus Tic20-like^91-265^E:9.1e-78	1	-0,685	1	-1,343	1	0,676	1	0,767	0	6,14	TI201_ARATH	Protein TIC 20-I, chloroplastic (Translocon at the inner envelope membrane of chloroplasts 20-I) (AtTIC20-I)	TIC20-I At1g04940 F13M7.5 F13M7.7	Arabidopsis thaliana (Mouse-ear cress)		Chloroplast; Complete proteome; Membrane; Plastid; Plastid inner membrane; Protein transport; Reference proteome; Transit peptide; Transmembrane; Transmembrane helix; Transport

SRR1271859_TR38007_c0_g1_i1_len=1290	RS92_ARATH	Q:1083-547,H:1-179	89.94%ID	E:2e-113	40S ribosomal protein S9-2	PF00163.16^Ribosomal_S4^Ribosomal protein S4/S9 N-terminal domain^8-64^E:2.6e-09`PF01479.22^S4^S4 domain^109-152^E:2.7e-11	1	-0,691	1	0,657	1	-0,629	1	-0,629	0	9,59	RS92_ARATH	40S ribosomal protein S9-2	RPS9C At5g39850 MYH19.1 MYH19.10	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; RNA-binding; Reference proteome; Ribonucleoprotein; Ribosomal protein; rRNA-binding
SRR1271859_TR38906_c1_g1_i6_len=793	RAN3_ARATH	Q:632-48,H:5-199	99.49%ID	E:1e-143	GTP-binding nuclear protein Ran-3	PF00025.18^Arf^ADP-ribosylation factor family^13-139^E:2.2e-11`PF00071.19^Ras^Ras family^15-171^E:3.2e-50`PF08477.10^Roc^Ras of Complex, Roc, domain of DAPkinase^15-128^E:1.3e-29`PF00910.19^RNA_helicase^RNA helicase^17-139^E:2.6e-05	0,705	-0,24	0,472	0,326	0,025	1,184	0,412	0,506	0	1,314	RAN3_ARATH	GTP-binding nuclear protein Ran-3 (Ras-related nuclear protein 3)	RAN3 At5g55190 MCO15.14	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; GTP-binding; Nucleotide-binding; Nucleus; Protein transport; Reference proteome; Transport
SRR1271859_TR41686_c4_g1_i1_len=775	NA	NA	NA	NA	NA	PF02496.13^ABA_WDS^ABA/WDS induced protein^109-185^E:1.1e-35	1	-0,621	1	-0,299	0,502	2,139	1	-1,697	0	1,549	.	.	.	.	.	.
SRR1271859_TR43983_c0_g1_i3_len=1847	G3PP1_ARATH	Q:207-1466,H:1-422	81.8%ID	E:0	Glyceraldehyde-3-phosphate dehydrogenase GAPCP1, chloroplastic	PF00044.21^Gp_dh_N^Glyceraldehyde 3-phosphate dehydrogenase, NAD binding domain^86-234^E:8.5e-57`PF02800.17^Gp_dh_C^Glyceraldehyde 3-phosphate dehydrogenase, C-terminal domain^239-396^E:3.2e-69	1	0	1	0	1	0	1	0	0	7,509	G3PP1_ARATH	Glyceraldehyde-3-phosphate dehydrogenase GAPCP1, chloroplastic (EC 1.2.1.12) (Glyceraldehyde-3-phosphate dehydrogenase of plastid 1) (NAD-dependent glyceraldehydephosphate dehydrogenase chloroplastic 1)	GAPCP1 At1g79530 T8K14.5	Arabidopsis thaliana (Mouse-ear cress)		Acetylation; Chloroplast; Complete proteome; Glycolysis; NAD; Oxidoreductase; Plastid; Reference proteome; Transit peptide
SRR1271859_TR44144_c1_g2_i2_len=895	SP1L1_ARATH	Q:699-379,H:1-110	64.86%ID	E:8e-29	Protein SPIRAL1-like 1	.	1	-0,444	1	0,07	1	0,821	1	1,484	0	6,738	SP1L1_ARATH	Protein SPIRAL1-like 1	SP1L1 At1g26355 T1K7.26	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Microtubule; Phosphoprotein; Reference proteome
SRR1271859_TR45325_c0_g1_i8_len=2399	NA	NA	NA	NA	NA	PF13417.3^GST_N_3^Glutathione S-transferase, N-terminal domain^141-216^E:1.1e-13	1	-0,037	1	-1,752	1	-1,436	1	-1,056	0	6,882	.	.	.	.	.	.
SRR1271859_TR45849_c0_g1_i1_len=2695	IQD1_ARATH	Q:1430-2383,H:137-444	47.75%ID	E:6e-70	Protein IQ-DOMAIN 1	PF13178.3^DUF4005^Protein of unknown function (DUF4005)^228-295^E:0.00015	1	-0,432	1	0,567	1	0,064	1	0,349	0,001	2,63	IQD1_ARATH	Protein IQ-DOMAIN 1	IQD1 At3g09710 F11F8.30	Arabidopsis thaliana (Mouse-ear cress)		Alternative splicing; Calmodulin-binding; Complete proteome; Nucleus; Reference proteome
SRR1271859_TR47370_c1_g1_i3_len=619	NLTP_PRUAV	Q:203-532,H:9-117	42.73%ID	E:2e-23	Non-specific lipid-transfer protein	PF14368.3^LTP_2^Probable lipid transfer^22-109^E:3.6e-06`PF00234.19^Tryp_alpha_amyl^Protease inhibitor/seed storage/LTP family^34-118^E:1.2e-06	0,355	-0,26	0,326	0,317	0,208	0,409	0,008	-1,052	0	2,088	NLTP_PRUAV	Non-specific lipid-transfer protein (LTP) (allergen Pru av 3)		Prunus avium (Cherry) (Cerasus avium)		Allergen; Disulfide bond; Lipid-binding; Signal; Transport
SRR342017_TR1488_c1_g2_i1_len=1762	PP153_ARATH	Q:332-1471,H:206-579	52.11%ID	E:2e-138	Pentatricopeptide repeat-containing protein At2g15690	PF01535.17^PPR^PPR repeat^166-187^E:0.048`PF01535.17^PPR^PPR repeat^192-220^E:0.00032`PF01535.17^PPR^PPR repeat^227-253^E:1.3`PF14432.3^DYW_deaminase^DYW family of nucleic acid deaminases^348-462^E:5.3e-34	1	-1,312	1	-0,715	1	0	1	0	0	6,698	PP153_ARATH	Pentatricopeptide repeat-containing protein At2g15690	PCMP-H66 At2g15690 F9O13.24	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Reference proteome; Repeat
SRR342017_TR4084_c1_g1_i3_len=702	GPX4_MESCR	Q:264-701,H:1-147	83.67%ID	E:3e-89	Probable phospholipid hydroperoxide glutathione peroxidase	PF08534.7^Redoxin^Redoxin^97-157^E:2.2e-06`PF00255.16^GSHPx^Glutathione peroxidase^98-206^E:4.8e-43`PF00578.18^AhpC-TSA^AhpC/TSA family^98-161^E:1.6e-09	1	1,398	1	0	1	0	1	0	0	7,994	GPX4_MESCR	Probable phospholipid hydroperoxide glutathione peroxidase (PHGPx) (EC 1.11.1.12)	GPXMC1	Mesembryanthemum crystallinum (Common ice plant) (Cryophytum crystallinum)		Cytoplasm; Oxidoreductase; Peroxidase
SRR342017_TR6085_c1_g1_i1_len=954	TI201_ARATH	Q:682-2,H:1-230	66.09%ID	E:5e-82	Protein TIC 20-I, chloroplastic {ECO:0000303|PubMed:23372012}	PF16166.2^TIC20^Chloroplast import apparatus Tic20-like^91-227^E:7.5e-57	1	0	1	0,82	1	-2,586	1	-2,586	0	4,054	TI201_ARATH	Protein TIC 20-I, chloroplastic (Translocon at the inner envelope membrane of chloroplasts 20-I) (AtTIC20-I)	TIC20-I At1g04940 F13M7.5 F13M7.7	Arabidopsis thaliana (Mouse-ear cress)		Chloroplast; Complete proteome; Membrane; Plastid; Plastid inner membrane; Protein transport; Reference proteome; Transit peptide; Transmembrane; Transmembrane helix; Transport
SRR342017_TR7190_c0_g2_i3_len=760	PS10B_ARATH	Q:199-759,H:3-190	92.02%ID	E:5e-118	26S protease regulatory subunit S10B homolog B	.	1	0	1	0	1	0	1	0	0	6,992	PS10B_ARATH	26S protease regulatory subunit S10B homolog B (26S proteasome AAA-ATPase subunit RPT4b) (26S proteasome subunit S10B homolog B) (Regulatory particle triple-A ATPase subunit 4b)	RPT4B At1g45000 F27F5.8	Arabidopsis thaliana (Mouse-ear cress)		ATP-binding; Alternative splicing; Complete proteome; Cytoplasm; Nucleotide-binding; Nucleus; Proteasome; Reference proteome
SRR342017_TR9404_c0_g5_i1_len=774	SL30A_ARATH	Q:242-742,H:34-194	67.66%ID	E:2e-51	Serine/arginine-rich SC35-like splicing factor SCL30A	PF00076.19^RRM_1^RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)^86-155^E:3.2e-20	0,5	-0,777	1	0	1	0	1	0	0	6,853	SL30A_ARATH	Serine/arginine-rich SC35-like splicing factor SCL30A (At-SCL30A) (AtSCL30A) (SC35-like splicing factor 30A) (Serine/arginine-rich splicing factor 30A)	SCL30A At3g13570 K20M4.1	Arabidopsis thaliana (Mouse-ear cress)		Alternative splicing; Complete proteome; Nucleus; Phosphoprotein; RNA-binding; Reference proteome; Spliceosome; mRNA processing; mRNA splicing
SRR342017_TR11303_c0_g1_i1_len=1129	NA	NA	NA	NA	NA	.	0,001	-0,896	0,681	-0,165	0,001	-0,983	0,026	-0,631	0,001	1,294	.	.	.	.	.	.
SRR342017_TR11530_c2_g1_i2_len=818	R10A1_ARATH	Q:1-534,H:39-216	95.51%ID	E:8e-107	60S ribosomal protein L10a-1	PF00687.18^Ribosomal_L1^Ribosomal protein L1p/L10e family^4-172^E:6.8e-40	1	0	1	0,879	1	2,126	1	0	0	8,118	R10A1_ARATH	60S ribosomal protein L10a-1	RPL10AA At1g08360 T27G7.6	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Reference proteome; Ribonucleoprotein; Ribosomal protein
SRR342017_TR12657_c1_g1_i1_len=630	USF_AQUPY	Q:534-1,H:26-207	34.76%ID	E:3e-22	Protein usf	PF01738.15^DLH^Dienelactone hydrolase family^9-125^E:4e-35	0,77	-0,157	0,075	0,709	0,273	0,363	0,228	0,409	0	1,13	USF_AQUPY	Protein usf	usf	Aquifex pyrophilus		
SRR342017_TR13616_c0_g1_i6_len=2277	FTZ22_ARATH	Q:314-1744,H:1-472	74.28%ID	E:0	Cell division protein FtsZ homolog 2-2, chloroplastic	PF00091.22^Tubulin^Tubulin/FtsZ family, GTPase domain^119-280^E:1.5e-37`PF12327.5^FtsZ_C^FtsZ family, C-terminal domain^330-424^E:7.4e-31	0,213	-0,395	0,16	-0,505	0,718	0,22	0,484	0,365	0	1,057	FTZ22_ARATH	Cell division protein FtsZ homolog 2-2, chloroplastic (AtFtsZ2-2) (Plastid division protein FTSZ2-2)	FTSZ2-2 At3g52750 F3C22.150	Arabidopsis thaliana (Mouse-ear cress)		Chloroplast; Complete proteome; GTP-binding; Membrane; Nucleotide-binding; Plastid; Reference proteome; Thylakoid; Transit peptide
SRR342017_TR14852_c1_g2_i1_len=1517	NA	NA	NA	NA	NA	.	1	0,01	1	0,013	1	-0,06	0,798	-0,291	0	6,453	.	.	.	.	.	.
SRR342017_TR14963_c0_g2_i2_len=942	HMGL_IPONI	Q:70-462,H:1-126	71.76%ID	E:1e-44	HMG1/2-like protein	PF09011.7^HMG_box_2^HMG-box domain^37-109^E:2.1e-15`PF00505.16^HMG_box^HMG (high mobility group) box^40-109^E:1.2e-22	0,113	0,444	0,006	-0,756	0,655	0,258	0,443	-0,42	0	4,387	HMGL_IPONI	HMG1/2-like protein		Ipomoea nil (Japanese morning glory) (Pharbitis nil)		DNA-binding; Nucleus
SRR342017_TR15164_c0_g2_i2_len=2891	NA	NA	NA	NA	NA	PF12796.4^Ank_2^Ankyrin repeats (3 copies)^196-279^E:1.2e-11`PF13637.3^Ank_4^Ankyrin repeats (many copies)^225-277^E:2.4e-06`PF13857.3^Ank_5^Ankyrin repeats (many copies)^250-298^E:2e-06`PF13857.3^Ank_5^Ankyrin repeats (many copies)^333-380^E:2.5e-06`PF00023.27^Ank^Ankyrin repeat^338-371^E:0.028	1	-0,146	0,502	1,783	1	-0,767	1	-0,462	0	2,051	.	.	.	.	.	.
SRR342017_TR15347_c0_g2_i2_len=1246	NA	NA	NA	NA	NA	.	0,643	0,367	0,017	-5,879	1	-0,27	0,239	-1,231	0	2,884	.	.	.	.	.	.
SRR342017_TR16388_c0_g1_i2_len=847	PSAG_ARATH	Q:191-613,H:27-160	72.34%ID	E:7e-67	Photosystem I reaction center subunit V, chloroplastic	PF01241.15^PSI_PSAK^Photosystem I psaG / psaK^53-144^E:2.5e-26	0,288	0,251	0	-1,58	0,04	-0,453	0,232	-0,261	0	1,027	PSAG_ARATH	Photosystem I reaction center subunit V, chloroplastic (PSI-G)	PSAG At1g55670 F20N2.21 F20N2.33 F20N2_3	Arabidopsis thaliana (Mouse-ear cress)		Chloroplast; Complete proteome; Membrane; Photosynthesis; Photosystem I; Plastid; Reference proteome; Thylakoid; Transit peptide; Transmembrane; Transmembrane helix
SRR342017_TR18707_c0_g1_i1_len=1596	CB23_TOBAC	Q:1136-342,H:1-265	92.45%ID	E:2e-178	Chlorophyll a-b binding protein 36, chloroplastic	PF00504.18^Chloroa_b-bind^Chlorophyll A-B binding protein^66-231^E:5.2e-50	0,546	-0,126	0	-0,817	0	-1,207	0	-0,981	0	0,8	CB23_TOBAC	Chlorophyll a-b binding protein 36, chloroplastic (LHCII type I CAB-36) (LHCP)	CAB36	Nicotiana tabacum (Common tobacco)		Acetylation; Chlorophyll; Chloroplast; Chromophore; Magnesium; Membrane; Metal-binding; Phosphoprotein; Photosynthesis; Photosystem I; Photosystem II; Plastid; Thylakoid; Transit peptide; Transmembrane; Transmembrane helix
SRR342017_TR19152_c1_g5_i2_len=1177	NA	NA	NA	NA	NA	.	1	-0,296	1	-0,864	1	0	1	1,362	0	4,569	.	.	.	.	.	.
SRR342017_TR20180_c0_g2_i6_len=1187	PGL1A_ARATH	Q:122-1093,H:1-324	72%ID	E:1e-140	PGR5-like protein 1A, chloroplastic	.	1	1,663	1	0	1	0	1	2,428	0	1,157	PGL1A_ARATH	PGR5-like protein 1A, chloroplastic (Ferredoxin-plastoquinone reductase 1)	PGRL1A At4g22890 F7H19.70	Arabidopsis thaliana (Mouse-ear cress)		Acetylation; Alternative splicing; Chloroplast; Complete proteome; Disulfide bond; Electron transport; Membrane; Plastid; Reference proteome; Thylakoid; Transit peptide; Transmembrane; Transmembrane helix; Transport
SRR342017_TR20345_c0_g2_i3_len=837	NA	NA	NA	NA	NA	.	1	0	1	0	1	0	1	0	0	7,78	.	.	.	.	.	.
SRR342017_TR22495_c2_g5_i8_len=2745	FLS2_ARATH	Q:1395-295,H:25-467	31.07%ID	E:2e-33	LRR receptor-like serine/threonine-protein kinase FLS2	PF08263.9^LRRNT_2^Leucine rich repeat N-terminal domain^86-119^E:4.2e-05`PF00560.30^LRR_1^Leucine Rich Repeat^167-187^E:0.054`PF13855.3^LRR_8^Leucine rich repeat^214-272^E:1.1e-08`PF00560.30^LRR_1^Leucine Rich Repeat^215-236^E:0.081`PF13516.3^LRR_6^Leucine Rich repeat^237-252^E:1.9`PF13855.3^LRR_8^Leucine rich repeat^283-342^E:6.8e-09`PF13516.3^LRR_6^Leucine Rich repeat^307-320^E:1.9`PF00560.30^LRR_1^Leucine Rich Repeat^308-326^E:0.31	1	-0,009	1	-1,668	1	-0,508	1	-0,294	0	4,642	FLS2_ARATH	LRR receptor-like serine/threonine-protein kinase FLS2 (EC 2.7.11.1) (Protein FLAGELLIN-SENSING 2) (Protein FLAGELLIN-SENSITIVE 2)	FLS2 At5g46330 MPL12.13 MPL12.8	Arabidopsis thaliana (Mouse-ear cress)		3D-structure; ATP-binding; Cell membrane; Complete proteome; Disulfide bond; Endosome; Glycoprotein; Kinase; Leucine-rich repeat; Membrane; Nucleotide-binding; Phosphoprotein; Plant defense; Receptor; Reference proteome; Repeat; Serine/threonine-protein kinase; Signal; Transferase; Transmembrane; Transmembrane helix; Ubl conjugation; Ubl conjugation pathway
SRR342017_TR23398_c0_g5_i1_len=697	ALF_SPIOL	Q:152-697,H:1-182	88.46%ID	E:5e-111	Fructose-bisphosphate aldolase, cytoplasmic isozyme	PF00274.16^Glycolytic^Fructose-bisphosphate aldolase class-I^11-182^E:3.2e-86	1	0,372	1	1,507	1	0,128	1	0,416	0	9,386	ALF_SPIOL	Fructose-bisphosphate aldolase, cytoplasmic isozyme (EC 4.1.2.13)		Spinacia oleracea (Spinach)	PATHWAY: Carbohydrate degradation; glycolysis; D-glyceraldehyde 3-phosphate and glycerone phosphate from D-glucose: step 4/4.	Cytoplasm; Glycolysis; Lyase; Schiff base
SRR342017_TR23398_c0_g6_i1_len=861	NA	NA	NA	NA	NA	.	1	-0,207	1	0,999	1	-0,562	1	-0,652	0	6,576	.	.	.	.	.	.
SRR342017_TR23665_c0_g6_i6_len=753	NA	NA	NA	NA	NA	.	1	0	1	0	1	0,976	1	0	0	6,246	.	.	.	.	.	.
SRR342017_TR25036_c0_g1_i1_len=566	NA	NA	NA	NA	NA	.	1	0	1	0	1	0	1	0	0	8,665	.	.	.	.	.	.
SRR342017_TR25222_c0_g2_i1_len=1299	NA	NA	NA	NA	NA	PF04949.10^Transcrip_act^Transcriptional activator^23-170^E:1.6e-74	0,548	0,227	0	-1,474	0,635	0,354	0,87	0,258	0	1,031	.	.	.	.	.	.
SRR342017_TR25536_c0_g1_i1_len=1037	NDK1_TOBAC	Q:141-584,H:1-148	95.95%ID	E:2e-87	Nucleoside diphosphate kinase 1	PF00334.16^NDK^Nucleoside diphosphate kinase^2-133^E:9.8e-55	0,006	-0,696	0,006	0,656	0,003	0,831	0,409	0,245	0	10,643	NDK1_TOBAC	Nucleoside diphosphate kinase 1 (EC 2.7.4.6) (Nucleoside diphosphate kinase I) (NDK I) (NDP kinase I) (NDPK I)		Nicotiana tabacum (Common tobacco)		ATP-binding; Kinase; Magnesium; Metal-binding; Nucleotide metabolism; Nucleotide-binding; Phosphoprotein; Transferase
SRR342017_TR25892_c2_g4_i3_len=1329	POLX_TOBAC	Q:1215-4,H:232-632	40.44%ID	E:3e-94	Retrovirus-related Pol polyprotein from transposon TNT 1-94	PF00098.20^zf-CCHC^Zinc knuckle^38-53^E:0.00023`PF13976.3^gag_pre-integrs^GAG-pre-integrase domain^208-275^E:2e-15`PF00665.23^rve^Integrase core domain^291-405^E:9.7e-26	1	1,242	1	-1,171	1	-1,18	1	-1,61	0	8,399	POLX_TOBAC	Retrovirus-related Pol polyprotein from transposon TNT 1-94 [Includes: Protease (EC 3.4.23.-); Reverse transcriptase (EC 2.7.7.49); Endonuclease]		Nicotiana tabacum (Common tobacco)		Aspartyl protease; Endonuclease; Hydrolase; Metal-binding; Nuclease; Nucleotidyltransferase; Protease; RNA-directed DNA polymerase; Transferase; Transposable element; Zinc; Zinc-finger
SRR342017_TR30126_c0_g1_i1_len=1309	PSBO_SOLTU	Q:1127-882,H:1-81	81.71%ID	E:2e-31	Oxygen-evolving enhancer protein 1, chloroplastic	.	0,249	-0,262	0,422	-0,194	0	-0,922	0,012	-0,546	0	0,838	PSBO_SOLTU	Oxygen-evolving enhancer protein 1, chloroplastic (OEE1) (33 kDa subunit of oxygen evolving system of photosystem II) (33 kDa thylakoid membrane protein) (OEC 33 kDa subunit)	PSBO	Solanum tuberosum (Potato)		Chloroplast; Complete proteome; Manganese; Membrane; Photosynthesis; Photosystem II; Plastid; Reference proteome; Thylakoid; Transit peptide
SRR342017_TR33136_c0_g3_i2_len=3709	FTSHC_ARATH	Q:1181-3163,H:348-1008	86.84%ID	E:0	ATP-dependent zinc metalloprotease FTSH 12, chloroplastic	PF00004.26^AAA^ATPase family associated with various cellular activities (AAA)^140-276^E:6.2e-32`PF07724.11^AAA_2^AAA domain (Cdc48 subfamily)^140-255^E:0.00026`PF01434.15^Peptidase_M41^Peptidase family M41^365-570^E:2.4e-23	0,854	0,25	0,811	0,263	1	0,331	0,811	0,492	0	1,898	FTSHC_ARATH	ATP-dependent zinc metalloprotease FTSH 12, chloroplastic (AtFTSH12) (EC 3.4.24.-)	FTSH12 At1g79560 T8K14.2	Arabidopsis thaliana (Mouse-ear cress)		ATP-binding; Chloroplast; Complete proteome; Hydrolase; Membrane; Metal-binding; Metalloprotease; Nucleotide-binding; Plastid; Protease; Reference proteome; Thylakoid; Transit peptide; Transmembrane; Transmembrane helix; Zinc
SRR342017_TR33575_c0_g1_i2_len=653	CSN7_ARATH	Q:40-348,H:156-258	72.82%ID	E:2e-37	COP9 signalosome complex subunit 7	.	1	0	1	0	1	0	1	0	0	7,618	CSN7_ARATH	COP9 signalosome complex subunit 7 (CSN complex subunit 7) (Protein FUSCA 5)	CSN7 FUS5 At1g02090 T7I23.24 T7I23.25	Arabidopsis thaliana (Mouse-ear cress)		3D-structure; Alternative splicing; Complete proteome; Cytoplasm; Developmental protein; Nucleus; Phosphoprotein; Phytochrome signaling pathway; Reference proteome; Signalosome
SRR342019_TR4213_c8_g3_i4_len=1198	GGAP1_ARATH	Q:610-62,H:1-179	73.22%ID	E:3e-77	GDP-L-galactose phosphorylase 1	.	0,108	0,702	1	0	0	-1,706	1	0,012	0	4,183	GGAP1_ARATH	GDP-L-galactose phosphorylase 1 (EC 2.7.7.69) (Protein VITAMIN C DEFECTIVE 2)	VTC2 At4g26850 F10M23.190	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Cofactor biosynthesis; L-ascorbate biosynthesis via GDP-alpha-D-mannose pathway; L-ascorbate from GDP-alpha-D-mannose: step 2/5.	Ascorbate biosynthesis; Complete proteome; Cytoplasm; Guanine-nucleotide releasing factor; Hydrolase; Nucleotide-binding; Nucleotidyltransferase; Nucleus; Reference proteome; Transferase
SRR342019_TR8850_c1_g4_i1_len=1085	RL9_PEA	Q:905-327,H:1-193	87.05%ID	E:1e-116	60S ribosomal protein L9	PF00347.20^Ribosomal_L6^Ribosomal protein L6^12-89^E:5.8e-12`PF00347.20^Ribosomal_L6^Ribosomal protein L6^101-180^E:5e-12	0,004	-0,765	0,556	-0,15	0,017	0,81	0,229	0,436	0	4,189	RL9_PEA	60S ribosomal protein L9 (Gibberellin-regulated protein GA)	RPL9	Pisum sativum (Garden pea)		Ribonucleoprotein; Ribosomal protein
SRR342019_TR11481_c2_g8_i1_len=1501	PRX2B_ARATH	Q:175-660,H:1-162	81.48%ID	E:2e-92	Peroxiredoxin-2B	PF08534.7^Redoxin^Redoxin^64-217^E:1.8e-34`PF00578.18^AhpC-TSA^AhpC/TSA family^64-179^E:3e-12	1	-0,434	0,461	-1,441	1	0,386	1	-0,091	0	1,261	PRX2B_ARATH	Peroxiredoxin-2B (EC 1.11.1.15) (Peroxiredoxin IIB) (Peroxiredoxin TPx1) (Thioredoxin reductase 2B) (Thioredoxin-dependent peroxidase 1)	PRXIIB TPX1 At1g65980 F12P19.14	Arabidopsis thaliana (Mouse-ear cress)		Alternative splicing; Antioxidant; Complete proteome; Cytoplasm; Disulfide bond; Oxidoreductase; Peroxidase; Redox-active center; Reference proteome
SRR342019_TR18824_c6_g1_i2_len=1026	NLTP_HELAN	Q:107-451,H:1-114	52.59%ID	E:2e-25	Non-specific lipid-transfer protein	PF14368.3^LTP_2^Probable lipid transfer^15-105^E:1.3e-05`PF00234.19^Tryp_alpha_amyl^Protease inhibitor/seed storage/LTP family^30-113^E:9.6e-08	0,266	0,548	0,003	1,349	0,004	1,217	0,077	0,801	0,001	1,137	NLTP_HELAN	Non-specific lipid-transfer protein (LTP) (NsLTP) (SDI-9)		Helianthus annuus (Common sunflower)		Disulfide bond; Lipid-binding; Signal; Transport
SRR342019_TR20493_c2_g5_i2_len=1742	HHT1_ARATH	Q:1621-308,H:28-454	33.41%ID	E:9e-59	Omega-hydroxypalmitate O-feruloyl transferase	PF02458.12^Transferase^Transferase family^17-453^E:2e-113	0,472	-0,709	1	0,014	0,545	-0,537	1	-0,088	0,001	0,999	HHT1_ARATH	Omega-hydroxypalmitate O-feruloyl transferase (EC 2.3.1.188) (Omega-hydroxyacid hydroxycinnamoyltransferase) (Protein ALIPHATIC SUBERIN FERULOYL TRANSFERASE)	HHT1 ASFT At5g41040 MEE6.11	Arabidopsis thaliana (Mouse-ear cress)		Acyltransferase; Alternative splicing; Cell wall biogenesis/degradation; Complete proteome; Reference proteome; Transferase
SRR342019_TR20560_c4_g2_i6_len=4978	POLX_TOBAC	Q:3498-1,H:1-1151	40.54%ID	E:0	Retrovirus-related Pol polyprotein from transposon TNT 1-94	PF14223.3^Retrotran_gag_2^gag-polypeptide of LTR copia-type^59-187^E:1.8e-33`PF00098.20^zf-CCHC^Zinc knuckle^227-242^E:0.00068`PF13976.3^gag_pre-integrs^GAG-pre-integrase domain^397-464^E:2.9e-14`PF00665.23^rve^Integrase core domain^480-594^E:6.2e-26`PF07727.11^RVT_2^Reverse transcriptase (RNA-dependent DNA polymerase)^854-1101^E:2.7e-92	1	0,056	1	0,983	1	0,622	1	0,13	0	8,275	POLX_TOBAC	Retrovirus-related Pol polyprotein from transposon TNT 1-94 [Includes: Protease (EC 3.4.23.-); Reverse transcriptase (EC 2.7.7.49); Endonuclease]		Nicotiana tabacum (Common tobacco)		Aspartyl protease; Endonuclease; Hydrolase; Metal-binding; Nuclease; Nucleotidyltransferase; Protease; RNA-directed DNA polymerase; Transferase; Transposable element; Zinc; Zinc-finger
SRR342019_TR22616_c0_g3_i2_len=1056	PRU1_PRUAR	Q:795-325,H:3-159	61.78%ID	E:5e-59	Major allergen Pru ar 1	PF00407.16^Bet_v_1^Pathogenesis-related protein Bet v I family^4-156^E:1e-19	0,177	-0,297	0,355	0,234	1	0,003	0,565	0,139	0	1,06	PRU1_PRUAR	Major allergen Pru ar 1 (allergen Pru ar 1)		Prunus armeniaca (Apricot) (Armeniaca vulgaris)		Allergen; Pathogenesis-related protein; Plant defense
SRR342019_TR29234_c2_g1_i6_len=720	C72A1_CATRO	Q:118-720,H:1-201	98.01%ID	E:2e-142	Secologanin synthase	PF00067.19^p450^Cytochrome P450^93-195^E:1.7e-10	0,133	-0,615	0,381	2,011	0,266	0,554	0,183	0,623	0,001	1,405	C72A1_CATRO	Secologanin synthase (SLS) (EC 1.3.3.9) (CYPLXXII) (Cytochrome P450 72A1)	CYP72A1 CYP72 P450CR3	Catharanthus roseus (Madagascar periwinkle) (Vinca rosea)	PATHWAY: Alkaloid biosynthesis; secologanin biosynthesis.	Alkaloid metabolism; Heme; Iron; Membrane; Metal-binding; Monooxygenase; NADP; Oxidoreductase; Transmembrane; Transmembrane helix; Vacuole
SRR342019_TR30344_c1_g9_i8_len=3925	IF2C_ARATH	Q:623-3496,H:37-1010	69.09%ID	E:0	Translation initiation factor IF-2, chloroplastic	PF00009.24^GTP_EFTU^Elongation factor Tu GTP binding domain^474-634^E:4e-33`PF01926.20^MMR_HSR1^50S ribosome-binding GTPase^475-583^E:5.9e-08`PF00071.19^Ras^Ras family^475-633^E:2.4e-06`PF11987.5^IF-2^Translation-initiation factor 2^779-870^E:3.5e-29	0,039	1,081	1	-0,186	0,056	-0,983	0,288	-0,504	0	1,356	IF2C_ARATH	Translation initiation factor IF-2, chloroplastic	At1g17220 F20D23.8	Arabidopsis thaliana (Mouse-ear cress)		Chloroplast; Complete proteome; GTP-binding; Initiation factor; Nucleotide-binding; Plastid; Protein biosynthesis; Reference proteome; Transit peptide
SRR342019_TR38591_c0_g2_i1_len=725	C3H49_ARATH	Q:105-725,H:3-176	55.56%ID	E:2e-72	Zinc finger CCCH domain-containing protein 49	PF00642.21^zf-CCCH^Zinc finger C-x8-C-x5-C-x3-H type (and similar)^157-177^E:1.1e-06`PF14608.3^zf-CCCH_2^RNA-binding, Nab2-type zinc finger^165-177^E:0.69`PF14608.3^zf-CCCH_2^RNA-binding, Nab2-type zinc finger^192-208^E:0.0068	1	-0,574	0,254	3,61	1	-0,636	1	-0,476	0	3,349	C3H49_ARATH	Zinc finger CCCH domain-containing protein 49 (AtC3H49)	At4g29190 F17A13.10	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; DNA-binding; Metal-binding; Reference proteome; Repeat; Zinc; Zinc-finger
SRR342019_TR38994_c3_g3_i2_len=1657	NA	NA	NA	NA	NA	PF05050.9^Methyltransf_21^Methyltransferase FkbM domain^65-217^E:2.4e-05	1	1,959	1	2,367	0,254	3,979	1	2,253	0	2,247	.	.	.	.	.	.
SRR342022_TR7506_c0_g1_i1_len=1191	RR6_ARATH	Q:199-756,H:17-206	73.16%ID	E:1e-73	30S ribosomal protein S6 alpha, chloroplastic	PF01250.14^Ribosomal_S6^Ribosomal protein S6^96-194^E:7.2e-19	0,031	-0,516	0	-1,195	0,346	-0,255	0,773	-0,076	0	6,374	RR6_ARATH	30S ribosomal protein S6 alpha, chloroplastic	RPS6 At1g64510 F1N19.8	Arabidopsis thaliana (Mouse-ear cress)		Chloroplast; Complete proteome; Plastid; RNA-binding; Reference proteome; Ribonucleoprotein; Ribosomal protein; Transit peptide; rRNA-binding
SRR342022_TR10375_c0_g1_i12_len=2737	OPT7_ARATH	Q:1437-175,H:346-764	72.21%ID	E:0	Oligopeptide transporter 7	PF03169.12^OPT^OPT oligopeptide transporter protein^12-387^E:6.1e-95	0,007	0,933	0,002	1,31	0,001	1,524	0,011	1,294	0	1,439	OPT7_ARATH	Oligopeptide transporter 7 (AtOPT7)	OPT7 At4g10770 T12H20.7	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Membrane; Peptide transport; Protein transport; Reference proteome; Transmembrane; Transmembrane helix; Transport
SRR342022_TR12295_c0_g1_i1_len=2579	RR1_SPIOL	Q:1633-365,H:1-408	82.08%ID	E:0	30S ribosomal protein S1, chloroplastic	PF00575.20^S1^S1 RNA binding domain^109-181^E:8.1e-05`PF00575.20^S1^S1 RNA binding domain^197-261^E:1.8e-08`PF00575.20^S1^S1 RNA binding domain^274-344^E:3.9e-22	0,394	-0,501	0,014	-1,498	1	-0,026	0,748	0,241	0	6,097	RR1_SPIOL	30S ribosomal protein S1, chloroplastic (CS1)	RPS1	Spinacia oleracea (Spinach)		Chloroplast; Direct protein sequencing; Plastid; RNA-binding; Repeat; Ribonucleoprotein; Ribosomal protein; Transit peptide
SRR342022_TR14927_c0_g1_i4_len=2019	C7A52_PANGI	Q:1714-284,H:1-479	80.79%ID	E:0	Beta-amyrin 28-oxidase	PF00067.19^p450^Cytochrome P450^36-451^E:2.2e-59	0,566	0,153	0,043	0,617	0,01	-0,673	0,119	-0,397	0,001	1,153	C7A52_PANGI	Beta-amyrin 28-oxidase (EC 1.14.13.-) (Cytochrome P450 CYP716A52v2)		Panax ginseng (Korean ginseng)		Heme; Iron; Membrane; Metal-binding; Monooxygenase; NADP; Oxidoreductase; Transmembrane; Transmembrane helix
SRR342022_TR15284_c5_g5_i2_len=2308	21KD_DAUCA	Q:361-846,H:28-189	56.17%ID	E:3e-60	21 kDa protein	.	0,241	-0,389	0,111	0,615	0,121	-0,849	0,518	-0,324	0	1,315	21KD_DAUCA	21 kDa protein (1.2 protein)		Daucus carota (Wild carrot)		Signal
SRR342022_TR17938_c0_g1_i1_len=1248	PSD8A_ARATH	Q:1142-342,H:1-267	80.9%ID	E:2e-149	26S proteasome non-ATPase regulatory subunit 8 homolog A	PF03399.13^SAC3_GANP^SAC3/GANP family^81-221^E:2.7e-06`PF10075.6^CSN8_PSD8_EIF3K^CSN8/PSMD8/EIF3K family^106-241^E:8.1e-28	0,506	-0,21	0,24	0,374	0,343	0,356	0,597	0,213	0	6,303	PSD8A_ARATH	26S proteasome non-ATPase regulatory subunit 8 homolog A (26S proteasome regulatory subunit RPN12a) (AtRPN12a) (26S proteasome regulatory subunit S14 homolog A)	RPN12A At1g64520 F1N19.9	Arabidopsis thaliana (Mouse-ear cress)		Acetylation; Complete proteome; Cytokinin signaling pathway; Proteasome; Reference proteome; Ubl conjugation
SRR342022_TR18074_c0_g3_i3_len=3143	AB26B_ARATH	Q:428-1597,H:99-485	69.23%ID	E:3e-163	ABC transporter B family member 26, chloroplastic	PF00664.20^ABC_membrane^ABC transporter transmembrane region^137-403^E:1e-38	0,547	-0,354	0,822	0,339	0,357	-0,725	0,471	-0,534	0	3,267	AB26B_ARATH	ABC transporter B family member 26, chloroplastic (ABC transporter ABCB.26) (AtABCB26) (Antigen peptide transporter-like 1) (Transporter associated with antigen processing-like protein 1) (AtTAP1)	ABCB26 TAP1 At1g70610 F24J13.18 F5A18.21	Arabidopsis thaliana (Mouse-ear cress)		ATP-binding; Chloroplast; Complete proteome; Membrane; Nucleotide-binding; Plastid; Reference proteome; Transit peptide; Transmembrane; Transmembrane helix; Transport
SRR342022_TR19824_c0_g1_i1_len=567	NA	NA	NA	NA	NA	.	0,763	-0,188	0,233	-0,808	1	0	1	0	0	7,262	.	.	.	.	.	.
SRR342022_TR21598_c2_g5_i1_len=4976	POLX_TOBAC	Q:22-2109,H:646-1323	46.72%ID	E:3e-176	Retrovirus-related Pol polyprotein from transposon TNT 1-94	PF07727.11^RVT_2^Reverse transcriptase (RNA-dependent DNA polymerase)^217-464^E:1.9e-93	0,007	0,686	0,014	-0,698	0,088	-0,483	0,021	-0,664	0	1,43	POLX_TOBAC	Retrovirus-related Pol polyprotein from transposon TNT 1-94 [Includes: Protease (EC 3.4.23.-); Reverse transcriptase (EC 2.7.7.49); Endonuclease]		Nicotiana tabacum (Common tobacco)		Aspartyl protease; Endonuclease; Hydrolase; Metal-binding; Nuclease; Nucleotidyltransferase; Protease; RNA-directed DNA polymerase; Transferase; Transposable element; Zinc; Zinc-finger
SRR342022_TR21598_c2_g5_i5_len=692	NA	NA	NA	NA	NA	.	1	0	1	0	1	0	1	0	0	7,105	.	.	.	.	.	.
SRR342022_TR23138_c3_g3_i12_len=1911	PLPD2_ARATH	Q:404-99,H:456-557	85.29%ID	E:2e-47	Dihydrolipoyl dehydrogenase 2, chloroplastic	PF13174.3^TPR_6^Tetratricopeptide repeat^219-245^E:0.013	0,577	0,181	0,048	0,576	0,176	0,501	0,118	0,574	0	1,369	PLPD2_ARATH	Dihydrolipoyl dehydrogenase 2, chloroplastic (ptLPD2) (EC 1.8.1.4) (Dihydrolipoamide dehydrogenase 2) (Protein LIPOAMIDE DEHYDROGENASE 2) (Pyruvate dehydrogenase complex E3 subunit 2) (E3-2) (PDC-E3 2)	LPD2 At4g16155 FCAALL.61	Arabidopsis thaliana (Mouse-ear cress)		Chloroplast; Complete proteome; Disulfide bond; FAD; Flavoprotein; NAD; Oxidoreductase; Plastid; Redox-active center; Reference proteome; Transit peptide
SRR342022_TR24136_c2_g2_i2_len=1019	BT3L4_DANRE	Q:137-502,H:1-123	58.54%ID	E:6e-41	Transcription factor BTF3 homolog 4	PF01849.15^NAC^NAC domain^36-91^E:5.1e-19	0,061	-0,719	0,644	-0,175	0,705	0,213	0,798	0,17	0	1,094	BT3L4_DANRE	Transcription factor BTF3 homolog 4 (Basic transcription factor 3-like 4)	btf3l4	Danio rerio (Zebrafish) (Brachydanio rerio)		Complete proteome; Reference proteome
SRR342022_TR26255_c0_g3_i2_len=702	NA	NA	NA	NA	NA	.	0,065	-1,53	0,381	-1,655	0	-5,868	0	-8,664	0,001	2,178	.	.	.	.	.	.
SRR342022_TR27941_c5_g1_i3_len=887	NA	NA	NA	NA	NA	.	0,022	1,449	0,381	1,547	0,043	2,564	0,043	2,569	0	1,166	.	.	.	.	.	.
SRR342022_TR29282_c0_g2_i1_len=693	PSAG_ARATH	Q:552-130,H:27-160	72.34%ID	E:2e-67	Photosystem I reaction center subunit V, chloroplastic	PF01241.15^PSI_PSAK^Photosystem I psaG / psaK^53-144^E:2.5e-26	0,659	-0,093	0	-1,45	0,004	-0,599	0,065	-0,382	0	1,478	PSAG_ARATH	Photosystem I reaction center subunit V, chloroplastic (PSI-G)	PSAG At1g55670 F20N2.21 F20N2.33 F20N2_3	Arabidopsis thaliana (Mouse-ear cress)		Chloroplast; Complete proteome; Membrane; Photosynthesis; Photosystem I; Plastid; Reference proteome; Thylakoid; Transit peptide; Transmembrane; Transmembrane helix
SRR342022_TR30154_c2_g10_i4_len=1487	PME3_CITSI	Q:1324-5,H:40-469	71.85%ID	E:0	Pectinesterase 3	PF04043.12^PMEI^Plant invertase/pectin methylesterase inhibitor^91-247^E:1.3e-28`PF01095.16^Pectinesterase^Pectinesterase^298-492^E:5.2e-97	0,17	-0,425	0,025	2,473	0,299	-1,872	0,034	-5,632	0	5,031	PME3_CITSI	Pectinesterase 3 (PE 3) (EC 3.1.1.11) (Pectin methylesterase 3)		Citrus sinensis (Sweet orange) (Citrus aurantium var. sinensis)	PATHWAY: Glycan metabolism; pectin degradation; 2-dehydro-3-deoxy-D-gluconate from pectin: step 1/5.	Aspartyl esterase; Cell wall; Cell wall biogenesis/degradation; Direct protein sequencing; Disulfide bond; Glycoprotein; Hydrolase; Secreted; Signal
SRR342022_TR31765_c1_g5_i1_len=1829	TBB8_ARATH	Q:901-1827,H:1-309	98.06%ID	E:0	Tubulin beta-8 chain	PF00091.22^Tubulin^Tubulin/FtsZ family, GTPase domain^43-251^E:1.5e-68`PF03953.14^Tubulin_C^Tubulin C-terminal domain^301-348^E:4.9e-13	0,065	-0,485	0,335	0,298	0,541	0,26	0,311	0,407	0	4,595	TBB8_ARATH	Tubulin beta-8 chain (Beta-8-tubulin)	TUBB8 TUB8 At5g23860 MRO11.10	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Cytoplasm; Cytoskeleton; GTP-binding; Microtubule; Nucleotide-binding; Reference proteome
SRR342022_TR34286_c0_g2_i1_len=1131	NA	NA	NA	NA	NA	PF11623.5^DUF3252^Protein of unknown function (DUF3252)^174-225^E:2e-28	0,723	0,134	0	-1,784	0,602	-0,118	0,94	-0,019	0	4,824	.	.	.	.	.	.
SRR342023_TR1054_c0_g5_i6_len=4915	AB3C_ARATH	Q:913-4659,H:245-1510	51.96%ID	E:0	ABC transporter C family member 3	PF00664.20^ABC_membrane^ABC transporter transmembrane region^285-548^E:1.4e-22`PF00005.24^ABC_tran^ABC transporter^619-749^E:3.1e-13`PF00664.20^ABC_membrane^ABC transporter transmembrane region^901-1135^E:2.5e-28`PF00005.24^ABC_tran^ABC transporter^1229-1377^E:7.8e-31	1	0,657	1	0,042	1	0,534	1	0,832	0,001	1,543	AB3C_ARATH	ABC transporter C family member 3 (ABC transporter ABCC.3) (AtABCC3) (EC 3.6.3.44) (ATP-energized glutathione S-conjugate pump 3) (Glutathione S-conjugate-transporting ATPase 3) (Multidrug resistance-associated protein 3)	ABCC3 EST2 MRP3 At3g13080 MJG19.3	Arabidopsis thaliana (Mouse-ear cress)		ATP-binding; Alternative splicing; Complete proteome; Hydrolase; Membrane; Nucleotide-binding; Phosphoprotein; Reference proteome; Repeat; Transmembrane; Transmembrane helix; Transport
SRR342023_TR2280_c0_g1_i4_len=757	NA	NA	NA	NA	NA	PF13920.3^zf-C3HC4_3^Zinc finger, C3HC4 type (RING finger)^72-118^E:8.9e-07`PF13639.3^zf-RING_2^Ring finger domain^73-113^E:1.5e-07	1	0	1	0	1	0	1	1,041	0	7,065	.	.	.	.	.	.
SRR342023_TR3519_c2_g1_i1_len=1064	PLAS_SOLLC	Q:219-695,H:11-170	76.54%ID	E:3e-67	Plastocyanin, chloroplastic	PF00127.17^Copper-bind^Copper binding proteins, plastocyanin/azurin family^73-170^E:4.2e-36	0,249	-0,244	0	-1,228	0	-0,788	0,007	-0,563	0	0,951	PLAS_SOLLC	Plastocyanin, chloroplastic	PETE	Solanum lycopersicum (Tomato) (Lycopersicon esculentum)		Chloroplast; Complete proteome; Copper; Electron transport; Membrane; Metal-binding; Plastid; Reference proteome; Thylakoid; Transit peptide; Transport
SRR342023_TR8311_c1_g4_i6_len=1105	Y5566_ARATH	Q:695-339,H:1-117	63.03%ID	E:8e-36	Uncharacterized protein At5g65660	.	0,187	-0,586	0,016	-1,143	1	0,355	0,517	-0,741	0	5,934	Y5566_ARATH	Uncharacterized protein At5g65660	At5g65660 K21L13.18	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Membrane; Reference proteome; Transmembrane; Transmembrane helix
SRR342023_TR9121_c5_g1_i3_len=1625	TBB7_GOSHI	Q:82-1359,H:1-426	94.84%ID	E:0	Tubulin beta-7 chain	PF00091.22^Tubulin^Tubulin/FtsZ family, GTPase domain^3-211^E:4e-69`PF03953.14^Tubulin_C^Tubulin C-terminal domain^261-381^E:5.8e-41	0,089	-0,42	0,444	-0,203	0,257	-0,903	0,874	0,129	0	8,852	TBB7_GOSHI	Tubulin beta-7 chain (Beta-7-tubulin)		Gossypium hirsutum (Upland cotton) (Gossypium mexicanum)		Cytoplasm; Cytoskeleton; GTP-binding; Microtubule; Nucleotide-binding
SRR342023_TR10616_c0_g1_i5_len=4184	ACA11_ARATH	Q:3684-493,H:1-1021	67.86%ID	E:0	Putative calcium-transporting ATPase 11, plasma membrane-type	PF12515.5^CaATP_NAI^Ca2+-ATPase N terminal autoinhibitory domain^7-50^E:2.4e-15`PF00690.23^Cation_ATPase_N^Cation transporter/ATPase, N-terminus^154-218^E:1.7e-15`PF00122.17^E1-E2_ATPase^E1-E2 ATPase^238-477^E:3.4e-45`PF00702.23^Hydrolase^haloacid dehalogenase-like hydrolase^484-801^E:2.5e-22`PF13246.3^Cation_ATPase^Cation transport ATPase (P-type)^540-624^E:3.7e-18`PF00689.18^Cation_ATPase_C^Cation transporting ATPase, C-terminus^872-1046^E:6.9e-45	0,69	-0,148	0,007	1,246	0,799	-0,109	0,325	0,368	0,001	1,71	ACA11_ARATH	Putative calcium-transporting ATPase 11, plasma membrane-type (EC 3.6.3.8) (Ca(2+)-ATPase isoform 11)	ACA11 At3g57330 F28O9.180	Arabidopsis thaliana (Mouse-ear cress)		ATP-binding; Calcium; Calcium transport; Calmodulin-binding; Complete proteome; Hydrolase; Ion transport; Magnesium; Membrane; Metal-binding; Nucleotide-binding; Reference proteome; Transmembrane; Transmembrane helix; Transport
SRR342023_TR18177_c2_g1_i2_len=1564	CLPAA_SOLLC	Q:1012-2,H:249-586	95.27%ID	E:0	ATP-dependent Clp protease ATP-binding subunit ClpA homolog CD4A, chloroplastic	PF00004.26^AAA^ATPase family associated with various cellular activities (AAA)^46-162^E:2.8e-15`PF07728.11^AAA_5^AAA domain (dynein-related subfamily)^46-124^E:2.3e-05`PF02151.16^UVR^UvrB/uvrC motif^258-293^E:3.1e-09	0,079	-0,849	1	1,712	0,052	-1,541	0,452	-0,612	0	1,541	CLPAA_SOLLC	ATP-dependent Clp protease ATP-binding subunit ClpA homolog CD4A, chloroplastic	CD4A	Solanum lycopersicum (Tomato) (Lycopersicon esculentum)		ATP-binding; Chaperone; Chloroplast; Complete proteome; Nucleotide-binding; Plastid; Reference proteome; Repeat; Transit peptide
SRR342023_TR20116_c0_g1_i1_len=534	NA	NA	NA	NA	NA	.	0,534	0,186	0	-1,758	0	-2,049	0	-2,412	0,001	1,176	.	.	.	.	.	.
SRR342023_TR20464_c3_g13_i1_len=952	NA	NA	NA	NA	NA	PF13920.3^zf-C3HC4_3^Zinc finger, C3HC4 type (RING finger)^48-94^E:3.2e-09`PF13639.3^zf-RING_2^Ring finger domain^49-89^E:8.9e-09`PF14447.3^Prok-RING_4^Prokaryotic RING finger family 4^51-93^E:1.2e-07`PF00097.22^zf-C3HC4^Zinc finger, C3HC4 type (RING finger)^51-88^E:1.6e-06`PF13445.3^zf-RING_UBOX^RING-type zinc-finger^51-86^E:0.00046	0,5	-0,532	0,195	-1,479	1	-0,33	1	-1,013	0	7,229	.	.	.	.	.	.
SRR342023_TR22207_c3_g7_i4_len=1603	NAGK_DICDI	Q:1257-298,H:4-316	37.58%ID	E:2e-59	N-acetyl-D-glucosamine kinase	PF01869.17^BcrAD_BadFG^BadF/BadG/BcrA/BcrD ATPase family^12-326^E:3.7e-57	0,802	0,115	0,812	0,087	0,152	0,838	0,25	0,644	0	7,457	NAGK_DICDI	N-acetyl-D-glucosamine kinase (N-acetylglucosamine kinase) (EC 2.7.1.59) (GlcNAc kinase)	nagk DDB_G0284433	Dictyostelium discoideum (Slime mold)		ATP-binding; Complete proteome; Kinase; Nucleotide-binding; Reference proteome; Transferase
SRR342023_TR23494_c5_g1_i1_len=651	PREP2_ARATH	Q:438-1,H:40-180	66.44%ID	E:8e-51	Presequence protease 2, chloroplastic/mitochondrial	.	1	0	1	0	1	0	1	0	0	8,749	PREP2_ARATH	Presequence protease 2, chloroplastic/mitochondrial (AtPreP2) (PreP 2) (EC 3.4.24.-) (Zinc metalloprotease 2) (AtZnMP2)	PREP2 ZNMP2 At1g49630 F14J22.13	Arabidopsis thaliana (Mouse-ear cress)		Chloroplast; Complete proteome; Hydrolase; Magnesium; Metal-binding; Metalloprotease; Mitochondrion; Plastid; Protease; Reference proteome; Transit peptide; Zinc
SRR342023_TR23701_c1_g3_i1_len=1180	CLPR2_ARATH	Q:1073-228,H:1-279	73.05%ID	E:5e-149	ATP-dependent Clp protease proteolytic subunit-related protein 2, chloroplastic {ECO:0000303|PubMed:11299370}	PF00574.20^CLP_protease^Clp protease^89-264^E:1.8e-63	0,287	-0,29	0,009	-0,755	0,528	-0,188	0,374	-0,266	0	7,405	CLPR2_ARATH	ATP-dependent Clp protease proteolytic subunit-related protein 2, chloroplastic (ClpR2) (nClpP2)	CLPR2 NCLPP2 At1g12410 F5O11.13	Arabidopsis thaliana (Mouse-ear cress)		3D-structure; Chloroplast; Complete proteome; Direct protein sequencing; Plastid; Reference proteome; Transit peptide
SRR342023_TR25396_c0_g3_i4_len=549	MD36B_ARATH	Q:357-506,H:67-116	84%ID	E:2e-22	Probable mediator of RNA polymerase II transcription subunit 36b	PF01269.14^Fibrillarin^Fibrillarin^77-117^E:1.9e-09	1	2,562	1	0	1	1,224	1	-1,914	0	7,361	MD36B_ARATH	Probable mediator of RNA polymerase II transcription subunit 36b (Histone-glutamine methyltransferase) (SKP1-interacting partner 7) (rRNA 2'-O-methyltransferase fibrillarin 1) (EC 2.1.1.-)	MED36B FBR1 FIB1 MED36_2 SKIP7 At5g52470 K24M7.22	Arabidopsis thaliana (Mouse-ear cress)		Alternative splicing; Complete proteome; Methyltransferase; Nucleus; RNA-binding; Reference proteome; Ribonucleoprotein; S-adenosyl-L-methionine; Transcription; Transcription regulation; Transferase; rRNA processing
SRR342023_TR25614_c1_g6_i1_len=732	METK1_CATRO	Q:589-2,H:1-196	99.49%ID	E:2e-141	S-adenosylmethionine synthase 1	PF00438.17^S-AdoMet_synt_N^S-adenosylmethionine synthetase, N-terminal domain^4-101^E:1.9e-43`PF02772.13^S-AdoMet_synt_M^S-adenosylmethionine synthetase, central domain^117-196^E:1e-32	0,103	1,59	0,502	3,834	0,001	-3,746	0	-6,815	0	1,31	METK1_CATRO	S-adenosylmethionine synthase 1 (AdoMet synthase 1) (EC 2.5.1.6) (Methionine adenosyltransferase 1) (MAT 1)	SAMS1	Catharanthus roseus (Madagascar periwinkle) (Vinca rosea)	PATHWAY: Amino-acid biosynthesis; S-adenosyl-L-methionine biosynthesis; S-adenosyl-L-methionine from L-methionine: step 1/1.	ATP-binding; Cobalt; Cytoplasm; Magnesium; Manganese; Metal-binding; Nucleotide-binding; One-carbon metabolism; Potassium; Transferase
SRR342023_TR27473_c2_g11_i6_len=698	ILV5_ARATH	Q:1-459,H:197-349	94.12%ID	E:1e-88	Ketol-acid reductoisomerase, chloroplastic	PF07991.9^IlvN^Acetohydroxy acid isomeroreductase, NADPH-binding domain^4-98^E:6.1e-13`PF01450.16^IlvC^Acetohydroxy acid isomeroreductase, catalytic domain^107-164^E:2.9e-17	0,014	-0,999	0,793	-0,211	0,484	-0,457	0,9	0,11	0	8,408	ILV5_ARATH	Ketol-acid reductoisomerase, chloroplastic (EC 1.1.1.86) (Acetohydroxy-acid reductoisomerase) (Alpha-keto-beta-hydroxylacyl reductoisomerase)	At3g58610 F14P22.200	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Amino-acid biosynthesis; L-isoleucine biosynthesis; L-isoleucine from 2-oxobutanoate: step 2/4.; PATHWAY: Amino-acid biosynthesis; L-valine biosynthesis; L-valine from pyruvate: step 2/4.	Amino-acid biosynthesis; Branched-chain amino acid biosynthesis; Chloroplast; Complete proteome; Magnesium; Metal-binding; NADP; Oxidoreductase; Plastid; Reference proteome; Transit peptide
SRR342023_TR27560_c2_g1_i2_len=588	NA	NA	NA	NA	NA	.	1	-0,379	1	-0,813	1	0,794	0,299	1,705	0	1,042	.	.	.	.	.	.
SRR342023_TR29871_c4_g1_i1_len=945	GPX8_ARATH	Q:120-614,H:2-166	79.39%ID	E:7e-95	Probable glutathione peroxidase 8	PF00255.16^GSHPx^Glutathione peroxidase^37-145^E:8.7e-42`PF00578.18^AhpC-TSA^AhpC/TSA family^37-98^E:5.4e-08	0,912	-0,082	0,458	-0,424	0,35	0,587	0,35	0,6	0	6,882	GPX8_ARATH	Probable glutathione peroxidase 8 (EC 1.11.1.9)	GPX8 At1g63460 F2K11.16	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Oxidoreductase; Peroxidase; Reference proteome
SRR342023_TR31010_c0_g1_i3_len=639	P2B11_ARATH	Q:93-584,H:88-255	36.69%ID	E:2e-21	F-box protein PP2-B11	PF14299.3^PP2^Phloem protein 2^37-194^E:4.2e-32	1	0	1	0	1	0	1	0	0	1,469	P2B11_ARATH	F-box protein PP2-B11 (Protein PHLOEM PROTEIN 2-LIKE B11) (AtPP2-B11) (SKP1-interacting partner 12)	PP2B11 SKIP12 At1g80110 F18B13.19	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Protein modification; protein ubiquitination.	Complete proteome; Nucleus; Reference proteome; Ubl conjugation pathway
SRR342023_TR31672_c2_g2_i4_len=927	KSG10_ARATH	Q:610-2,H:1-199	76.85%ID	E:3e-108	Shaggy-related protein kinase kappa	PF00069.22^Pkinase^Protein kinase domain^89-203^E:5.6e-20`PF07714.14^Pkinase_Tyr^Protein tyrosine kinase^90-203^E:4.2e-10	1	0	1	0	1	0	1	0	0	6,753	KSG10_ARATH	Shaggy-related protein kinase kappa (EC 2.7.11.1) (ASK-kappa) (AtK-1)	ASK10 At1g09840 F21M12.23	Arabidopsis thaliana (Mouse-ear cress)		ATP-binding; Complete proteome; Kinase; Nucleotide-binding; Phosphoprotein; Reference proteome; Serine/threonine-protein kinase; Transferase
SRR646572_TR429_c0_g1_i4_len=1286	NA	NA	NA	NA	NA	.	1	-0,634	1	0	1	-1,052	1	-1,052	0	7,368	.	.	.	.	.	.
SRR646572_TR1408_c1_g1_i3_len=1502	POLX_TOBAC	Q:64-1500,H:5-484	33.06%ID	E:1e-74	Retrovirus-related Pol polyprotein from transposon TNT 1-94	PF14223.3^Retrotran_gag_2^gag-polypeptide of LTR copia-type^39-169^E:1.8e-33`PF00098.20^zf-CCHC^Zinc knuckle^209-224^E:0.00024`PF13976.3^gag_pre-integrs^GAG-pre-integrase domain^379-446^E:2.1e-11	0,732	0,68	1	0,159	1	0,062	1	-0,978	0	3,889	POLX_TOBAC	Retrovirus-related Pol polyprotein from transposon TNT 1-94 [Includes: Protease (EC 3.4.23.-); Reverse transcriptase (EC 2.7.7.49); Endonuclease]		Nicotiana tabacum (Common tobacco)		Aspartyl protease; Endonuclease; Hydrolase; Metal-binding; Nuclease; Nucleotidyltransferase; Protease; RNA-directed DNA polymerase; Transferase; Transposable element; Zinc; Zinc-finger
SRR646572_TR7228_c0_g1_i1_len=1069	PLAS_SOLLC	Q:847-371,H:11-170	77.16%ID	E:3e-68	Plastocyanin, chloroplastic	PF00127.17^Copper-bind^Copper binding proteins, plastocyanin/azurin family^73-170^E:2.1e-36	0,535	-0,272	0,004	-1,053	0,14	-0,441	0,648	-0,141	0	3,336	PLAS_SOLLC	Plastocyanin, chloroplastic	PETE	Solanum lycopersicum (Tomato) (Lycopersicon esculentum)		Chloroplast; Complete proteome; Copper; Electron transport; Membrane; Metal-binding; Plastid; Reference proteome; Thylakoid; Transit peptide; Transport
SRR646572_TR7923_c0_g1_i1_len=949	NA	NA	NA	NA	NA	.	0,581	0,468	0,429	-0,522	0,214	0,825	0,694	0,355	0	3,978	.	.	.	.	.	.
SRR646572_TR9880_c0_g1_i3_len=3102	NA	NA	NA	NA	NA	PF02536.11^mTERF^mTERF^209-282^E:7.4e-09`PF02536.11^mTERF^mTERF^271-462^E:5.7e-38	0,266	-0,477	0,046	-0,913	0,848	-0,218	1	-0,087	0	6,924	.	.	.	.	.	.
SRR646572_TR14099_c0_g1_i2_len=825	GASA4_ARATH	Q:535-278,H:20-106	70.45%ID	E:5e-34	Gibberellin-regulated protein 4	PF02704.11^GASA^Gibberellin regulated protein^47-106^E:3.7e-22	1	0	1	0	1	0	1	0	0,001	6,638	GASA4_ARATH	Gibberellin-regulated protein 4 (GAST1 protein homolog 4)	GASA4 At5g15230 F8M21.120	Arabidopsis thaliana (Mouse-ear cress)		Alternative splicing; Complete proteome; Disulfide bond; Gibberellin signaling pathway; Reference proteome; Secreted; Signal
SRR646572_TR21106_c0_g1_i1_len=866	R27A3_ARATH	Q:134-571,H:1-146	89.04%ID	E:8e-89	60S ribosomal protein L27a-3	PF00828.16^Ribosomal_L27A^Ribosomal proteins 50S-L15, 50S-L18e, 60S-L27A^72-187^E:6.7e-23	1	0	1	0	1	-0,145	1	-0,769	0	7,766	R27A3_ARATH	60S ribosomal protein L27a-3	RPL27AC At1g70600 F24J13.17 F5A18.22	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Reference proteome; Ribonucleoprotein; Ribosomal protein
SRR646572_TR21462_c0_g1_i1_len=1231	NA	NA	NA	NA	NA	PF03652.12^RuvX^Holliday junction resolvase^23-158^E:1.9e-23	1	-0,011	1	-0,02	1	0,094	1	-0,068	0	6,855	.	.	.	.	.	.
SRR646572_TR23472_c0_g2_i1_len=2432	ORP3C_ARATH	Q:697-2067,H:1-457	82.53%ID	E:0	Oxysterol-binding protein-related protein 3C	PF01237.15^Oxysterol_BP^Oxysterol-binding protein^70-423^E:5.5e-101	1	0	1	-0,141	1	-0,091	1	-0,403	0	4,138	ORP3C_ARATH	Oxysterol-binding protein-related protein 3C (OSBP-related protein 3C)	ORP3C At5g59420 F2O15.10	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Lipid transport; Lipid-binding; Reference proteome; Transport
SRR646572_TR29822_c0_g1_i1_len=1582	GEDH1_OCIBA	Q:161-1228,H:3-358	65.73%ID	E:8e-142	Geraniol dehydrogenase 1	PF08240.9^ADH_N^Alcohol dehydrogenase GroES-like domain^39-151^E:6.3e-28`PF00107.23^ADH_zinc_N^Zinc-binding dehydrogenase^195-318^E:7.5e-19`PF13602.3^ADH_zinc_N_2^Zinc-binding dehydrogenase^228-347^E:2.8e-07	1	0	1	1,979	1	0	1	0	0	7,306	GEDH1_OCIBA	Geraniol dehydrogenase 1 (ObaGEDH1) (EC 1.1.1.183)	GEDH1	Ocimum basilicum (Sweet basil)		Metal-binding; NADP; Oxidoreductase; Zinc
SRR646572_TR29822_c0_g1_i3_len=1634	MTDH_FRAAN	Q:278-1336,H:4-356	70.54%ID	E:1e-157	Probable mannitol dehydrogenase	PF08240.9^ADH_N^Alcohol dehydrogenase GroES-like domain^92-204^E:2.6e-26`PF00107.23^ADH_zinc_N^Zinc-binding dehydrogenase^248-371^E:1.3e-19	0,012	0,813	0,002	0,909	0,622	0,137	0,759	0,094	0	1,159	MTDH_FRAAN	Probable mannitol dehydrogenase (EC 1.1.1.255) (NAD-dependent mannitol dehydrogenase)	CAD	Fragaria ananassa (Strawberry)		Metal-binding; NAD; Oxidoreductase; Zinc
SRR646572_TR30079_c0_g1_i1_len=1778	PRP18_HUMAN	Q:477-1319,H:77-342	38.18%ID	E:7e-54	Pre-mRNA-splicing factor 18	PF08799.8^PRP4^pre-mRNA processing factor 4 (PRP4) like^15-41^E:1.9e-11`PF02840.12^Prp18^Prp18 domain^136-277^E:2.4e-62	1	0	1	0	0,76	-0,595	0,132	-2,104	0	6,801	PRP18_HUMAN	Pre-mRNA-splicing factor 18 (PRP18 homolog) (hPRP18)	PRPF18 HPRP18	Homo sapiens (Human)		3D-structure; Acetylation; Alternative splicing; Complete proteome; Nucleus; Reference proteome; Spliceosome; mRNA processing; mRNA splicing
SRR646572_TR34696_c0_g3_i1_len=637	NA	NA	NA	NA	NA	.	1	0,35	1	0,63	1	0,061	1	0,025	0	3,405	.	.	.	.	.	.
SRR646572_TR35457_c0_g1_i2_len=872	NA	NA	NA	NA	NA	.	1	-0,059	1	-1,82	1	0,554	1	-0,553	0	2,015	.	.	.	.	.	.
SRR646596_TR2901_c0_g1_i1_len=1885	CBDAS_CANSA	Q:162-1661,H:30-538	43.24%ID	E:3e-137	Cannabidiolic acid synthase	PF01565.20^FAD_binding_4^FAD binding domain^79-215^E:2.1e-28`PF08031.9^BBE^Berberine and berberine like^468-526^E:6e-23	0,381	1,474	0,502	3,639	0,381	2,622	0,381	2,496	0	4,919	CBDAS_CANSA	Cannabidiolic acid synthase (EC 1.21.3.8) (CBDA synthase.)	CBDAS	Cannabis sativa (Hemp) (Marijuana)		Apoplast; Direct protein sequencing; Disulfide bond; FAD; Flavoprotein; Glycoprotein; Oxidoreductase; Secreted; Signal
SRR646596_TR5516_c0_g1_i1_len=1977	OSB2_ARATH	Q:1641-694,H:84-366	40.69%ID	E:7e-66	Protein OSB2, chloroplastic	.	1	-1,257	1	0,472	1	-0,996	1	-0,054	0,001	5,556	OSB2_ARATH	Protein OSB2, chloroplastic (Organellar single-stranded DNA-binding protein 2) (Protein FLORAL ABSCISSION ASSOCIATED) (Protein PLASTID TRANSCRIPTIONALLY ACTIVE 9)	OSB2 FAA PTAC9 At4g20010 F18F4.110	Arabidopsis thaliana (Mouse-ear cress)		Alternative splicing; Chloroplast; Complete proteome; DNA-binding; Plastid; Reference proteome; Repeat; Transit peptide
SRR646596_TR6655_c0_g1_i2_len=1322	NA	NA	NA	NA	NA	.	1	1,529	1	0,691	1	1,155	1	-0,153	0	5,613	.	.	.	.	.	.
SRR646596_TR7727_c0_g1_i1_len=994	Y5957_ARATH	Q:299-862,H:19-183	45.45%ID	E:5e-29	Uncharacterized protein At5g39570	.	1	-0,724	0,692	0,799	1	-0,93	1	-0,146	0	5,635	Y5957_ARATH	Uncharacterized protein At5g39570	At5g39570 MIJ24_40	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Direct protein sequencing; Phosphoprotein; Reference proteome
SRR646596_TR11634_c0_g1_i1_len=1661	NA	NA	NA	NA	NA	PF12678.4^zf-rbx1^RING-H2 zinc finger domain^83-130^E:8.3e-11`PF13639.3^zf-RING_2^Ring finger domain^87-130^E:3.1e-15`PF17123.2^zf-RING_11^RING-like zinc finger^87-116^E:4.2e-11`PF13923.3^zf-C3HC4_2^Zinc finger, C3HC4 type (RING finger)^87-129^E:7.6e-10`PF13445.3^zf-RING_UBOX^RING-type zinc-finger^88-127^E:2.9e-08`PF00097.22^zf-C3HC4^Zinc finger, C3HC4 type (RING finger)^88-129^E:2.7e-08	0,874	0,13	1	-0,128	0,272	0,484	0,231	0,502	0	5,638	.	.	.	.	.	.
SRR646596_TR12031_c0_g2_i1_len=780	NA	NA	NA	NA	NA	PF10950.5^DUF2775^Protein of unknown function (DUF2775)^42-152^E:2.5e-22`PF10950.5^DUF2775^Protein of unknown function (DUF2775)^159-230^E:2.5e-15	0,061	0,493	0,001	-3,029	1	1,311	1	1,875	0	0,937	.	.	.	.	.	.
SRR646596_TR16647_c0_g1_i1_len=763	Y5258_ARATH	Q:123-401,H:6-98	64.52%ID	E:5e-35	Uncharacterized protein At5g22580	PF07876.9^Dabb^Stress responsive A/B Barrel Domain^5-97^E:6.4e-23	1	2,594	1	3,683	0,502	3,756	1	0	0	8,97	Y5258_ARATH	Uncharacterized protein At5g22580	At5g22580 MQJ16.12	Arabidopsis thaliana (Mouse-ear cress)		3D-structure; Complete proteome; Magnesium; Metal-binding; Reference proteome

SRR646596_TR17100_c0_g3_i2_len=810	P2B11_ARATH	Q:73-564,H:88-255	36.31%ID	E:1e-21	F-box protein PP2-B11	PF14299.3*PP2*Phloem protein 2*3-160*E:1.9e-32	1	0	1	0	0,502	-4,266	0,502	-4,266	0	1,018	P2B11_ARATH	F-box protein PP2-B11 (Protein PHLOEM PROTEIN 2-LIKE B11) (AIPP2-B11) (SKP1-interacting partner 12)	PP2B11 SKIP12 At1g60110 F18B13.19	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Protein modification; protein ubiquitination.	Complete proteome; Nucleus; Reference proteome; Ubl conjugation pathway
SRR646596_TR20825_c0_g1_i3_len=722	EF1A_MANES	Q:130-594,H:1-155	99.35%ID	E:2e-106	Elongation factor 1-alpha	PF00009.24*GTP_EFTU*Elongation factor Tu GTP binding domain*49-198*E:4.7e-44	0,056	-0,808	0,017	1,472	0,104	-0,877	0,142	-0,735	0,001	0,924	EF1A_MANES	Elongation factor 1-alpha (EF-1-alpha)	EF1	Manihot esculenta (Cassava) (Jatropha manihot)	-	Cytoplasm; Elongation factor; GTP-binding; Nucleotide-binding; Phosphoprotein; Protein biosynthesis
SRR646596_TR26974_c0_g2_i2_len=1953	MDAR_SOLLC	Q:245-150,H:18-433	86.4%ID	E:0	Monodehydroascorbate reductase	PF07992.11*Pyr_redox_2*Pyridine nucleotide-disulphide oxidoreductase*2-132*E:3e-23	1	2,675	0,502	2,108	0	7,847	MDAR_SOLLC	Monodehydroascorbate reductase (MDAR) (EC 1.6.5.4) (Ascorbate free radical reductase) (AFR reductase)	Solanum lycopersicum (Tomato) (Lycopersicon esculentum)	AFRR	-	Complete proteome; Cytoplasm; FAD; Flavoprotein; NAD; Oxidoreductase; Redox-active center; Reference proteome
SRR646596_TR30857_c1_g1_i3_len=2797	PAL1_TOBAC	Q:2065-218,H:100-715	90.75%ID	E:0	Phenylalanine ammonia-lyase	PF00221.16*Lyase_aromatic*Aromatic amino acid lyase*2-440*E:1e-144	1	7,736	0,254	-4,601	1	0,006	1	-0,611	0	7,74	PAL1_TOBAC	Phenylalanine ammonia-lyase (EC 4.3.1.24)	TPA1 PALB	Nicotiana tabacum (Common tobacco)	PATHWAY: Phenylpropanoid metabolism; trans-cinnamate biosynthesis; trans-cinnamate from L-phenylalanine: step 1/1.	Cytoplasm; Lyase; Phenylpropanoid metabolism
SRR646596_TR30884_c0_g1_i1_len=1048	BGLT_TRIRP	Q:851-165,H:25-254	67.39%ID	E:8e-101	Cyanogenic beta-glucosidase	PF00232.15*Glyco_hydro_1*Glycosyl hydrolase family 1*69-293*E:1.1e-84	0,692	-0,88	1	0,727	1	-3,139	1	-3,139	0	1,503	BGLT_TRIRP	Cyanogenic beta-glucosidase (EC 3.2.1.21) (Linamarase) (Fragment)	LI	Trifolium repens (Creeping white clover)	-	3D-structure; Direct protein sequencing; Disulfide bond; Glycoprotein; Glycosidase; Hydrolase; Signal
SRR646596_TR33990_c0_g1_i1_len=770	NDUA2_ARATH	Q:636-352,H:1-95	66.32%ID	E:1e-36	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2	-	-	-	-	-	-	-	-	-	-	7,707	NDUA2_ARATH	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2	At5g47890 MCA23_23	Arabidopsis thaliana (Mouse-ear cress)	-	Complete proteome; Disulfide bond; Electron transport; Membrane; Mitochondrion; Mitochondrion inner membrane; Reference proteome; Respiratory chain; Transport
SRR646596_TR34697_c0_g1_i2_len=3167	PMT8_ARATH	Q:2813-951,H:1-623	79.01%ID	E:0	Probable methyltransferase PMT8	PF03141.13*Methyltransf_29*Putative Sadenosyl-L-methionine-dependent methyltransferase*97-608*E:5.6e-225 PF05724.3*Methyltransf_11*Methyltransferase domain*225-318*E:2.2e-06	0,816	-0,112	0	0,012	0,548	-0,287	0,415	-0,367	0	3,373	PMT8_ARATH	Probable methyltransferase PMT8 (EC 2.1.1.-)	At1g00430 F19P19.11	Arabidopsis thaliana (Mouse-ear cress)	-	Complete proteome; Glycoprotein; Golgi apparatus; Membrane; Methyltransferase; Reference proteome; Signal-anchor; Transferase; Transmembrane; Transmembrane helix
SRR646596_TR34714_c0_g3_i1_len=1888	GUN6_ARATH	Q:1888-548,H:74-619	75.06%ID	E:0	Endoglucanase 6	PF00759.16*Glyco_hydro_9*Glycosyl hydrolase family 9*2-312*E:5e-80 PF09478.7*PCBM9*Carbohydrate binding domain CBM49*356-433*E:3e-27	0,692	1,139	0,517	-0,878	1	-0,557	0,629	-0,998	0	4,164	GUN6_ARATH	Endoglucanase 6 (EC 3.2.1.4) (Endo-1,4-beta glucanase 6)	At1g64390 F15H21.9	Arabidopsis thaliana (Mouse-ear cress)	-	Carbohydrate metabolism; Cell wall biogenesis/degradation; Cellulose degradation; Complete proteome; Glycoprotein; Glycosidase; Hydrolase; Polysaccharide degradation; Reference proteome; Secreted; Signal
SRR646604_TR174_c3_g1_i1_len=2299	HSP72_SOLLC	Q:2100-1633,H:1-644	94.27%ID	E:0	Heat shock cognate 70 kDa protein 2	PF00012.17*HSP70*Hsp70 protein*9-618*E:4.5e-270 PF06723.10*MreB_Mbl*MreB/Mbl protein*131-389*E:4.1e-14	1	0,335	1	1,31	1	0,148	1	-0,5	0	9,079	HSP72_SOLLC	Heat shock cognate 70 kDa protein 2	HSC-2	Solanum lycopersicum (Tomato) (Lycopersicon esculentum)	-	ATP-binding; Complete proteome; Nucleotide-binding; Reference proteome; Stress response
SRR646604_TR607_c1_g2_i4_len=2319	RFS2_ARATH	Q:2-1423,H:172-653	80.79%ID	E:0	Probable galactinol--sucrose galactosyltransferase 2	PF05691.9*Raffinose_syn*Raffinose synthase or seed imbibition protein Sip1*1-456*E:5.6e-230	1	0,114	0,004	1,876	0	0,006	0,935	0,424	0,314	0	1,292	RFS2_ARATH	Probable galactinol--sucrose galactosyltransferase 2 (EC 2.4.1.82) (Protein SEED IMBIBITION 2) (Raffinose synthase 2)	RFS2 RS2 SIP2 At3g57520 T8H10.120	Arabidopsis thaliana (Mouse-ear cress)	-	Alternative splicing; Carbohydrate metabolism; Complete proteome; Glycosyltransferase; Reference proteome; Transferase
SRR646604_TR2448_c0_g12_i1_len=623	TSJT1_TOBAC	Q:442-2,H:1-148	44.97%ID	E:7e-38	Stem-specific protein TSJT1	PF12481.5*DUF3700*Aluminium induced protein*2-147*E:1.7e-54	1	0,312	0,023	1,79	0,136	0,597	0,004	1,046	0	1,159	TSJT1_TOBAC	Stem-specific protein TSJT1	TSJT1	Nicotiana tabacum (Common tobacco)	-	-
SRR646604_TR5426_c0_g1_i1_len=6108	CLAH1_ARATH	Q:2778-5543,H:736-1657	93.49%ID	E:0	Clathrin heavy chain 1	PF00637.17*Clathrin*Region in Clathrin and VPS*73-201*E:5.3e-29 PF00637.17*Clathrin*Region in Clathrin and VPS*216-354*E:2e-31 PF00637.17*Clathrin*Region in Clathrin and VPS*368-504*E:1.1e-26 PF00637.17*Clathrin*Region in Clathrin and VPS*512-654*E:5.5e-29 PF00637.17*Clathrin*Region in Clathrin and VPS*662-802*E:5.4e-31	1	-0,272	1	0,427	1	-0,094	1	1,577	0	5,654	CLAH1_ARATH	Clathrin heavy chain 1	CHC1 At3g11130 F11B9.30 F9F8.6	Arabidopsis thaliana (Mouse-ear cress)	-	Acetylation; Coated pit; Complete proteome; Cytoplasmic vesicle; Endocytosis; Membrane; Reference proteome; Repeat
SRR646604_TR7370_c0_g2_i3_len=928	NA	NA	NA	NA	NA	-	-	-	-	-	1	-0,611	1	-0,238	0	5,965	.	-	-	-	-	-
SRR646604_TR9504_c0_g1_i1_len=2929	SSY2_SOLTU	Q:326-2650,H:1-767	65.95%ID	E:0	Granule-bound starch synthase 2, chloroplast/amyloplastic	PF08323.8*Glyco_transf_5*Starch synthase catalytic domain*299-541*E:1.2e-64 PF00534.17*Glycos_transf_1*Glycosyl transferases group 1*601-742*E:2.6e-16 PF13692.3*Glyco_trans_1_4*Glycosyl transferases group 1*604-743*E:5.9e-15	1	0	1	0,174	1	-0,535	1	-0,094	0	5,441	SSY2_SOLTU	Granule-bound starch synthase 2, chloroplast/amyloplastic (EC 2.4.1.21) (Granule-bound starch synthase II) (GBSS-II) (SS II)	SS2 SSII	Solanum tuberosum (Potato)	PATHWAY: Glycan biosynthesis; starch biosynthesis.	Amyloplast; Chloroplast; Complete proteome; Direct protein sequencing; Glycosyltransferase; Plastid; Polymorphism; Reference proteome; Starch biosynthesis; Transferase; Transit peptide
SRR646604_TR14248_c1_g2_i1_len=2835	POLX_TOBAC	Q:8-2218,H:605-1323	47.11%ID	E:0	Retrovirus-related Pol polyprotein from transposon TNT 1-94	PF07727.11*RVT_2*Reverse transcriptase (RNA-dependent DNA polymerase)*253-600*E:3.9e-93	1	-0,912	1	0,224	1	0,047	1	-0,4	0	6,034	POLX_TOBAC	Retrovirus-related Pol polyprotein from transposon TNT 1-94 [Includes: Protease (EC 3.4.23.-); Reverse transcriptase (EC 2.7.7.49); Endonuclease]	-	Nicotiana tabacum (Common tobacco)	-	-
SRR646604_TR16577_c2_g1_i3_len=962	GOLS1_AJURE	Q:124-849,H:1-235	78.93%ID	E:3e-134	Galactinol synthase 1	PF01501.17*Glyco_transf_8*Glycosyl transferase family 8*73-254*E:1.8e-28	1	1,34	1	1,653	1	-0,034	1	0,886	0	1,493	GOLS1_AJURE	Galactinol synthase 1 (ArGolS1) (GolS-1) (EC 2.4.1.123)	GOLS1	Ajuga reptans (Bugle)	-	Aspartyl protease; Endonuclease; Hydrolase; Metal-binding; Nuclease; Nucleotidyltransferase; Protease; RNA-directed DNA polymerase; Transferase; Transposable element; Zinc; Zinc-finger
SRR646604_TR19244_c0_g1_i1_len=3008	EFGC2_SOYBN	Q:457-2766,H:13-780	87.05%ID	E:0	Elongation factor G-2, chloroplastic	PF00009.24*GTP_EFTU*Elongation factor Tu GTP binding domain*98-370*E:4.7e-71 PF03144.22*GTP_EFTU_D2*Elongation factor Tu domain 2*413-480*E:1.4e-15 PF14492.3*EFG_III*Elongation Factor G, domain III*493-566*E:4.7e-33 PF03764.18*EFG_IV*Elongation factor G, domain IV*568-686*E:2.3e-45 PF00679.21*EFG_C*Elongation factor G C-terminus*690-776*E:4.5e-26	0,073	-0,697	0,058	-0,96	0,008	-0,73	0,717	-0,105	0	1,185	EFGC2_SOYBN	Elongation factor G-2, chloroplastic (cEF-G 2)	fusA2	Glycine max (Soybean) (Glycine hispida)	PATHWAY: Protein biosynthesis; polypeptide chain elongation. (ECO:0000255|HAMAP-Rule:MF_00063).	Chloroplast; Complete proteome; Elongation factor; GTP-binding; Nucleotide-binding; Plastid; Protein biosynthesis; Reference proteome; Transit peptide
SRR646604_TR19799_c2_g1_i3_len=1245	POLX_TOBAC	Q:1210-275,H:125-437	31.78%ID	E:2e-48	Retrovirus-related Pol polyprotein from transposon TNT 1-94	PF14223.3*Retrotran_gag_2*gag-polypeptide of LTR copia-type*3-74*E:2.1e-14 PF00098.20*zf-CCHC*Zinc knuckle*114-129*E:0.00012	1	0,808	1	0,111	1	-1,475	1	-1,591	0	6,129	POLX_TOBAC	Retrovirus-related Pol polyprotein from transposon TNT 1-94 [Includes: Protease (EC 3.4.23.-); Reverse transcriptase (EC 2.7.7.49); Endonuclease]	-	Nicotiana tabacum (Common tobacco)	-	Aspartyl protease; Endonuclease; Hydrolase; Metal-binding; Nuclease; Nucleotidyltransferase; Protease; RNA-directed DNA polymerase; Transferase; Transposable element; Zinc; Zinc-finger
SRR646604_TR19799_c2_g2_i1_len=518	NA	NA	NA	NA	NA	PF14223.3*Retrotran_gag_2*gag-polypeptide of LTR copia-type*112-170*E:4.3e-13	1	-0,173	1	-1,547	1	-1,649	1	0,198	0	6,683	.	-	-	-	-	-
SRR646604_TR20238_c0_g1_i2_len=574	NA	NA	NA	NA	NA	-	-	-	-	-	-	-	-	-	0,001	6,566	.	-	-	-	-	-
SRR646604_TR20314_c0_g1_i1_len=2243	ASNS3_ARATH	Q:180-1841,H:1-554	87.55%ID	E:0	Asparagine synthetase [glutamine-hydrolyzing] 3	PF13522.3*GATase_6*Glutamine amidotransferase domain*92-219*E:1.3e-35 PF13537.3*GATase_7*Glutamine amidotransferase domain*107-224*E:1e-43 PF12481.5*DUF3700*Aluminium induced protein*171-258*E:5e-10 PF00733.18*Asn_synthase*Asparagine synthase*269-570*E:5.6e-98	1	-0,329	1	0,784	1	-0,51	1	-0,482	0	4,739	ASNS3_ARATH	Asparagine synthetase [glutamine-hydrolyzing] 3 (EC 6.3.5.4) (Glutamine-dependent asparagine synthetase 3)	ASN3 At5g10240 F18D22.10 T31P16.230	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Amino-acid biosynthesis; L-asparagine biosynthesis.	-
SRR646604_TR23580_c0_g2_i1_len=1832	SCP51_ARATH	Q:204-1493,H:21-459	66.74%ID	E:0	Serine carboxypeptidase-like 51	PF00450.19*Peptidase_S10*Serine carboxypeptidase*36-449*E:9e-71	0,581	0,335	1	-0,045	1	0,306	1	0,074	0	3,458	SCP51_ARATH	Serine carboxypeptidase-like 51 (EC 3.4.16.-)	SCPL51 At2g27920 T1E2.16	Arabidopsis thaliana (Mouse-ear cress)	-	-
SRR646604_TR23924_c0_g2_i2_len=2113	GSH1_TOBAC	Q:288-1862,H:1-522	83.84%ID	E:0	Glutamate--cysteine ligase, chloroplastic	PF04107.10*GCS2*Glutamate-cysteine ligase family 2(GCS2)*147-435*E:1.3e-94	0,641	-0,257	0,13	0,671	0,691	0,26	0,183	0,646	0	1,955	GSH1_TOBAC	Glutamate--cysteine ligase, chloroplastic (EC 6.3.2.2) (Gamma-ECS) (GCS) (Gamma-glutamylcysteine synthetase)	GSH1	Nicotiana tabacum (Common tobacco)	PATHWAY: Sulfur metabolism; glutathione biosynthesis; glutathione from L-cysteine and L-glutamate: step 1/2.	ATP-binding; Chloroplast; Disulfide bond; Glutathione biosynthesis; Ligase; Nucleotide-binding; Plastid; Transit peptide
SRR646604_TR25316_c0_g2_i2_len=2192	APX1_ARATH	Q:168-419,H:1-250	85.2%ID	E:5e-141	L-ascorbate peroxidase 1, cytosolic	PF00141.20*peroxidase*Peroxidase*22-227*E:4.9e-49	0,87	-0,225	0,114	0,872	0,052	1,507	0,111	1,338	0	3,134	APX1_ARATH	L-ascorbate peroxidase 1, cytosolic (AP) (AtAPx01) (EC 1.11.1.11)	APX1 At1g07890 F24B9.2	Arabidopsis thaliana (Mouse-ear cress)	-	Alternative splicing; Calcium; Complete proteome; Cytoplasm; Direct protein sequencing; Heme; Hydrogen peroxide; Iron; Metal-binding; Oxidoreductase; Peroxidase; Reference proteome; Phosphoprotein; Potassium; Reference proteome
SRR646604_TR28714_c0_g1_i2_len=945	CB23_TOBAC	Q:45-734,H:38-265	92.17%ID	E:1e-151	Chlorophyll a-b binding protein 36, chloroplastic	PF00504.18*Chlorophyll a-b binding*Chlorophyll A-B binding protein*1-126*E:4e-30	0,099	-0,347	0	-1,9	0	-1,076	0	-0,855	0	1,744	CB23_TOBAC	Chlorophyll a-b binding protein 36, chloroplastic (LHCII type I CAB-36) (LHCP)	CAB36	Nicotiana tabacum (Common tobacco)	-	Acetylation; Chloroplast; Chromophore; Magnesium; Membrane; Metal-binding; Phosphoprotein; Photosynthesis; Photosystem I; Photosystem II; Plastid; Thylakoid; Transit peptide; Transmembrane; Transmembrane helix
SRR646604_TR30519_c0_g2_i1_len=2811	NA	NA	NA	NA	NA	PF00575.20*S1*S1 RNA binding domain*551-621*E:3.7e-11	1	0,056	1	-0,893	1	0,012	1	0,192	0	8,976	.	-	-	-	-	-
SRR646604_TR33779_c0_g1_i1_len=1957	CTD55_HYOMU	Q:1827-403,H:26-497	55.23%ID	E:1e-178	Premnaspirodiene oxygenase	PF00067.19*p450*Cytochrome P450*51-504*E:9.7e-104	1	-0,64	1	0	1	0,291	0	0,047	0	1,017	CTD55_HYOMU	Premnaspirodiene oxygenase (HPO) (EC 1.14.13.121) (Cytochrome P450 7ID55)	CYP7ID55	Hyoscyamus muticus (Egyptian henbane)	-	Heme; Iron; Membrane; Metal-binding; Monooxygenase; NADP; Oxidoreductase; Transmembrane; Transmembrane helix
SRR646604_TR34861_c0_g1_i1_len=1000	NA	NA	NA	NA	NA	-	1	0	1	1,579	1	-3,182	1	-1,67	0	6,869	.	-	-	-	-	-
SRR646604_TR37133_c2_g1_i4_len=1013	POLX_TOBAC	Q:520-1011,H:424-587	46.34%ID	E:1e-68	Retrovirus-related Pol polyprotein from transposon TNT 1-94	PF07727.11*RVT_2*Reverse transcriptase (RNA-dependent DNA polymerase)*2-135*E:4.8e-41	1	-0,139	1	-1,424	1	-1,439	0,502	-2,58	0	3,717	POLX_TOBAC	Retrovirus-related Pol polyprotein from transposon TNT 1-94 [Includes: Protease (EC 3.4.23.-); Reverse transcriptase (EC 2.7.7.49); Endonuclease]	-	Nicotiana tabacum (Common tobacco)	-	Aspartyl protease; Endonuclease; Hydrolase; Metal-binding; Nuclease; Nucleotidyltransferase; Protease; RNA-directed DNA polymerase; Transferase; Transposable element; Zinc; Zinc-finger
SRR648705_TR4879_c1_g1_i1_len=840	POLX_TOBAC	Q:2-292,H:1227-1323	52.58%ID	E:2e-24	Retrovirus-related Pol polyprotein from transposon TNT 1-94	PF07727.11*RVT_2*Reverse transcriptase (RNA-dependent DNA polymerase)*2-135*E:4.8e-41	1	2,046	1	-0,169	1	0,33	1	0,273	0	6,71	POLX_TOBAC	Retrovirus-related Pol polyprotein from transposon TNT 1-94 [Includes: Protease (EC 3.4.23.-); Reverse transcriptase (EC 2.7.7.49); Endonuclease]	-	Nicotiana tabacum (Common tobacco)	-	Aspartyl protease; Endonuclease; Hydrolase; Metal-binding; Nuclease; Nucleotidyltransferase; Protease; RNA-directed DNA polymerase; Transferase; Transposable element; Zinc; Zinc-finger
SRR648705_TR4879_c1_g4_i1_len=506	NA	NA	NA	NA	NA	-	1	0	1	0	1	0	1	0	0	8,93	.	-	-	-	-	-
SRR648705_TR4879_c1_g5_i1_len=956	POLX_TOBAC	Q:882-49,H:943-1218	52.52%ID	E:7e-93	Retrovirus-related Pol polyprotein from transposon TNT 1-94	PF07727.11*RVT_2*Reverse transcriptase (RNA-dependent DNA polymerase)*2-135*E:4.8e-41	1	-1,937	1	-2,373	1	2,049	1	1,191	0	6,242	POLX_TOBAC	Retrovirus-related Pol polyprotein from transposon TNT 1-94 [Includes: Protease (EC 3.4.23.-); Reverse transcriptase (EC 2.7.7.49); Endonuclease]	-	Nicotiana tabacum (Common tobacco)	-	Aspartyl protease; Endonuclease; Hydrolase; Metal-binding; Nuclease; Nucleotidyltransferase; Protease; RNA-directed DNA polymerase; Transferase; Transposable element; Zinc; Zinc-finger
SRR648705_TR5530_c0_g1_i1_len=1946	NA	NA	NA	NA	NA	PF05368.10*NmrA*NmrA-like family*20-91*E:2.4e-06 PF01370.18*Epimerase*NAD dependent epimerase/dehydratase family*20-80*E:9.5e-05 PF13460.3*NAD_binding_10*NAD(P)H-binding*24-140*E:1.2e-11 PF08547.9*CLAS0*Complex I intermediate-associated protein 30 (CIA30)*154-323*E:1.2e-41 PF13460.3*NAD_binding_10*NAD(P)H-binding*335-435*E:2e-13	0,002	6,396	0,059	1,674	0,6	-0,319	1	0,014	0	2,139	.	-	-	-	-	-
SRR648705_TR6339_c0_g1_i1_len=1235	21KD_DAUCA	Q:869-369,H:28-192	49.7%ID	E:3e-52	21 kDa protein	PF40443.12*PMEI*Plant invertase/pectin methylesterase inhibitor*31-189*E:2.4e-36	0,286	-0,861	0,004	-2,893	1	-0,631	1	-1,616	0	4,871	21KD_DAUCA	21 kDa protein (1.2 protein)	Daucus carota (Wild carrot)	Ipomoea nil (Japanese morning glory) (Pharbitis nil)	-	Signal
SRR648705_TR7307_c0_g1_i2_len=657	HMGL_IPONI	Q:615-166,H:1-126	63.33%ID	E:1e-43	HMG1/2-like protein	PF09011.7*HMG_box_2*HMG1/2-like protein domain*37-109*E:3.4e-15 PF00505.16*HMG_box*HMG (high mobility group) box*40-109*E:1.9e-22	1	-0,08	0,454	-0,393	1	0,239	0,158	1,677	0	5,619	HMGL_IPONI	HMG1/2-like protein	-	-	-	DNA-binding; Nucleus
SRR648705_TR13253_c0_g2_i1_len=3955	ALFC2_ARATH	Q:3425-2235,H:1-398	88.72%ID	E:0	Probable fructose-bisphosphate aldolase 2, chloroplastic	PF00274.16*Glycolytic*Fructose-bisphosphate aldolase class-I*53-397*E:2.1e-158	1	0	1	0	1	0	1	0	0	8,077	ALFC2_ARATH	Probable fructose-bisphosphate aldolase 2, chloroplastic (EC 4.1.2.13)	FBA2 At4g38970 F19H22.70	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Carbohydrate degradation; glycolysis; D-glyceraldehyde 3-phosphate and glycerone phosphate from D-glucose: step 4/4.	Alternative splicing; Chloroplast; Complete proteome; Glycolysis; Lyase; Methylation; Phosphoprotein; Plastid; Reference proteome; Schiff base; Transit peptide
SRR648705_TR13253_c0_g2_i2_len=3854	ALFC2_ARATH	Q:3324-2134,H:1-398	88.72%ID	E:0	Probable fructose-bisphosphate aldolase 2, chloroplastic	PF00274.16*Glycolytic*Fructose-bisphosphate aldolase class-I*53-397*E:2.1e-158	0,552	-0,233	1	0,031	0	-0,925	0,019	-0,515	0	2,167	ALFC2_ARATH	Probable fructose-bisphosphate aldolase 2, chloroplastic (EC 4.1.2.13)	FBA2 At4g38970 F19H22.70	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Carbohydrate degradation; glycolysis; D-glyceraldehyde 3-phosphate and glycerone phosphate from D-glucose: step 4/4.	Alternative splicing; Chloroplast; Complete proteome; Glycolysis; Lyase; Methylation; Phosphoprotein; Plastid; Reference proteome; Schiff base; Transit peptide
SRR648705_TR13379_c0_g1_i3_len=692	RS212_ARATH	Q:180-422,H:1-81	81.48%ID	E:3e-44	40S ribosomal protein S21-2	-	-	-	-	-	0	-7,167	-2,282	-0,271	0	1,174	.	40S ribosomal protein S21-2	4,454 RS212_ARATH	RPS21C At5g27700 T1G16.30	Arabidopsis thaliana (Mouse-ear cress)	-	Acetylation; Complete proteome; Reference proteome; Ribonucleoprotein; Ribosomal protein
SRR648705_TR14618_c0_g1_i3_len=3093	4CLL7_ARATH	Q:441-208,H:1-544	68.74%ID	E:0	4-coumarate--CoA ligase-like 7	PF00501.25*AMP-binding*AMP-binding enzyme*36-449*E:1.1e-101 PF13193.3*AMP-binding_C*AMP-binding enzyme C-terminal domain*458-533*E:1.2e-14	0,254	-4,759	1	0	0,009	-6,002	0,009	-6,002	0	1,666	4CLL7_ARATH	4-coumarate--CoA ligase-like 7 (EC 6.2.1.-) (4-coumarate--CoA ligase isoform 6) (At4CL6)	4CLL7 At4g05160 C17L7.80	Arabidopsis thaliana (Mouse-ear cress)	-	Complete proteome; Ligase; Nucleotide-binding; Oxylipin biosynthesis; Peroxisome; Reference proteome
SRR648705_TR23292_c0_g2_i1_len=833	NA	NA	NA	NA	NA	-	0,254	4,779	0,454	-0,446	0,004	-2,36	0,278	-0,732	0	8,047	.	-	-	-	-	-
SRR648705_TR23308_c0_g3_i3_len=2394	SPDE_COFAR	Q:1183-1979,H:116-316	90.05%ID	E:5e-121	Spermidine synthase	PF01564.14*Spermine_synth*Spermine/spermidine synthase*1-133*E:2.8e-44	0,648	-0,281	0,405	0,327	0,736	-0,156	0,329	-0,4	0	5,42	SPDE_COFAR	Spermidine synthase (SPDSY) (EC 2.5.1.16) (Putrescine aminopropyltransferase)	-	Coffea arabica (Arabian coffee)	-	Polyamine biosynthesis; Spermidine biosynthesis; Transferase
SRR648705_TR27096_c1_g1_i1_len=652	RS191_ARATH	Q:535-107,H:1-143	86.71%ID	E:2e-88	40S ribosomal protein S19-1	PF01090.16*Ribosomal_S19e*Ribosomal protein S19e*6-140*E:7.4e-59	0	-1,286	0,003	0,999	0,657	0,17	0,53	-0,22	0	1,55	RS191_ARATH	40S ribosomal protein S19-1	RPS19A At3g02080 F1C9.13	Arabidopsis thaliana (Mouse-ear cress)	-	Complete proteome; Reference proteome; Ribonucleoprotein; Ribosomal protein
SRR648705_TR28356_c0_g4_i1_len=1138	C84A1_ARATH	Q:134-757,H:313-520	82.21%ID	E:2e-110	Cytochrome P450 84A1	PF00067.19*p450*Cytochrome P450*1-188*E:7.6e-62	1	0,142	1	0,506	1	0,111	1	-0,28	0,001	5,666	C84A1_ARATH	Cytochrome P450 84A1 (EC 1.14.-.-) (Ferulate-5-hydroxylase) (F5H)	CYP84A1 FAH1 At4g36220 F22E13.110	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Aromatic compound metabolism; phenylpropanoid biosynthesis.	Oxidoreductase; Reference proteome; Transferase; Transmembrane helix
SRR648705_TR35052_c0_g1_i1_len=1056	PR1_MEDTR	Q:665-255,H:40-173	57.25%ID	E:5e-48	Pathogenesis-related protein PR-1	PF00188.23*CAP*Cysteine-rich secretory protein family*65-185*E:8.4e-24	0,239	1,254	1	-0,8	0,01	-1,157	0	-4,108	0,001	1,713	PR1_MEDTR	Pathogenesis-related protein PR-1	PR-1	Medicago truncatula (Barrel medic) (Medicago tribuloides)	-	Disulfide bond; Pathogenesis-related protein; Plant defense; Signal
SRR648705_TR37308_c0_g1_i1_len=506	NA	NA	NA	NA	NA	-	0,083	-0,389	0,003	-0,69	0	-0,917	0	-0,948	0	0,925	.	-	-	-	-	-
SRR648705_TR41240_c0_g2_i2_len=1159	VPS29_ARATH	Q:840-277,H:1-188	86.7%ID	E:1e-116	Vacuolar protein sorting-associated protein 29	PF12850.4*Metallophos_2*Calcineurin-like phosphoesterase superfamily domain*4-157*E:2.1e-19	0,798	0,525	1	-0,334	0,56	0,899	0,132	1,524	0	3,735	VPS29_ARATH	Vacuolar protein sorting-associated protein 29 (Protein MAIGO 1) (Vesicle protein sorting 29)	VPS29 MAG1 At3g47810 T23J7.140	Arabidopsis thaliana (Mouse-ear cress)	-	Complete proteome; Cytoplasm; Endosome; Golgi apparatus; Membrane; Protein transport; Reference proteome; Transport
SRR648705_TR43844_c0_g2_i1_len=1151	TIP21_ARATH	Q:138-875,H:1-247	82.19%ID	E:4e-92	Aquaporin TIP2-1	PF00230.17*MIP*Major intrinsic protein*16-232*E:1.7e-73	1	0,459	1	0	1	0,107	1	-0,743	0	10,07	TIP21_ARATH	Aquaporin TIP2-1 (Delta-tonoplast intrinsic protein) (Delta-TIP) (Tonoplast intrinsic protein 2-1) (AtTIP2;1) (Cleaved into: Aquaporin TIP2-1, Normrally processed)	TIP2-1 At3g16240 MYA6.10	Arabidopsis thaliana (Mouse-ear cress)	-	Aquaporin; Complete proteome; Kinase; Nucleotide-binding; Phosphoprotein; Reference proteome; Serine/threonine protein kinase; Transferase
SRR648705_TR7693_c0_g1_i2_len=3595	CAPP2_ARATH	Q:580-3483,H:1-963	87.1%ID	E:0	Phosphoenolpyruvate carboxylase 2	PF00311.14*PEPcase*Phosphoenolpyruvate carboxylase*163-968*E:0	0,355	-0,326	0,684	0,221	0	-2,213	0	-1,384	0	1,399	CAPP2_ARATH	Phosphoenolpyruvate carboxylase 2 (ARPPC2) (PEPC 2) (PEPCase 2) (EC 4.1.1.31)	PPC2 At2g42600 F14N22.13	Arabidopsis thaliana (Mouse-ear cress)	-	Calcium; Cell wall; Complete proteome; Direct protein sequencing; Glycoprotein; Hydrolase; Protease; Reference proteome; Secreted; Serine protease; Signal; Zymogen
SRR648707_TR1124_c1_g1_i2_len=1052	HTOMT_CATRO	Q:32-1051,H:1-338	93.53%ID	E:0	Tabersonine 16-O-methyltransferase	PF01596.21*NARS*AIR synthase related protein, N-terminal domain*39-493*E:5.021 PF02269.19*ARS_C*AIR synthase related protein, C-terminal domain*535-680*E:2.2e-21 PF02769.19*AIRS_C*AIR synthase related protein, C-terminal domain*945-1075*E:3.3e-16 PF13507.3*GATase_5*CobB/CobQ-like glutamine amidotransferase domain*1143-1196*E:2.4e-15 PF01190.14*Pollen_Ole_e_1*Pollen proteins Ole e I like*29-110*E:1.2e-15	1	0,001	1	0,001	0	0,001	1	0,011	HTOMT_CATRO	Tabersonine 16-O-methyltransferase (EC 2.1.1.94)	16OMT	Catharanthus roseus (Madagascar periwinkle) (Vinca rosea)	-	Cytoplasm; Methyltransferase; S-adenosyl-L-methionine; Transferase
SRR648707_TR7601_c4_g2_i1_len=6090	PUR4_ARATH	Q:5873-2213,H:9-1192	78.69%ID	E:0	Probable phosphoribosylformylglycinamidine synthase, chloroplastic/mitochondrial	PF00586.21*AIRS*AIR synthase related protein, N-terminal domain*339-493*E:5.021 PF02769.19*AIRS_C*AIR synthase related protein, C-terminal domain*535-680*E:2.2e-21 PF02769.19*AIRS_C*AIR synthase related protein, C-terminal domain*945-1075*E:3.3e-16 PF13507.3*GATase_5*CobB/CobQ-like glutamine amidotransferase domain*1143-1196*E:2.4e-15 PF01190.14*Pollen_Ole_e_1*Pollen proteins Ole e I like*29-110*E:1.2e-15	1	1,559	0,882	0,059	0,694	0,217	0,626	0,233	0,564	0,418	PUR4_ARATH	Probable ph

SRR342022_TR9794_c0_g20_i1_len=1639	STSY_RAUSE	Q:819-1544,H:83-324	40.91%ID	E:4e-59	Strictosidine synthase	PF03088.13*Str_synth*Strictosidine synthase*73-160:E:1.5e-25	0,001	1,704	0,103	1,523	0,692	0,563	1	-0,471	1	0,026	STSY_RAUSE	Strictosidine synthase (EC 4.3.3.2)	STR1	Rauvolfia serpentina (Serpentine wood) (Ophioxylon serpentinum)	PATHWAY: Alkaloid biosynthesis; 3alpha(S)-strictosidine biosynthesis; 3alpha(S)-strictosidine from secologanin and tryptamine: step 1/1.	3D-structure; Alkaloid metabolism; Direct protein sequencing; Glycoprotein; Lyase; Signal; Vacuole
SRR342022_TR9794_c0_g20_i3_len=1230	STSY_RAUMA	Q:278-1135,H:37-332	43.71%ID	E:1e-81	Strictosidine synthase	PF03088.13*Str_synth*Strictosidine synthase*17-264*E:3e-25	0	1,31	0,002	1,389	1	-0,037	0,076	-1,503	0,938	0,04	STSY_RAUMA	Strictosidine synthase (EC 4.3.3.2) (Fragment)	STR1	Rauvolfia mannii	PATHWAY: Alkaloid biosynthesis; 3alpha(S)-strictosidine biosynthesis; 3alpha(S)-strictosidine from secologanin and tryptamine: step 1/1.	Alkaloid metabolism; Glycoprotein; Lyase; Signal; Vacuole
SRR342022_TR22888_c2_g4_i1_len=1175	14335_SOLTU	Q:1081-317,H:1-256	93.75%ID	E:3e-172	14-3-3-like protein 16R	PF00244.17*14-3-3*14-3-3 protein*32-257*E:7.4e-105	0	3,144	0,029	-0,567	0,111	-0,519	0,004	-0,958	0,003	-0,77	14335_SOLTU	14-3-3-like protein 16R	-	-	-	Solanum tuberosum (Potato)	-	Complete proteome; Reference proteome
SRR342022_TR26103_c2_g5_i1_len=1165	NA	NA	NA	NA	NA	-	0	4,122	0,402	0,979	0,002	2,443	0,026	1,901	0,949	0,033		-	-	-	-	-	-	-
SRR342022_TR26348_c3_g6_i6_len=717	MECR_ARATH	Q:58-525,H:220-375	78.21%ID	E:3e-81	Probable trans-2-enoyl-CoA reductase, mitochondrial	-	0,001	6,615	0,623	-0,38	0,076	1,397	0,44	0,767	0,003	-1,47	MECR_ARATH	Probable trans-2-enoyl-CoA reductase, mitochondrial (EC 1.3.1.38)	At3g45770 T6D9.100	Arabidopsis thaliana (Mouse-ear cress)	-	-	-	Alternative splicing; Complete proteome; Fatty acid biosynthesis; Fatty acid metabolism; Lipid biosynthesis; Lipid metabolism; Mitochondrion; NADP; Oxidoreductase; Reference proteome; Transit peptide
SRR342023_TR2846_c0_g5_i2_len=1227	ABP20_PRUPE	Q:258-782,H:28-202	69.89%ID	E:3e-72	Auxin-binding protein ABP20	PF00190.19*Cupin_1*Cupin*54-199*E:4.1e-32	0	1,428	0	-3,732	0	-2,648	0	-1,69	0,615	0,105	ABP20_PRUPE	Auxin-binding protein ABP20	ABP20	Prunus persica (Peach) (Amygdalus persica)	-	-	-	Apoplast; Auxin signaling pathway; Cell wall; Disulfide bond; Glycoprotein; Manganese; Metal-binding; Receptor; Secreted; Signal
SRR342023_TR17123_c5_g1_i3_len=829	NA	NA	NA	NA	NA	-	0	1,079	0,724	-0,199	1	-0,424	0,381	-1,563	1	0		-	-	-	-	-	-	-
SRR342023_TR22890_c2_g1_i3_len=708	TBL21_ARATH	Q:634-5,H:179-391	62.91%ID	E:2e-100	Protein trichome birefringence-like 21	PF14416.3*PMR5N*PMR5 N terminal Domain*12-64*E:1.6e-22 PF13839.3*PC-Esterase*GDSL/SGNH-like Acyl-Esterase family found in Pmr5 and Cas1p*65-216*E:2.4e-44	0	6,951	0,282	1,239	0,564	-0,477	0,312	-0,817	1	0	TBL21_ARATH	Protein trichome birefringence-like 21	TBL21 At5g15890 F1N13.30	Arabidopsis thaliana (Mouse-ear cress)	-	-	-	Complete proteome; Membrane; Reference proteome; Signal-anchor; Transmembrane; Transmembrane helix
SRR342023_TR27467_c3_g4_i8_len=1394	NA	NA	NA	NA	NA	PF06108.9*DUF952*Protein of unknown function (DUF952)*19-54*E:7.6e-08	0	1,571	0	-2,315	0,132	0,762	0,496	0,388	1	-2,002		-	-	-	-	-	-	-
SRR64657_TR24195_c1_g6_i3_len=578	NU5C_COFAR	Q:4474-2276,H:1-733	85.68%ID	E:0	NAD(P)H-quinone oxidoreductase subunit 5, chloroplastic	PF00662.17*Proton_antipo_N*NADH-Ubiquinone oxidoreductase (complex I), chain 5 N-terminus*72-129*E:5e-20 PF00361.17*Proton_antipo_M*Proton-conducting membrane transporter*141-442*E:1.9e-96 PF10110.16*Proton_antipo_C*NADH-dehydrogenase subunit F, TMs, (complex I) C-terminus*448-688*E:2.7e-112	0	1,62	0,927	0,999	0,203	-0,597	0,203	-0,581	0,363	-0,277	NU5C_COFAR	NAD(P)H-quinone oxidoreductase subunit 5, chloroplastic (EC 1.6.5.-) (NAD(P)H dehydrogenase subunit 5) (NADH-plastoquinone oxidoreductase subunit 5)	ndhF	Coffea arabica (Arabian coffee)	-	-	-	Chloroplast; Membrane; NAD; NADP; Oxidoreductase; Plastid; Plastoquinone; Quinone; Thylakoid; Transmembrane; Transmembrane helix; Transport
SRR64657_TR30031_c0_g1_i2_len=1681	NA	NA	NA	NA	NA	-	0	4,175	0,594	0,124	0,012	0,612	0,002	0,752	0,423	-0,174		-	-	-	-	-	-	-
SRR64657_TR30268_c0_g1_i1_len=737	NA	NA	NA	NA	NA	-	0	8,205	0	-10,998	1	0	1	0	1	0		-	-	-	-	-	-	-
SRR64696_TR11266_c4_g7_i3_len=553	NA	NA	NA	NA	NA	-	0	3,2	0,579	-0,117	0,745	0,071	0,383	0,187	0,708	0,192		-	-	-	-	-	-	-
SRR64696_TR32001_c0_g1_i1_len=2993	SIR1_TOBAC	Q:187-2271,H:1-691	82.21%ID	E:0	Sulfite reductase 1 [ferredoxin], chloroplastic	PF03460.14*NIR_SIR_ferr*Nitrite/Sulfite reductase ferredoxin-like half domain*195-252*E:2e-15 PF01077.19*NIR_SIR*Nitrite and sulphite reductase 4Fe-4S domain*289-467*E:2.1e-50 PF03460.14*NIR_SIR_ferr*Nitrite/Sulfite reductase ferredoxin-like half domain*485-538*E:1e-13 PF01077.19*NIR_SIR*Nitrite and sulphite reductase 4Fe-4S domain*563-701*E:1.2e-09	0	2,577	0,321	-0,289	0,339	-0,32	0,708	0,123	0,695	0,125	SIR1_TOBAC	Sulfite reductase 1 [ferredoxin], chloroplastic (NiSiR1) (EC 1.8.7.1)	SIR1	Nicotiana tabacum (Common tobacco)	-	-	-	4Fe-4S; Chloroplast; DNA-binding; Direct protein sequencing; Heme; Iron; Iron-sulfur; Metal-binding; Oxidoreductase; Plastid; Thioether bond; Transit peptide
SRR64604_TR17021_c2_g3_i3_len=2306	NA	NA	NA	NA	NA	-	0	1,632	1	-0,003	0,776	0,081	0,799	-0,092	0,29	-0,399		-	-	-	-	-	-	-
SRR64604_TR26908_c0_g1_i1_len=551	NA	NA	NA	NA	NA	-	0	1,357	0,129	0,4	0,045	0,505	0,004	0,724	0,001	-0,946		-	-	-	-	-	-	-
SRR64705_TR1118_c0_g1_i1_len=935	NA	NA	NA	NA	NA	-	0	1,086	0,008	0,606	0,254	4,414	1	2,551	0,049	0,468		-	-	-	-	-	-	-
SRR64705_TR17279_c0_g2_i8_len=2030	TLP8_ORYSJ	Q:1602-313,H:1-445	73.66%ID	E:0	Tubbylike F-box protein 8	PF00646.30*F-box*F-box domain*52-105*E:7.7e-11 PF12937.4*F-boxlike*F-boxlike*53-95*E:1.2e-06 PF01167.15*Tub*Tub family*117-424*E:7.4e-97	0	6,996	0,03	-1,073	0,103	1,709	0,356	1,251	1	-0,398	TLP8_ORYSJ	Tubby-like F-box protein 8 (OsTLP8) (Tubby-like F-box protein 1) (OsTLP1)	TULP8 TULP1 Os05g0437900 LOC_Os05g36190 OJ1058_F05.11 Os J_01918 OSJNBb0042217.6	Oryza sativa subsp. japonica (Rice)	-	-	-	Complete proteome; Reference proteome
SRR64705_TR17428_c0_g2_i1_len=1299	SWT17_ARATH	Q:310-999,H:1-241	60.17%ID	E:1e-82	Bidirectional sugar transporter SWEET17	PF03083.13*MtN3_slv*Sugar efflux transporter for intercellular exchange*7-92*E:2.6e-26 PF03083.13*MtN3_slv*Sugar efflux transporter for intercellular exchange*128-212*E:1.8e-25	0	1,755	0,057	1,42	0,282	0,398	0,562	-0,268	0,211	-0,466	SWT17_ARATH	Bidirectional sugar transporter SWEET17 (AtSWEET17) (Protein SUGARS WILL EVENTUALLY BE EXPORTED TRANSPORTERS 17)	SWEET17 At4g15920 dl4000c FCAALL.237	Arabidopsis thaliana (Mouse-ear cress)	-	-	-	Complete proteome; Membrane; Reference proteome; Repeat; Sugar transport; Transmembrane; Transmembrane helix; Transport; Vacuole
SRR64705_TR18459_c0_g2_i1_len=609	NA	NA	NA	NA	NA	-	0	1,644	0,165	-0,297	0,037	-0,461	0,612	-0,114	0,782	0,075		-	-	-	-	-	-	-
SRR64705_TR23045_c0_g2_i1_len=4443	AL221_ARATH	Q:142-1917,H:1-596	80.2%ID	E:0	Aldehyde dehydrogenase 22A1	PF00171.19*Aldedh*Aldehyde dehydrogenase family*59-523*E:1.4e-121	0,001	6,608	0,381	1,365	1	0	1	0	0,629	-1,623	AL221_ARATH	Aldehyde dehydrogenase 22A1 (EC 1.2.1.3) (Novel aldehyde dehydrogenase family 22 member A1)	ALDH22A1 At3g66658 T8E24.4	Arabidopsis thaliana (Mouse-ear cress)	-	-	-	Alternative splicing; Complete proteome; NAD; Oxidoreductase; Reference proteome; Secreted; Signal
SRR64705_TR25614_c3_g2_i6_len=1277	NA	NA	NA	NA	NA	-	0	1,722	0,554	-0,134	0,301	0,255	0,18	0,324	0,405	0,202		-	-	-	-	-	-	-
SRR64705_TR25781_c0_g1_i1_len=2293	GAE6_ARATH	Q:1864-539,H:4-452	79.33%ID	E:0	UDP-glucuronate 4-epimerase 6	PF04321.14*RmlD_sub_bind*RmlD substrate binding domain*118-302*E:1e-10 PF01370.18*Epimerase*NAD dependent epimerase/dehydratase family*120-357*E:5.1e-46 PF02719.12*Polysacc_synt_2*Polysaccharide biosynthesis protein*120-356*E:3.4e-08 PF16363.2*GDP_Man_Dehyd*GDP-mannose 4,6 dehydratase*121-440*E:3.6e-48 PF10073.16*Beta_HSD*3-beta hydroxysteroid dehydrogenase/isomerase family*121-399*E:1.4e-12 PF07993.9*NAD_binding_4*Male sterility protein*158-299*E:3.9e-05	0	1,295	0,023	0,648	0,538	-0,203	0,611	-0,16	0,255	-0,539	GAE6_ARATH	UDP-glucuronate 4-epimerase 6 (EC 5.1.3.6) (UDP-glucuronic acid epimerase 6) (AtUGlcAE2)	GAE6 UGlcAE2 At3g23820 F14D13.1	Arabidopsis thaliana (Mouse-ear cress)	-	-	-	Carbohydrate metabolism; Complete proteome; Golgi apparatus; Isomerase; Membrane; NAD; Reference proteome; Transmembrane; Transmembrane helix
SRR648705_TR41790_c2_g1_i2_len=6940	NA	NA	NA	NA	NA	-	0	1,665	0,064	-0,383	0,967	0,009	1	0	0,764	-0,101		-	-	-	-	-	-	-
SRR648705_TR17051_c0_g3_i2_len=1066	NA	NA	NA	NA	NA	-	0	3,415	0,045	1,511	0,006	1,808	1	0,219	0,663	-0,443		-	-	-	-	-	-	-
SRR648707_TR2930_c2_g2_i5_len=3561	PSBA_CUCSA	Q:2927-1569,H:1-353	99.72%ID	E:0	Photosystem II protein D1 [ECO:0000255]HAMAP-Rule:MF_01379]	PF00124.16*Photo_RC*Photosynthetic reaction centre protein*28-327*E:3.7e-98	0	3,35	0,095	0,503	0,19	0,41	0,097	0,503	0,003	-0,77	PSBA_CUCSA	Photosystem II protein D1 (PSII D1 protein) (EC 1.10.3.9) (Photosystem II Q(B) protein)	psbA	Cucumis sativus (Cucumber)	-	-	-	Acetylation; Calcium; Chlorophyll; Chloroplast; Chromophore; Electron transport; Herbicide resistance; Iron; Magnesium; Manganese; Membrane; Metal-binding; Oxidoreductase; Phosphoprotein; Photosynthesis; Photosystem II; Plastid; Thylakoid; Transmembrane; Transmembrane helix; Transport
SRR648707_TR8102_c0_g1_i2_len=1197	FK151_ARATH	Q:67-379,H:57-153	80.61%ID	E:1e-45	Peptidyl-prolyl cis-trans isomerase FKBP15-1	PF00254.25*FKBP_C*FKBP-type peptidyl-prolyl cis-trans isomerase*6-84*E:5.7e-30	0,001	2,135	0,006	2,333	0,042	-2,103	0,042	-2,083	1	-0,204	FK151_ARATH	Peptidyl-prolyl cis-trans isomerase FKBP15-1 (PPIase FKBP15-1) (EC 5.2.1.8) (15 kDa FK506-binding protein) (15 kDa FKBP) (FK506-binding protein 15-1) (AtFKBP15-1) (FK506-binding protein 2-1) (Immunophilin FKBP15-1) (Rotamase)	FKBP15-1 At3g25220 MJL12.17	Arabidopsis thaliana (Mouse-ear cress)	-	-	-	Complete proteome; Endoplasmic reticulum; Isomerase; Reference proteome; Rotamase; Signal
SRR648707_TR35408_c0_g2_i3_len=1189	YCX91_PHAAO	Q:833-1105,H:1-91	97.8%ID	E:3e-56	Uncharacterized protein ORF91	-	0	2,777	0,211	-0,282	0,017	-0,581	0,01	-0,629	0,258	0,989	YCX91_PHAAO	Uncharacterized protein ORF91	-	Phalaenopsis aphrodite subsp. formosana (Moth orchid)	-	-	-	Chloroplast; Plastid
SRR648707_TR39754_c0_g3_i6_len=3641	NA	NA	NA	NA	NA	-	0	5,664	0,034	5,508	0,882	-0,163	0,763	-0,243	0,319	1,051		-	-	-	-	-	-	-
SRR648707_TR39808_c0_g1_i10_len=2016	ALMT9_ARATH	Q:476-1174,H:134-365	56.65%ID	E:1e-91	Aluminum-activated malate transporter 9	PF11744.5*ALMT*Aluminium activated malate transporter*2-216*E:1.2e-82	0,001	6,577	1	0,131	0,258	-1,05	0,679	-0,412	0,719	0,276	ALMT9_ARATH	Aluminum-activated malate transporter 9 (AtALMT9)	ALMT9 At3g18440 MYF24.16	Arabidopsis thaliana (Mouse-ear cress)	-	-	-	Chloride; Complete proteome; Ion channel; Ion transport; Membrane; Reference proteome; Transmembrane; Transmembrane helix; Transport; Vacuole
SRR924147_TR23104_c0_g1_i7_len=659	NA	NA	NA	NA	NA	-	0	2,54	0,705	-0,186	0,865	-0,144	0,865	-0,115	0,781	0,441		-	-	-	-	-	-	-

Ms8h

Transcript (CDF97)	Uniprot homolog	BLASTX Position	BLASTX %Identity	BLASTX evalue	Uniprot descr	Pfam	PValue_Ms6h	logFC_Ms6h	PValue_Ms8h	logFC_Ms8h	PValue_MsDamaged24h	logFC_MsDamaged24h	PValue_MsIntact24h	logFC_MsIntact24h	PValue_MsTwk	logFC_MsTwk	Entry.name	Protein names	Gene names	Organism	Pathway	Keywords
SRR114633_TR7479_c0_g2_i1_len=507	RER1A_ARATH	Q:292-117,H:26-116	68.48%ID	E:2e-25	Protein RER1A	PF03248.10*Rer1*Rer1 family*27-126*E:6.7e-37	0,113	0,573	0	1,824	0,526	-0,242	0,678	-0,147	0,031	0,874	RER1A_ARATH	Protein RER1A (AtRER1A)	RER1A At4g39220 T22F8.120	Arabidopsis thaliana (Mouse-ear cress)	-	Acetylation; Complete proteome; Membrane; Reference proteome; Transmembrane; Transmembrane helix
SRR114633_TR2604_c0_g1_i1_len=1488	PXN_ARATH	Q:335-1296,H:22-326	73.94%ID	E:8e-160	Peroxisomal nicotinamide adenine dinucleotide carrier	PF00153.24*Mito_carr*Mitochondrial carrier protein*7-90*E:7.9e-17 PF00153.24*Mito_carr*Mitochondrial carrier protein*109-217*E:3.1e-20 PF00153.24*Mito_carr*Mitochondrial carrier protein*228-318*E:1.1e-18	0,298	0,5	0	1,835	0,001	1,616	0,044	1,087	0,255	0,621	PXN_ARATH	Peroxisomal nicotinamide adenine dinucleotide carrier (Peroxisomal NAD carrier) (Peroxisomal membrane protein 38. (PMP38)) (AtPMP38) (Protein ABERRANT PEROXISOME MORPHOLOGY 3) (Solute carrier family 25 member 17)	PXN APEM3 At2g39970 T28M21.13	Arabidopsis thaliana (Mouse-ear cress)	-	-
SRR114633_TR5687_c0_g2_i1_len=2190	ORYA_ORYSJ	Q:1916-639,H:22-444	66.36%ID	E:0	Oryzain alpha chain	PF08246.9*Inhibitor_I29*Cathepsin propeptide inhibitor domain (I29)*116-173*E:1.3e-16 PF00112.20*Peptidase_C1*Papain family cysteine protease*204-419*E:2.2e-84 PF00396.15*Granulin*Granulin*453-499*E:9.6e-11	0,002	0,695	0	1,422	0,002	1,301	0,528	0,327	0,076	-2,996	ORYA_ORYSJ	Oryzain alpha chain (EC 3.4.22.-)	Os04g0650000 LOC_Os04g55650 H0212B02.7 OSJNBb0059K02.8	Oryza sativa subsp. japonica (Rice)	-	Complete proteome; Direct protein sequencing; Disulfide bond; Glycoprotein; Hydrolase; Protease; Reference proteome; Signal; Thiol protease; Zymogen
SRR114633_TR8390_c0_g2_i1_len=3017	LACS7_ARATH	Q:2389-320,H:4-697	75.79%ID	E:0	Long chain acyl-CoA synthetase 7, peroxisomal	PF00501.25*AMP-binding*AMP-binding enzyme*105-550*E:8.5e-109	0,698	0,253	0,000	-1,055	0,521	0,475	0,568	0,044	1	0,57	LACS7_ARATH	Long chain acyl-CoA synthetase 7, peroxisomal (EC 6.2.1.3)	LACS7 At5g27600 F15A18.60	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Lipid metabolism; fatty acid metabolism.	-
SRR114633_TR10084_c0_g2_i1_len=1911	NA	NA	NA	NA	NA	PF10250.6*O-FucT*GDP-fucose protein O-fucosyltransferase*97-379*E:7.9e-24	0,008	0,85	0	1,609	0,411	0,319	0,248	-0,46	0,524	0,229		-	-	-	-	-
SRR114633_TR11177_c0_g1_i1_len=752	NA	NA	NA	NA	NA	-	1	2,971	0	5,782	1	0	1	1,45	1	2,622		-	-	-	-	-
SRR114633_TR15026_c0_g1_i3_len=2476	DHQS_SOLLC	Q:1276-2472,H:40-439	87.25%ID	E:0	3-dehydroquinate synthase, chloroplastic	PF13685.3*Fe-ADH_2*Iron-containing alcohol dehydrogenase*98-318*E:1.8e-11 PF01761.17*DHQ_synthase*3-dehydroquinate synthase*150-408*E:5.4e-106	0,272	0,499	0	2,085	0,378	0,348	0,23	0,464	0,021	1,093	DHQS_SOLLC	3-dehydroquinate synthase, chloroplastic (EC 4.2.3.4)	DHQS AROB Solyc02g083590 LOC544275	Solanum lycopersicum (Tomato) (Lycopersicon esculentum)	PATHWAY: Metabolic intermediate biosynthesis; chorismate biosynthesis; chorismate from D-erythrose-4-phosphate and phosphoenolpyruvate: step 2/7.	Amino-acid biosynthesis; Aromatic amino acid biosynthesis; Chloroplast; Complete proteome; Lyase; Metal-binding; NAD; Plastid; Reference proteome; Transit peptide
SRR114633_TR15043_c0_g1_i2_len=1758	GR82_ORYSJ	Q:682-356,H:61-169	81.65%ID	E:5e-58	Probable phospholipid hydroperoxide glutathione peroxidase	PF00255.16*GSHPx*Glutathione peroxidase*85-141*E:4.5e-16 PF00578.18*AhpC-TSA*AhpC/TSA family*85-141*E:2.7e-08	0,241	0,716	0	1,958	0,705	0,724	0,951	0,066	1	0,765	GPX4_SPICI	Probable phospholipid hydroperoxide glutathione peroxidase (PHGPx) (EC 1.11.1.12)	-	Spinacia oleracea (Spinach)	-	Cytoplasm; Oxidoreductase; Reference proteome
SRR114633_TR15250_c0_g1_i1_len=646	BI1L_ARATH	Q:528-37,H:24-192	68.86%ID	E:2e-66	BI1-like protein	PF10027.17*Bax1-I*Inhibitor of apoptosis-promoting Bax1*61-203*E:2.3e-23	0,064	0,507	0	1,45	0,076	0,483	0,115	0,431	1	-1,548	BI1L_ARATH	BI1-like protein	At4g15470 dl3775w FCAALL.58	Arabidopsis thaliana (Mouse-ear cress)	-	Complete proteome; Membrane; Reference proteome; Transmembrane; Transmembrane helix
SRR114633_TR17118_c0_g1_i1_len=2301	HSP72_SOLLC	Q:2145-208,H:1-644	94.58%ID	E:0	Heat shock cognate 70 kDa protein 2	PF00012.17*HSP70*Hsp70 protein*9-618*E:1.3e-268 PF06723.10*MreB_Mbl*MreB/Mbl protein*127-380*E:8.4e-14	0,161	-0,362	0	5,349	0	-9,168	0	-2,364	0,663	0,476	HSP72_SOLLC	Heat shock cognate 70 kDa protein 2	HSC-2	Solanum lycopersicum (Tomato) (Lycopersicon esculentum)	-	ATP-binding; Complete proteome; Nucleotide-binding; Reference proteome; Stress response
SRR114633_TR17118_c0_g1_i3_len=2377	HSP7C_PETHY	Q:2221-275,H:1-651	93.09%ID	E:0	Heat shock cognate 70 kDa protein	PF00012.17*HSP70*Hsp70 protein*9-618*E:2.2e-268 PF06723.10*MreB_Mbl*MreB/Mbl protein*127-380*E:5.9e-14	0,103	1,723	0	2,461	0,002	1,241	0,006	1,106	1	0,979	HSP7C_PETHY	Heat shock cognate 70 kDa protein	HSP70	Petunia hybrida (Petunia)	-	ATP-binding; Nucleotide-binding; Stress response
SRR114633_TR19576_c0_g1_i1_len=2196	IMA_SOLLC	Q:334-1917,H:1-526	85.82%ID	E:0	Importin subunit alpha	PF01749.17*IBB*Importin beta binding domain*12-94*E:1.5e-22 PF00514.20*Arm*Armadillo/beta-catenin-like repeat*105-145*E:8.4e-11 PF13646.3*HEAT_2*HEAT repeats*118-187*E:3.5e-07 PF13513.3*HEAT_EZ*HEAT-like repeat*130-185*E:5.1e-08 PF00514.20*Arm*Armadillo/beta-catenin-like repeat*147-186*E:1.4e-13 PF02985.19*HEAT*HEAT repeat*160-186*E:0.00018 PF00514.20*Arm*Armadillo/beta-catenin-like repeat*189-230*E:5.4e-07 PF00514.20*Arm*Armadillo/beta-catenin-like repeat*245-270*E:1.8e-07 PF00514.20*Arm*Armadillo/beta-catenin-like repeat*274-312*E:3.8e-09 PF00514.20*Arm*Armadillo/beta-catenin-like repeat*318-356*E:1.7e-09 PF00514.20*Arm*Armadillo/beta-catenin-like repeat*358-397*E:3.4e-13 PF00514.20*Arm*Armadillo/beta-catenin-like repeat*402-439*E:1.4e-06 PF16186.2*Arm_3*Atypical Arm repeat*456-502*E:7e-21	1	-0,036	0,001	1,393	0,481	0,281	0,385	0,043	1	0,283	0,452	IMA_SOLLC	Importin subunit alpha (Karyopherin subunit alpha) (KAP alpha)	-	Solanum lycopersicum (Tomato) (Lycopersicon esculentum)	-	Complete proteome; Cytoplasm; Protein transport; Reference proteome; Repeat; Transport
SRR114633_TR22199_c0_g3_i1_len=1959	STP13_ARATH	Q:266-1822,H:14-526	83.82%ID	E:0	Sugar transport protein 13	PF00083.21*Sugar_tr*Sugar (and other) transporter*29-491*E:5.8e-119 PF07690.13*MFS_1*Major Facilitator Superfamily*77-440*E:1.3e-25	0,267	0,648	0	2,688	0,019	1,555	0,112	1,161	1	-0,349	STP13_ARATH	Sugar transport protein 13 (Hexose transporter 13) (Multicopy suppressor of snf4 deficiency protein 1)	STP13 MSS1 At5g26340 F9D12.17	Arabidopsis thaliana (Mouse-ear cress)	-	Cell membrane; Complete proteome; Membrane; Reference proteome; Sugar transport; Symport; Transmembrane; Transmembrane helix; Transport
SRR114633_TR22975_c0_g1_i1_len=2997	PAO4_ARATH	Q:1771-431,H:48-497	70.07%ID	E:0	Probable polyamine oxidase 4	PF1593.21*Amino_oxidase*Flavin containing amine oxidoreductase*12-416*E:1.1e-81 PF13450.3*NAD_binding_8*NAD(P)-binding Rossmann-like domain*12-58*E:1.5e-05	0,042	0,69	0	1,25	0,312	0,718	0,235	0,838	0,593	-0,646	PAO4_ARATH	Probable polyamine oxidase 4 (AtPAO4) (EC 1.5.3.16) (Amine oxidase 2)	PAO4 At1g65840 F1E22.18	Arabidopsis thaliana (Mouse-ear cress)	-	Complete proteome; Reference proteome
SRR114633_TR23146_c0_g1_i3_len=3060	ACD10_MOUSE	Q:42-1284,H:282-962	47.35%ID	E:0	Acyl-CoA dehydrogenase family member 10	PF16136.20*APH*Phosphotransferase enzyme family*43-278*E:7.5e-41 PF02771.13*Acyl-CoA_dh_N*Acyl-CoA dehydrogenase, N-terminal domain*414-556*E:8.4e-11 PF02770.16*Acyl-CoA_dh_M*Acyl-CoA dehydrogenase, middle domain*561-662*E:5.4e-18 PF00441.21*Acyl-CoA_dh_1*Acyl-CoA dehydrogenase, C-terminal domain*674-733*E:7e-09	1	0,341	0	3,829	0,034	3,617	0,009	4,132	0,62	0,665	ACD10_MOUSE	Acyl-CoA dehydrogenase family member 10 (ACAD-10) (EC 1.3.99.-)	Acad10	Mus musculus (Mouse)	-	Acetylation; Complete proteome; Reference proteome; FAD; Flavoprotein; Oxidoreductase; Reference proteome; FAD; Flavoprotein; Oxidoreductase; Reference proteome
SRR114633_TR25914_c0_g1_i1_len=1846	YIP6_XENTR	Q:775-177,H:55-230	36.67%ID	E:1e-30	Protein YIPF6	PF04893.14*Yip1*Yip1 domain*137-268*E:3.5e-13	0,593	0,681	0	2,811	0,611	0,408	1	0,104	1	-0,078	YIPF6_XENTR	Protein YIPF6 (YIP1 family member 6)	yip16 TGas105o14.1	Xenopus tropicalis (Western clawed frog) (Silurana tropicalis)	-	Complete proteome; Glycoprotein; Membrane; Reference proteome; Transmembrane; Transmembrane helix
SRR114633_TR29750_c0_g1_i1_len=1236	NA	NA	NA	NA	NA	PF02544.13*Steroid_dh*3-oxo-5-alpha-steroid 4-dehydrogenase*132-266*E:2.4e-28 PF06966.9*DUF1295*Protein of unknown function (DUF1295)*133-236*E:2.9e-05	0,691	0,224	0	2,021	0,609	0,304	0,793	0,179	0,407	0,633		-	-	-	-	-
SRR114633_TR30547_c0_g1_i1_len=2085	BH062_ARATH	Q:160-1845,H:1-456	39.72%ID	E:3e-97	Transcription factor bHLH62	PF00010.23*HLH*Helix-loop-helix DNA-binding domain*381-428*E:3.2e-06	0,593	0,603	0	2,877	0,073	2,52	0,01	3,023	1	0,281	BH062_ARATH	Transcription factor bHLH62 (Basic helix-loop-helix protein 62) (AtbHLH62) (bHLH 62) (Transcription factor EN 85) (bHLH transcription factor bHLH062)	BHLH62 EN85 At3g07340 F21O3.5	Arabidopsis thaliana (Mouse-ear cress)	-	Complete proteome; DNA-binding; Nucleus; Reference proteome; Transcription; Transcription regulation
SRR114633_TR33197_c0_g2_i1_len=3093	2A5B_ARATH	Q:1916-441,H:1-492	78.54%ID	E:0	Serine/threonine protein phosphatase 2A 57 kDa regulatory subunit B' beta isoform	PF16063.17*B56*Protein phosphatase 2A regulatory B subunit (B56 family)*74-485*E:8.2e-189	1	0,621	0	7,617	0,502	3,945	1	0,704	1	0	2A5B_ARATH	Serine/threonine protein phosphatase 2A 57 kDa regulatory subunit B' beta isoform (AtB' beta) (PP2A, B' subunit, beta isoform)	B'BETA At3g09880 F8A24.7	Arabidopsis thaliana (Mouse-ear cress)	-	Complete proteome; Reference proteome
SRR114633_TR34904_c0_g1_i1_len=2150	C76B6_CATRO	Q:189-1664,H:6-490	50.61%ID	E:2e-163	Geraniol 8-hydroxylase	PF00067.19*p450*Cytochrome P450*35-484*E:9e-114	1	0,235	0	2,458	0	-1,505	0	-1,446	1	0,236	C76B6_CATRO	Geraniol 8-hydroxylase (EC 1.14.13.152) (Cytochrome P450 76B6) (Geraniol 10-hydroxylase) (CrG10H)	CYP76B6 G10H	Catharanthus roseus (Madagascar periwinkle) (Vinca rosea)	-	Direct protein sequencing; Endoplasmic reticulum; Heme; Iron; Membrane; Metal-binding; Monooxygenase; NADP; Oxidoreductase; Transmembrane; Transmembrane helix
SRR114633_TR35396_c1_g5_i2_len=1933	CLPP_COFAR	Q:1866-1273,H:1-196	97.96%ID	E:6e-134	ATP-dependent Clp protease proteolytic subunit [ECO:0000255]HAMAP-Rule:MF_00444]	PF00574.20*CLP_protease*Clp protease*17-194*E:2.4e-67	0,028	0,801	0	2,117	0,904	0,067	0,753	-0,113	0,004	1,235	CLPP_COFAR	ATP-dependent Clp protease proteolytic subunit (EC 3.4.21.92) (Endopeptidase Clp)	clpP	Coffea arabica (Arabian coffee)	-	Chloroplast; Hydrolase; Plastid; Protease; Serine protease
SRR114633_TR37078_c0_g1_i1_len=1691	CXE18_ARATH	Q:1369-804,H:17-333	57.23%ID	E:7e-129	Probable carboxylesterase 18	PF00135.25*Coesterase*Carboxylesterase family*111-168*E:6.3e-08 PF07859.10*Abhydrolase_3*alpha/beta hydrolase fold*127-348*E:5e-09	0,496	0,406	0	1,704	0,376	0,443	0,053	0,872	1	0,083	CXE18_ARATH	Probable carboxylesterase 18 (AtCXE18) (EC 3.1.1.1)	CXE18 At5g23530 MQM1.21	Arabidopsis thaliana (Mouse-ear cress)	-	Acetylation; Complete proteome; Hydrolase; Reference proteome; Serine esterase
SRR114633_TR1364_c0_g2_i1_len=1646	PUMP5_ARATH	Q:1167-193,H:1-311	76.31%ID	E:8e-153	Mitochondrial uncoupling protein

SRR122238_TR17315_c0_g1_i1_len=978	ISCAP_ARATH	Q:678-304;H:56-180	83.2%ID	E:6e-71	Iron-sulfur assembly protein IscA, chloroplastic	PF01521.1*Fe-S_biosyn*Iron-sulphur cluster biosynthesis*117-219*E:2.5e-21	0,87	0,229	0	2,264	0,049	1,206	1	-0,084	1	-0,046	ISCAP_ARATH	Iron-sulfur assembly protein IscA, chloroplastic (Plastid SufA-like protein) (Protein scaffold protein AtCpIscA)	ISCA.At1g10500 T10D24.11	Arabidopsis thaliana (Mouse-ear cress)	-	-	Chloroplast; Complete proteome; Iron; Iron-sulfur; Metal-binding; Plastid; Reference proteome; Transit peptide
SRR122238_TR22165_c0_g1_i2_len=1106	SRP_VITRI	Q:129-666;H:1-241	65.04%ID	E:2e-89	Stress-related protein	PF0755.9*REP*Rubber elongation factor protein (REP)*60-274*E:4e-92	0,452	0,281	0,001	1,249	0,147	0,489	0,64	-0,177	0,256	0,379	SRP_VITRI	Stress-related protein	SRP	Vitis riparia (Frost grape) (Vitis vulpina)	-	-	Stress response
SRR122238_TR22541_c0_g1_i4_len=1860	NA	NA	NA	NA	NA	-	0,76	0,775	0,001	2,271	0,356	1,253	0,356	1,269	0,461	1,559		-	-	-	-	-	
SRR122238_TR23102_c0_g1_i5_len=1620	LEU1A_SOLPN	Q:209-1507;H:23-454	85.22%ID	E:0	2-isopropylmalate synthase A	PF00682.16*HMGL-like*HMGL-like*73-352*E:6.6e-92	0,174	-0,56	0	2,632	0,547	-0,339	0,317	0,541	0,145	0,512	LEU1A_SOLPN	2-isopropylmalate synthase A (EC 2.3.3.13) (Alpha-IPM synthase A) (Alpha-isopropylmalate synthase A)	IPMSA	Solanum pennellii (Tomato) (Lycopersicon pennellii)	PATHWAY: Amino-acid biosynthesis; Leucine biosynthesis; Leucine from 3-methyl-2-oxobutanoate: step 1/4.		Amino-acid biosynthesis; Branched-chain amino acid biosynthesis; Leucine biosynthesis; Transferase
SRR122238_TR23144_c0_g2_i1_len=965	DNAJ8_ARATH	Q:483-1537;H:55-162	69.09%ID	E:2e-35	Chaperone protein dnaJ 8, chloroplastic	PF00226.28*DnaJ*DnaJ domain*43-96*E:3.5e-15	0,326	-0,329	0	9,182	1	-1,482	1	-1,482	0,006	0,908	DNAJ8_ARATH	Chaperone protein dnaJ 8, chloroplastic (AtDjC8) (AtJ8)	ATJ8 C8 J8 At1g80920 F23A5.28	Arabidopsis thaliana (Mouse-ear cress)	-	-	Chaperone; Chloroplast; Complete proteome; Plastid; Reference proteome; Transit peptide
SRR122238_TR29113_c0_g1_i2_len=1378	NA	NA	NA	NA	NA	PF06232.8*ATS3*Embryo-specific protein 3, (ATS3)*43-161*E:7.4e-53	0,618	0,279	0,001	2,283	1	0,218	1	0,119	0,166	0,779		-	-	-	-	-	
SRR122238_TR29256_c0_g1_i1_len=1272	RL5_CUCSA	Q:75-923;H:1-283	85.51%ID	E:1e-157	60S ribosomal protein L5	PF17144.1*Ribosomal_L5e*Ribosomal large subunit proteins 60S L5, and 50S L18*14-175*E:3.4e-83*PF14204.3*Ribosomal_L18_c*Ribosomal 18 C-terminal region*192-280*E:2.5e-26	1	-0,087	1	-0,046	0,404	-0,187	RL5_CUCSA	60S ribosomal protein L5	RPL5	Cucumis sativus (Cucumber)	-	-	RNA-binding; Ribonucleoprotein; Ribosomal protein; rRNA-binding
SRR122238_TR29998_c0_g2_i2_len=1776	UG76_CATRO	Q:74-1534;H:1-487	99.59%ID	E:0	7-deoxyloganetin glucosyltransferase	PF03201.15*UDPGT*UDP-glucuronosyl and UDP-glucosyl transferase*97-447*E:3.6e-30	0,066	4,062	0	7,142	0,129	3,661	0,502	2,764	1	0,509	UG76_CATRO	7-deoxyloganetin glucosyltransferase (EC 2.4.1.324) (Iridoid 1-O-glucosyltransferase) (UDP-glucose glucosyltransferase 6) (CrUGT6) (UDP-glycosyltransferase 85A23)	UGT85A23 UGT6	Catharanthus roseus (Madagascar periwinkle) (Vinca rosea)	-	-	Transferase
SRR122238_TR30997_c0_g2_i2_len=2686	SFH8_ARATH	Q:2340-484;H:1-620	76%ID	E:0	Phosphatidylinositol/phosphatidylcholine transfer protein SFH8	PF03765.12*CRAL_TRIO_N*CRAL/TRIO, N-terminal domain*108-131*E:1.3e-05 PF00650.17*CRAL_TRIO*CRAL/TRIO domain*155-321*E:8e-34	0,154	0,459	0	1,418	0,037	0,672	0,037	0,661	0,108	-0,612	SFH8_ARATH	Phosphatidylinositol/phosphatidylcholine transfer protein SFH8 (Protein SEC FOURTEEN HOMOLOGS 8) (AtSFH8)	SFH8 At2g21520 F3K23.28	Arabidopsis thaliana (Mouse-ear cress)	-	-	Chloroplast; Complete proteome; Membrane; Reference proteome; Transfer complex
SRR122238_TR34562_c0_g2_i2_len=1584	IDH1_ARATH	Q:1420-290;H:1-367	84.88%ID	E:0	Isocitrate dehydrogenase [NAD] regulatory subunit 1, mitochondrial	PF00180.17*Iso_dh*Isocitrate/isopropylmalate dehydrogenase*50-372*E:2.3e-78	0,921	-0,088	0	1,382	0,415	0,357	0,601	0,242	0,666	-0,347	IDH1_ARATH	Isocitrate dehydrogenase [NAD] regulatory subunit 1, mitochondrial (EC 1.1.1.41) (IDH-I) (Isocitric dehydrogenase 1) (NAD(+)-specific ICDH 1)	IDH1 At4g35260 F23E12.180	Arabidopsis thaliana (Mouse-ear cress)	-	-	Complete proteome; Magnesium; Manganese; Metal-binding; Mitochondrion; NAD; Oxidoreductase; Reference proteome; Transit peptide; Tricarboxylic acid cycle
SRR122238_TR35386_c0_g1_i18_len=2319	2AAB_ARATH	Q:265-2025;H:1-687	94.38%ID	E:0	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform	PF02985.19*HEAT*HEAT repeat*242-270*E:0.00019 PF13646.3*HEAT_2*HEAT repeats*361-461*E:2.2e-11 PF02985.19*HEAT*HEAT repeat*440-465*E:0.0027	0,756	-0,13	0	1,707	0,732	0,147	0,613	0,2	0,048	0,685	2AAB_ARATH	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform (A6A beta) (PP2A, subunit A, beta isoform)	PP2AA2 DF1 At3g25800 K13N2.14	Arabidopsis thaliana (Mouse-ear cress)	-	-	Acetylation; Alternative splicing; Complete proteome; Reference proteome; Repeat
SRR122238_TR35731_c0_g1_i3_len=604	CD48D_ARATH	Q:505-47;H:1-153	91.5%ID	E:6e-95	Cell division control protein 48 homolog D	PF02359.15*CDC48_N*Cell division protein 48 (CDC48), N-terminal domain*63-144*E:3.6e-24	0,955	-0,032	0	1,901	0,744	0,113	0,744	0,122	0,019	0,834	CD48D_ARATH	Cell division control protein 48 homolog D (AtCDC48d) (Transitional endoplasmic reticulum ATPase D)	CDC48D At3g53230 T4D2.160	Arabidopsis thaliana (Mouse-ear cress)	-	-	ATP-binding; Acetylation; Cell cycle; Cell division; Complete proteome; Cytoplasm; Cytoskeleton; Nucleotide-binding; Nucleus; Phosphoprotein; Protein transport; Reference proteome; Repeat; Transport; Ubl conjugation
SRR122238_TR36321_c1_g2_i1_len=724	ADF5_ARATH	Q:582-154;H:1-143	86.71%ID	E:2e-86	Actin-depolymerizing factor 5	PF00241.17*Cofilin_ADF*Cofilin/tropomyosin-type actin-binding protein*65-187*E:4.2e-32	0,407	-0,468	0	2,836	1	-0,02	0,623	-0,342	1	1,139	ADF5_ARATH	Actin-depolymerizing factor 5 (ADF-5) (AtADF5)	ADF5 At2g16700 T24I21.11	Arabidopsis thaliana (Mouse-ear cress)	-	-	Actin-binding; Alternative splicing; Complete proteome; Reference proteome
SRR122238_TR36833_c0_g1_i6_len=949	VATO2_ARATH	Q:828-304;H:4-178	90.86%ID	E:2e-87	V-type proton ATPase subunit c''2	PF00137.18*ATP-synt_C*ATP synthase subunit C*23-82*E:6.1e-15 PF00137.18*ATP-synt_C*ATP synthase subunit C*107-166*E:4.5e-10	0,886	0,049	0	7,143	1	-0,217	1	-1,113	0,462	-0,204	VATO2_ARATH	V-type proton ATPase subunit c''2 (V-ATPase subunit c''2) (Vacuolar H(+)-ATPase subunit c'' isoform 2) (Vacuolar proton pump subunit c''2)	VHAc''2 VMA16 At2g25610 F3N11.6	Arabidopsis thaliana (Mouse-ear cress)	-	-	Complete proteome; Endoplasmic reticulum; Golgi apparatus; Hydrogen ion transport; Ion transport; Membrane; Reference proteome; Transmembrane; Transmembrane helix; Transport
SRR122238_TR37722_c0_g1_i2_len=1208	IF4E3_WHEAT	Q:881-324;H:48-232	84.41%ID	E:1e-114	Eukaryotic translation initiation factor NCBP	PF10652.15*IF4E*Eukaryotic initiation factor 4E*58-217*E:1.3e-51	0,129	5,063	0	7,775	0,117	5,915	1	0	0,154	0,818	IF4E3_WHEAT	Eukaryotic translation initiation factor NCBP (Novel cap-binding protein) (nCBP) (mRNA cap-binding protein)	NCBP	Triticum aestivum (Wheat)	-	-	Complete proteome; Initiation factor; Protein biosynthesis; RNA-binding; Reference proteome; Translation regulation
SRR122238_TR41245_c1_g2_i13_len=2585	NA	NA	NA	NA	NA	-	0,694	0,36	0	7,096	1	-0,307	1	0,239	1	-0,021		-	-	-	-	-	
SRR122238_TR41386_c0_g1_i2_len=1936	TAL_RENSM	Q:442-1485;H:12-366	50.42%ID	E:1e-96	Transaldolase (ECO:0000025)HAMAP-Rule:MF_00493)	PF00923.16*Transaldolase*Transaldolase*110-433*E:2.5e-78	0,962	-0,029	0	1,398	0,072	0,599	0,035	0,686	0,234	0,421	TAL_RENSM	Transaldolase (EC 2.2.1.2)	tal RSal33209_2247	Reniibacterium salminiinarum (strain ATCC 33209 / DSM 20767 / JCM 11484 / NBRC 15589 / NCIMB 2235)	PATHWAY: Carbohydrate degradation; pentose phosphate pathway; D-glyceraldehyde 3-phosphate and beta-D-fructose 6-phosphate from D-fructose 6-phosphate and D-xylulose 5-phosphate (non-oxidative stage): step 2/3. [ECO:0000255]HAMAP-Rule:MF_00493;		Complete proteome; Cytoplasm; Pentose shunt; Reference proteome; Schiff base; Transferase
SRR122238_TR42679_c0_g1_i1_len=751	ERG3_ORYSJ	Q:10-543;H:1-144	66.21%ID	E:9e-61	Elicitor-responsive protein 3	PF01168.27*C2*C2 domain*4-104*E:4.5e-21	0,025	1,467	0	3,338	0,004	2,1	0,059	1,561	1	-0,192	ERG3_ORYSJ	Elicitor-responsive protein 3 (16 kDa phloem protein) (RPP16)	ERG3 Os04g0531100 LOC_Os04g44870 OsJ_01949 OSJNBa0081C01.13	Oryza sativa subsp. japonica (Rice)	-	-	Complete proteome; Reference proteome
SRR122238_TR43809_c0_g1_i1_len=832	SDF2_ARATH	Q:141-536;H:8-215	78.79%ID	E:5e-74	Stromal cell-derived factor 2-like protein	PF02815.16*MIR*MIR domain*3-81*E:4.4e-06	0,524	-0,623	0,001	5,911	1	-0,017	1	-0,456	0,438	-0,398	SDF2_ARATH	Stromal cell-derived factor 2-like protein (AtSDF2) (SDF2-like protein)	SDF2 At2g25110 F13D4.70	Arabidopsis thaliana (Mouse-ear cress)	-	-	3D-structure; Complete proteome; Endoplasmic reticulum; Glycoprotein; Plant defense; Reference proteome; Repeat; Signal
SRR122238_TR45965_c0_g1_i1_len=1251	NA	NA	NA	NA	NA	-	0,226	1,862	0	2,253	0,03	1,051	0,002	1,386	1	0,123		-	-	-	-	-	
SRR122238_TR47400_c1_g1_i2_len=1835	C72A1_CATRO	Q:106-1674;H:1-523	97.13%ID	E:0	Secologanin synthase	PF00067.19*p450*Cytochrome P450*90-497*E:3.1e-87	0,037	0,668	0	2,033	0,819	-0,16	0,329	-0,546	0,427	0,27	C72A1_CATRO	Secologanin synthase (SLS) (EC 1.3.3.9) (CYPLXXII) (Cytochrome P450 72A1)	CYP72A1 CYP72 P450CR3	Catharanthus roseus (Madagascar periwinkle) (Vinca rosea)	PATHWAY: Alkaloid biosynthesis; secologanin biosynthesis.		Alkaloid metabolism; Heme; Iron; Membrane; Metal-binding; Monooxygenase; NADP; Oxidoreductase; Transferase; Transmembrane; Transmembrane helix; Vacuole
SRR122238_TR47649_c1_g1_i4_len=1154	NA	NA	NA	NA	NA	-	0,352	0,267	0	1,476	0,031	0,655	0,01	0,772	0,195	-0,344		-	-	-	-	-	
SRR122238_TR50801_c0_g2_i2_len=1006	TOM20_SOLTU	Q:122-703;H:1-192	73.71%ID	E:9e-92	Mitochondrial import receptor subunit TOM20	PF06552.9*TOM20_plant*Plant specific mitochondrial import receptor subunit TOM20*7-193*E:1.7e-94	1	-0,015	0,001	0,956	0,034	0,68	0,093	0,558	0,902	-0,048	TOM20_SOLTU	Mitochondrial import receptor subunit TOM20 (Translocase of outer membrane 20 kDa subunit)	TOM20	Solanum tuberosum (Potato)	-	-	Complete proteome; Direct protein sequencing; Membrane; Mitochondrion; Mitochondrion outer membrane; Protein transport; Reference proteome; TPR repeat; Transmembrane; Transmembrane helix; Transport
SRR122238_TR54170_c2_g7_i6_len=1422	LEA14_SOYBN	Q:167-6113;H:4-152	72.48%ID	E:5e-72	Desiccation protectant protein Lea14 homolog	PF03168.10*LEA_2*Late embryogenesis abundant protein*96-192*E:5.4e-18	0,692	0,595	0	3,458	0,133	1,13	0,187	1,04	0,708	0,175	LEA14_SOYBN	Desiccation protectant protein Lea14 homolog	-	Glycine max (Soybean) (Glycine hispida)	-	-	Complete proteome; Reference proteome
SRR122238_TR57409_c0_g2_i1_len=939	NA	NA	NA	NA	NA	-	0,56	0,861	0	2,855	0,471	0,569	0,707	0,441	1	0,54		-	-	-	-	-	
SRR122238_TR57866_c0_g2_i1_len=3327	CDKF4_ORYSJ	Q:1072-1833;H:1-252	71.09%ID	E:2e-117	Cyclin-dependent kinase F-4	PF00069.22*Pkinase*Protein kinase domain*4-203*E:1.6e-67 PF07714.14*Pkinase_Tyr*Protein tyrosine kinase*6-195*E:3.1e-38	0,081	0,689	0	1,589	0,859	0,074	0,683	0,145	0,006	1,348	CDKF4_ORYSJ	Cyclin-dependent kinase F-4 (CDKF;4) (EC 2.7.11.22) (EC 2.7.11.23) (Serine/threonine-protein kinase MHK-like protein 2)	CDKF-4 Os02g0700600 LOC_Os02g47220 OJ1111_E07.13-1 P0459B01.42-1	Oryza sativa subsp. japonica (Rice)	-	-	ATP-binding; Complete proteome; Kinase; Nucleotide-binding; Phosphoprotein; Reference proteome; Serine/threonine-protein kinase; Transferase
SRR122238_TR59227_c0_g2_i1_len=725	NDBAA_ARATH	Q:132-401;H:10-99	88.89%ID	E:2e-52	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10-A	PF00069.22*Pkinase*Protein kinase domain*13-53*E:2.1e-05	0,803	-0,1	0	1,266	0,336	0,328	0,255	0,389	0,742	0,108	NDBAA_ARATH	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10-A	At1g49140 F27J15.9	Arabidopsis thaliana (Mouse-ear cress)	-	-	Complete proteome; Electron transport; Membrane; Mitochondrion; Mitochondrion inner membrane; Reference proteome; Respiratory chain; Transport
SRR122238_TR61114_c0_g1_i1_len=2620	AROC2_SOLLC	Q:102-1166;H:34-388	88.17%ID	E:0	Chorismate synthase 2, chloroplastic	PF01264.18*Chorismate_synt*Chorismate synthase*57-387*E:8.5e-132	0,545	0,46	0,001	1,909	0,298	0,589	0,034	1,039	1	-0,002	AROC2_SOLLC	Chorismate synthase 2, chloroplastic (EC 4.2.3.5) (5-enolpyruvylshikimate-3-phosphate phospholyase 2)	CS2	Solanum lycopersicum (Tomato) (Lycopersicon esculentum)	PATHWAY: Metabolic intermediate biosynthesis; chorismate biosynthesis; chorismate	Amino-acid biosynthesis	Amino-acid biosynthesis; Aromatic amino acid biosynthesis; Chloroplast; Complete proteome; Lyase; Plastid; Reference proteome; Transit peptide
SRR122238_TR65674_c0_g1_i3_len=1260	FK126_ARATH	Q:1222-149;H:1-359	48.07%ID	E:3e-108	F-box/kelch-repeat protein At1g15670	PF03069.20*FBOX*F-box domain*16-68*E:0.0011 PF13964.3*Kelch_6*Kelch motif*119-168*E:1.3e-07 PF01344.22*Kelch_1*Kelch motif*125-165*E:1e-05 PF01344.22*Kelch_1*Kelch motif*179-214*E:8e-08	1	-0,01	0	3,563	0,017	-4,193	0,017	-4,342	0,153	0,69	FK126_ARATH	F-box/kelch-repeat protein At1g15670	At1g15670 F7H2.1	Arabidopsis thaliana (Mouse-ear cress)	-	-	Complete proteome; Kelch repeat; Reference proteome; Repeat
SRR122238_TR67135_c0_g2_i1_len=3431	SND1_HUMAN	Q:3321-442;H:21-602	34.7%ID	E:3e-147	Staphylococcal nuclease domain-containing protein 1	PF00565.14*Snase*Staphylococcal nuclease homologue*636-753*E:3.2e-13 PF00567.21*TUDOR*Tudor domain*753-876*E:7.8e-21 PF00565.14*Snase*Staphylococcal nuclease homologue*884-988*E:9.4e-08	0,626	-0,223	0	1,513	1	-0,081	0,77	-0,228	1	-0,377	SND1_HUMAN	Staphylococcal nuclease domain-containing protein 1 (100 kDa coactivator) (EBNA2 coactivator p100) (Tudor domain-containing protein 11) (p100 co-activator)	SND1 TDRD11	Homo sapiens (Human)	-	-	3D-structure; Activation; Complete proteome; Cytoplasm; Direct protein sequencing; Nostrovirus interaction; Nucleus; Phosphoprotein; Reference proteome; Repeat; Transcription; Transcription regulation
SRR122238_TR68263_c1_g1_i1_len=1439	NA	NA	NA	NA	NA	PF00076.19*RRM_1*RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)*74-6*E:1.5e-08	0,254	4,746	0	6,665	1	0	1	0	1	-3,406		-	-	-	-	-	
SRR122238_TR73330_c1_g1_i2_len=557	UBQ11_ARATH	Q:1-555;H:34-218	100%ID	E:1e-129	Polyubiquitin 11	PF00240.20*ubiquitin*Ubiquitin family*1-141*E:3.3e-17 PF11976.5*Rad60-SLD*Ubiquitin-2 like Rad60 SUMO-like*44-114*E:3.7e-16 PF00240.20*ubiquitin*Ubiquitin family*46-117*E:5.4e-34 PF13881.3*Rad60-SLD_2*Ubiquitin-2 like Rad60 SUMO-like*53-114*E:0.062 PF14560.3*Ubiquitin_2*Ubiquitin-like domain*55-112*E:0.00024 PF11976.5*Rad60-SLD*Ubiquitin-2 like Rad60 SUMO-like*120-185*E:3.9e-14 PF00240.20*ubiquitin*Ubiquitin family*122-185*E:2.3e-29 PF14560.3*Ubiquitin_2*Ubiquitin-like domain*131-180*E:0.0032	0,857	0,063	0	1,405	0,725	0,125	0,905	0,048	0,008	1,019	UBQ11_ARATH	Polyubiquitin 11 [Cleaved into: Ubiquitin]	UBQ11 At4g05050 C17L7.6 T32N4.13	Arabidopsis thaliana (Mouse-ear cress)	-	-	Alternative splicing; Complete proteome; Cytoplasm; Isopeptide bond; Nucleus; Reference proteome; Repeat; Ubl conjugation; Ubl conjugation pathway
SRR122238_TR74772_c1_g1_i2_len=983	SRP14_ARATH	Q:121-462;H:1-114	74.56%ID	E:3e-45	Signal recognition particle 14 kDa protein	PF02290.12*SRP14*Signal recognition particle, 14kD protein*4-93*E:3e-26	1	0	0	7,787	1	0	0	0,444	-0,484	SRP14_ARATH	Signal recognition particle 14 kDa protein (SRP14)	SRP14 At2g43640 F18O19.25	Arabidopsis thaliana (Mouse-ear cress)	-	-	Alternative splicing; Complete proteome; Cytoplasm; RNA-binding; Reference proteome; Ribonucleoprotein; Signal recognition particle
SRR122238_TR76412_c0_g1_i2_len=1501	NA	NA	NA	NA	NA	PF02341.12*RcbX*RbcX protein*98-198*E:2.2e-18	0,109	1,11	0	1,882	0,29	0,243	0,803	0,059	0,73	0,138		-	-	-	-	-	
SRR122238_TR78053_c0_g1_i2_len=996	NA	NA	NA	NA	NA	PF06364.9*DUF1068*Protein of unknown function (DUF1068)*10-174*E:2.2e-64	0,626	0,23	0	7,591	1	0	1	0,508	0,581	-0,449		-	-	-	-	-	
SRR122238_TR79862_c0_g3_i1_len=765	SNAK2_SOLTU	Q:581-333;H:22-104	68.67%ID	E:2e-33	Snakin-2	PF20704.11*GASA*Gibberellin regulated protein*49-108*E:2.1e-21	0,629	1,675	0	3,547	0,76	0,458	0,282	1,042	0,732	-0,631	SNAK2_SOLTU	Snakin-2	SN2	Solanum tuberosum (Potato)	-	-	Antimicrobial; Cell wall; Complete proteome; Direct protein sequencing; Disulfide bond; Plant defense; Reference proteome; Secreted; Signal
SRR122238_TR79977_c0_g1_i1_len=851	DNJ11_ARATH	Q:375-285;H:65-161	67.35%ID	E:5e-38	Chaperone protein dnaJ 11, chloroplastic	PF00226.28*DnaJ*DnaJ domain*94-157*E:1.9e-21	0,08	1,109	0	1,759	0,704	-0,179	0,051	-0,89	1	0,08	DNJ11_ARATH	Chaperone protein dnaJ 11, chloroplastic (AtDjC11) (AtJ11)	ATJ11 C11 J11 At4g36040 T19K4.170	Arabidopsis thaliana (Mouse-ear cress)	-	-	Chaperone; Chloroplast; Complete proteome; Direct protein sequencing; Plastid; Reference proteome; Transit peptide
SRR122238_TR79291_c1_g2_i2_len=2169	PIF4_ARATH	Q:146-1603;H:6-413	33.27%ID	E:8e-46	Transcription factor PIF4	PF03010.23*HLH*Helix-loop-helix DNA-binding domain*326-372*E:2e-13	0,025	0,61	0	1,645	0,054	0,536	0,003	0,801	0,234	-0,475	PIF4_ARATH	Transcription factor PIF4 (Basic helix-loop-helix protein 9) (bHLH9) (bHLH 9) (Phytochrome-interacting factor 4) (Short under red-light 2) (Transcription factor EN 102) (bHLH transcription factor bHLH009)	PIF4 BHLH9 EN102 SRL2 At2g43010 MFL8.13	Arabidopsis thaliana (Mouse-ear cress)	-	-	Alternative splicing; Complete proteome; DNA-binding; Nucleus; Phytochrome signaling pathway; Reference proteome; Transcription; Transcription regulation
SRR122238_TR79711_c1_g2_i1_len=1153	SERA1_ARATH	Q:59-946;H:308-603	86.15%ID	E:3e-160	D-3-phosphoglycerate dehydrogenase 1, chloroplastic	PF02826.16*2-Hacid_dh_C*D-isomer specific 2-hydroxyacid dehydrogenase, NAD binding domain*7-38*E:1.7e-07 PF01842.22*ACT*ACT domain*229-289*E:2e-07	0,183	0,392	0	2,912	0,011	0,86	0,17	0,5	0,031	-0,629	SERA1_ARATH	D-3-phosphoglycerate dehydrogenase 1, chloroplastic (EC 1.1.1.95) (Protein EMBRYO SAC DEVELOPMENT ARREST 9)	PGDH1 EDA9 At4g34200 F10M10.7	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Amino-acid biosynthesis; L-serine biosynthesis; L-serine from 3-phosphoglycerate: step 1/3.		Chloroplast; Complete proteome; NAD; Oxidoreductase; Plastid; Reference proteome; Transit peptide
SRR122238_TR80349_c0_g1_i1_len=2880	NA	NA	NA	NA	NA	-	0,333	0,636	0	1,82	0,121	0,514	0,108	0,518	0,031	1,392		-	-	-	-	-	
SRR122238_TR81963_c0_g1_i1_len=1197	KAI2_ARATH	Q:1029-229;H:1-267	79.78%ID	E:7e-161	Probable esterase KAI2	PF12146.5*Hydrolase_4*Serine aminopeptidase, S33*17-124*E:1.4e-07 PF00561.17*Abhydrolase_1*alpha/beta hydrolase fold*19-156*E:2.4e-11 PF12697.4*Abhydrolase_6*Alpha/beta hydrolase family*20-257*E:2e-11	0,76	0,443	0	3,634	1	-0,145	0,132	-2,334	0,732	0,695	KAI2_ARATH	Probable esterase KAI2 (Protein DWARF-14-like) (Protein D14-like) (Protein HYPOSENSITIVE TO LIGHT) (Protein KARRIKIN INSENSITIVE 2)	KAI2 D14L HTL At4g37470 F6G17.120	Arabidopsis thaliana (Mouse-ear cress)	-	-	3D-structure; Complete proteome; Cytoplasm; Hydrolase; Nucleus; Reference proteome
SRR122238_TR85786_c0_g1_i1_len=1017	NA	NA	NA	NA	NA	-	1	3,673	0	8,31	0,254	4,721	0,502	4,255	1	0		-	-	-	-	-	
SRR122238_TR86442_c0_g1_i1_len=609	NA	NA	NA	NA	NA	-	0,533	0,25	0,001	1,088	0,936	0,032	0,804	-0,079	0,015	0,765		-	-	-	-	-	
SRR122238_TR89533_c0_g1_i1_len=804	NA	NA	NA	NA	NA	-	1	-0,207	0	4,603	0,005	4,918	0,017	4,506	1	0,123		-	-	-	-	-	
SRR122238_TR90465_c0_g1_i6_len=2093	ACOX4_ARATH	Q:1941-754;H:1-396	80.05%ID	E:0	Acyl-coenzyme A oxidase 4, peroxisomal	PF07771.13*Acyl-CoA_dh_N*Acyl-CoA dehydrogenase, N-terminal domain*56-165*E:2e-23 PF02770.16*Acyl-CoA_dh_M*Acyl-CoA dehydrogenase, middle domain*171-263*E:9.5e-23 PF00441.21*Acyl-CoA_dh_1*Acyl-CoA dehydrogenase, C-terminal domain*280-398*E:7.8e-22	0,189	1,699	0	7,46	0,132	2,206	0,132	2,353	1	-0,201	ACOX4_ARATH	Acyl-coenzyme A oxidase 4, peroxisomal (AOX 4) (EC 1.3.3.6) (G6p) (Short-chain acyl-CoA oxidase) (AtCX4) (AtG6) (SAOX)	ACX4 G6 At3g51840 ATEM1.9	Arabidopsis thaliana (Mouse-ear cress)	-	-	3D-structure; Activation; Complete proteome; Cytoplasm; FAD; Fatty acid metabolism; Flavoprotein; Glycoprotein; Lipid metabolism; Oxidoreductase; Peroxisome; Reference proteome
SRR121857_TR3205_c1_g5_i1_len=996	TBA2_GOSHI	Q:783-457;H:1-109	94.5%ID	E:9e-113	Tubulin alpha-2 chain	PF00091.22*Tubulin*Tubulin/FtsZ family, GTPase domain*3-111*E:7.6e-29	0,662	0,115	0	2,17	0,707	0,34	0,044	1,174	1	1,76	TBA2_GOSHI	Tubulin alpha-2 chain (Alpha-2-tubulin)	-	Gossypium hirsutum (Upland cotton) (Gossypium mexicanum)	-	-	Acetylation; Cytoplasm; Cytoskeleton; GTP-binding; Microtubule; Nucleotide-binding
SRR121857_TR3504_c0_g1_i3_len=1075	RL71_ARATH	Q:95-829;H:1-247	55.87%ID	E:5e-86	60S ribosomal protein L7-1	PF00879.9*Ribosomal_L30_N*Ribosomal L30 N-terminal domain*13-75*E:1.4e-09 PF00327.17*Ribosomal_L30*Ribosomal protein L30p/L7e*97-137*E:1.3e-17	0,044	-0,628	0	6,476	1	-2,34	1	0,979	0,753	-0,112	RL71_ARATH	60S ribosomal protein L7-1	RPL7A At1g80750 F23A5.10	Arabidopsis thaliana (Mouse-ear cress)	-	-	Complete proteome; Reference proteome; Ribonucleoprotein; Ribosomal protein
SRR121857_TR3680_c3_g1_i1_len=987	UBIQP_AVEFA	Q:95-985;H:1-297	100%ID	E:0	Polyubiquitin	PF11976.5*Rad60-SLD*Ubiquitin-2 like Rad60 SUMO-like*25-95*E:4.9e-16 PF00240.20*ubiquitin*Ubiquitin family*27-98*E:7.1e-34 PF13881.3*Rad60-SLD_2*Ubiquitin-2 like Rad60 SUMO-like*35-95*E:0.08 PF14560.3*Ubiquitin_2*Ubiquitin-like domain*32-100*E:0.0037 PF00240.20*ubiquitin*Ubiquitin family*34-103*E:1.6e-33 PF13881.3*Rad60-SLD_2*Ubiquitin-2 like Rad60 SUMO-like*41-102*E:0.14 PF11976.5*Rad60-SLD*Ubiquitin-2 like Rad60 SUMO-like*108-178*E:1.1e-15 PF00240.20*ubiquitin*Ubiquitin family*110-181*E:1.6e-33 PF14560.3*Ubiquitin_2*Ubiquitin-like domain*119-176*E:0.00069 PF13881.3*Rad60-SLD_2*Ubiquitin-2 like Rad60 SUMO-like*120-178*E:0.16 PF11976.5*Rad60-SLD*Ubiquitin-2 like Rad60 SUMO-like*184-254*E:1.1e-15 PF00240.20*ubiquitin*Ubiquitin family*186-257*E:1.6e-33 PF14560.3*Ubiquitin_2*Ubiquitin-like domain*195-252*E:0.00069 PF13881.3*Rad60-SLD_2*Ubiquitin-2 like Rad60 SUMO-like*198-254*E:0.16 PF11976.5*Rad60-SLD*Ubiquitin-2 like Rad60 SUMO-like*260-320*E:8e-15 PF00240.20*ubiquitin*Ubiquitin family*262-328*E:4.3e-31 PF14560.3*Ubiquitin_2*Ubiquitin-like domain*271-327*E:0.0011	0,55	0,129	0	1,334	0,023	0,486	0,193	0,28	0,023	0,5	UBIQP_AVEFA	Polyubiquitin [Cleaved into: Ubiquitin]	Avena fatua (Wild oats)	-	-	Cytoplasm; Isopeptide bond; Nucleus; Repeat; Ubl conjugation
SRR121857_TR7086_c0_g2_i1_len=2109	GAT1_ARATH	Q:110-1444;H:4-451	60.49%ID	E:0	GABA transporter 1	PF01490.15*Aa_trans*Transmembrane amino acid transporter protein*38-445*E:5.2e-64	0,502	1,768	0	5,424	0,066	4,588	0,502	3,137	1	0,304	GAT1_ARATH	GABA transporter 1 (AtGAT1) (Bidirectional amino acid transporter 1)	GAT1 BAT1 At1g08230 T23G18.9	Arabidopsis thaliana (Mouse-ear cress)	-	-	Amino-acid transport; Cell membrane; Complete proteome; Membrane; Reference proteome; Transmembrane; Transmembrane helix; Transport
SRR121857_TR8549_c0_g2_i1_len=1927	P2C44_ORYSJ	Q:583-1431;H:37-319	78.95%ID	E:2e-153	Probable protein phosphatase 2C 44	PF00481.18*PP2C*Protein phosphatase 2C*58-286*E:2.8e-56

SRR1271858_TR40310_c0_g1_i1_len=2097	PLAT1_ARATH	2340.H47:671	90.49%ID	E0	Phosphosulfolipid synthase 1 (PSL1)	acyltransferase*473:630*E:9.9e-19	0.305	0.01	0	2.72	0.012	0.31	0.352	0.101	0.401	0.352 PLAT1_ARATH	Phosphosulfolipid synthase 1 (PSL1) (EC 4.2.1.158)	T6I14.2	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Glycerolipid metabolism, Glycerophospholipids.	Glycerolipids; Lipid metabolism; Membrane; Reference proteome; Transferase; Transmembrane; Transmembrane helix
SRR1271858_TR32130_c0_g1_i1_len=748	CB12_SOLLC	Q:32-694.H:46-266	91.4%ID	E1e-148	Chlorophyll a-b binding protein 7, chloroplastic	PF00504.18*Chloroa_b-bind*Chlorophyll A-B binding protein*39-205*E:6.8e-52	0	-6.679	0	7.321	0.001	-6.538	0.352	-1.041	1	0.048 CB12_SOLLC	Chlorophyll a-b binding protein 7, chloroplastic (LHCI type II CAB-7)	CAB7	Solanum lycopersicum (Tomato) Lycopersicon esculentum)		Chlorophyll; Chloroplast; Chromosome; Cytoplasm; Cytoskeleton; Nucleus; Plastid; Reference proteome; Thylakoid; Transit peptide; Transmembrane; Transmembrane helix
SRR1271858_TR34670_c0_g1_i3_len=1808	METK3_CATRO	Q:1588-819,H:1-390	99.49%ID	E0	S-adenosylmethionine synthase 3	PF00438.17*S-AdoMet_synt*S-adenosylmethionine synthase, N-terminal domain*4-101*E:1.5e-42*PF02772.13*S-AdoMet_synt_M*S-adenosylmethionine synthetase, central domain*117-238*E:6.3e-47*PF02773.13*S-AdoMet_synt_C*S-adenosylmethionine synthetase, C-terminal domain*240-381*E:8.8e-43	0.92	-0.044	0.001	1.086	0.221	-0.369	0.166	-0.421	0.152	-0.431 METK3_CATRO	S-adenosylmethionine synthase 3 (AdoMet synthase 3) (EC 2.5.1.6) (Methionine adenosyltransferase 3) (MAT 3)	SAM53		PATHWAY: Amino-acid biosynthesis; Sadenosyl-L-methionine biosynthesis; S-adenosyl-L-methionine from L-methionine: step 1/1.	ATP-binding; Cobalt; Cytoplasm; Magnesium; Manganese; Metal-binding; Nucleotide-binding; One-carbon metabolism; Polassium; Transferase
SRR1271858_TR36855_c0_g1_i1_len=1654	TRPB_CAMAC	Q:1-1654	93.84%ID	E0	Tryptophan synthase beta chain 2, chloroplastic	PF00291.22*PALP*Pyridoxal-phosphate dependent enzyme*13-342*E:1.5e-49	0.118	-1.697	0	7.676	0.034	5.672	1	0	0	0 TRPB_CAMAC	Tryptophan synthase beta chain 2, chloroplastic (EC 4.2.1.20)	TSB	Camptotheca acuminata (Happy tree)	PATHWAY: Amino-acid biosynthesis; L-tryptophan biosynthesis; L-tryptophan from chorismate: step 5/5.	Amino-acid biosynthesis; Aromatic amino acid biosynthesis; Chloroplast; Lyase; Plastid; Pyridoxal phosphate; Transit peptide; Tryptophan biosynthesis
SRR1271858_TR41214_c0_g1_i1_len=2975	METE_CATRO	Q:143-2668,H:1-765	90.14%ID	E0	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	PF08267.9*Meth_synt_1*Cobalamin-independent synthase, N-terminal domain*3-315*E:1.9e-121*PF01717.15*Meth_synt_2*Cobalamin-independent synthase, Catalytic domain*432-576*E:2.1e-68	0.42	0.274	0	2.46	0.51	-0.329	0.37	-0.43	0.05	0.473 METE_CATRO	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase (EC 2.1.1.14) (Cobalamin-independent methionine synthase isozyme) (Vitamin-B12-independent methionine synthase isozyme)	METE	Catharanthus roseus (Madagascar periwinkle) (Vinca rosea)	PATHWAY: Amino-acid biosynthesis; Lmethionine biosynthesis via de novo pathway; L-methionine from L-homocysteine (MetE route): step 1/1.	Amino-acid biosynthesis; Cytoplasm; Metal-binding; Methionine biosynthesis; Methyltransferase; Transferase; Zinc
SRR1271858_TR41214_c0_g1_i5_len=2963	METE_CATRO	Q:143-2656,H:1-765	90.57%ID	E0	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	PF08267.9*Meth_synt_1*Cobalamin-independent synthase, N-terminal domain*3-315*E:1.2e-121*PF01717.15*Meth_synt_2*Cobalamin-independent synthase, Catalytic domain*432-492*E:6.5e-20	0.876	0.085	0	1.717	0.206	-0.638	0.6	-0.259	0.543	0.151 METE_CATRO	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase (EC 2.1.1.14) (Cobalamin-independent methionine synthase isozyme) (Vitamin-B12-independent methionine synthase isozyme)	METE	Catharanthus roseus (Madagascar periwinkle) (Vinca rosea)	PATHWAY: Amino-acid biosynthesis; Lmethionine biosynthesis via de novo pathway; L-methionine from L-homocysteine (MetE route): step 1/1.	Amino-acid biosynthesis; Cytoplasm; Metal-binding; Methionine biosynthesis; Methyltransferase; Transferase; Zinc
SRR1271858_TR41800_c0_g1_i3_len=3104	TLC1_SOLTU	Q:630-2153,H:1-511	85.52%ID	E0	Plastidic ATP/ADP-transporter	PF03219.11*TLC*TLC ATP/ADP transporter*100-509*E:4.6e-170	0.634	0.225	0	1.946	1	0.9	1	0.259	0.155	0.472 TLC1_SOLTU	Plastidic ATP/ADP-transporter		Solanum tuberosum (Potato)		ATP-binding; Chloroplast; Complete proteome; Membrane; Nucleotide-binding; Plastid; Reference proteome; Transmembrane; Transmembrane helix; Transport
SRR1271858_TR42899_c0_g3_i1_len=3309	TPS11_ARATH	Q:579-3101,H:10-835	69.31%ID	E0	Probable alpha,alpha-trehalose-phosphate synthase [UDP-forming] 11	PF00982.18*Glyco_transf_20*Glycosyltransferase family 20*63-549*E:2e-184*PF02358.13*Trehalose_PPase*Trehalose-phosphatase*399-632*E:3e-77*PF08282.9*Hydrolase_3*haloacid dehalogenase-like hydrolase*727-803*E:3e-05	0.564	0.361	0.001	2.391	0.189	1.669	0.118	1.815	0.472	0.708 TPS11_ARATH	Probable alpha,alpha-trehalose-phosphate synthase [UDP-forming] 11 (EC 2.4.1.15) (Trehalose-6-phosphate synthase 11) (ATPS11)	TPS11 TPSB Ai2g18700 MSF3.8	Arabidopsis thaliana (Mouse-ear cress)		Alternative splicing; Chloroplast; Complete proteome; Glycosyltransferase; Phosphoprotein; Reference proteome; Transferase
SRR1271858_TR43396_c1_g3_i1_len=2746	PTR28_ARATH	Q:2437-1532,H:4-302	63.58%ID	E2e-122	Protein NRT1/ PTR FAMILY 5.6	PF00854.18*PTR2*POT family*112-275*E:3.2e-41	0.254	3.969	0.001	6.584	0.001	6.433	0.034	5.633	1	0 PTR28_ARATH	Protein NRT1/ PTR FAMILY 5.6 (AINPP5.6)	NPF5.6 At2g37900 T8P21.19	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Membrane; Phosphoprotein; Reference proteome; Transmembrane; Transmembrane helix; Transport
SRR1271858_TR43523_c0_g2_i1_len=1206	NBSR1_ARATH	Q:231-986,H:30-281	88.89%ID	E2e-166	NADH-cytochrome b5 reductase 1	PF00970.21*FAD_binding_6*Oxidoreductase FAD-binding domain*46-144*E:8.3e-33*PF00175.18*NAD_binding_1*Oxidoreductase NAD-binding domain*154-260*E:3.4e-31	0.044	0.54	0	1.676	0.019	0.65	0.065	0.52	0.465	-0.21 NBSR1_ARATH	NADH-cytochrome b5 reductase 1 (EC 1.6.2.2)	CBR1 CBR At5g17770 MVA3.13	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; FAD; Flavoprotein; Membrane; Mitochondrion; Mitochondrion outer membrane; NAD; Oxidoreductase; Phosphoprotein; Reference proteome; Transmembrane; Transmembrane helix
SRR1271858_TR46029_c0_g1_i1_len=822	NA	NA	NA	NA	NA		0.254	3.758	0.001	5	0.043	3.142	0.381	2.394	1	-1.059					
SRR1271858_TR48059_c0_g4_i3_len=1423	MTDH_FRAAN	Q:1257-220,H:8-353	64.74%ID	E9e-119	Probable mannitol dehydrogenase	PF08240.9*ADH_N*Alcohol dehydrogenase GroES-like domain*32-144*E:5.2e-27*PF02826.16*2-Hacid_dh_C*D-isomer specific 2-hydroxyacid dehydrogenase, NAD binding domain*167-217*E:1.1e-06*PF00107.23*ADH_zinc_N*Zinc-binding dehydrogenase*158-311*E:2.8e-19	0.006	0.607	0	2.982	0.119	0.372	0.035	-0.518	0.34	0.461 MTDH_FRAAN	Probable mannitol dehydrogenase (EC 1.1.1.255) (NAD-dependent mannitol dehydrogenase)	CAD	Fragaria ananassa (Strawberry)		Metal-binding; NAD; Oxidoreductase; Zinc
SRR1271858_TR48059_c0_g4_i2_len=1243	10HGO_CATRO	Q:1074-889,H:11-72	74.19%ID	E1e-23	8-hydroxyeugenol dehydrogenase		0.047	0.71	0	2.24	0.641	0.252	0.268	-0.647	1	0.004 10HGO_CATRO	8-hydroxyeugenol dehydrogenase (Cr10HGO) (EC 1.1.1.324)	10HGO	Catharanthus roseus (Madagascar periwinkle) (Vinca rosea)		Metal-binding; NADP; Oxidoreductase; Zinc
SRR1271858_TR48572_c0_g1_i1_len=2696	ABKC_DICDI	Q:1653-3674,H:158-631	34.5%ID	E9e-84	Probable serine/threonine-protein kinase abkC	PF03109.13*ABC1*ABC1 family*275-399*E:1.3e-31	0.505	-0.486	0	1.821	1	0.091	1	0.062	0.86	0.21 ABKC_DICDI	Probable serine/threonine-protein kinase abkC (EC 2.7.11.-)	abkC adckC DDB_G0267774	Dictyostelium discoideum (Slime mold)		ATP-binding; Coiled coil; Complete proteome; Kinase; Nucleotide-binding; Reference proteome; Serine/threonine-protein kinase; Transferase
SRR1271858_TR48586_c1_g3_i1_len=2124	DCE_PETHY	Q:283-1740,H:1-485	86.83%ID	E0	Glutamate decarboxylase	PF00282.16*Pyridoxal_deC*Pyridoxal-dependent decarboxylase conserved domain*33-381*E:1.8e-110	0.195	1.352	0	3.95	0.402	1.045	0.195	1.309	0.76	0.631 DCE_PETHY	Glutamate decarboxylase (GAD) (EC 4.1.1.15)	GAD	Petunia hybrida (Petunia)		3D-structure; Calmodulin-binding; Decarboxylase; Lyase; Pyridoxal phosphate
SRR1271858_TR50158_c0_g1_i3_len=1789	B561J_ARATH	Q:1452-385,H:24-384	55.4%ID	E5e-140	Cytochrome b561 and DOMON domain-containing protein At5g47530	PF04526.10*DUF568*Protein of unknown function (DUF568)*89-186*E:1.6e-23*PF03188.13*Cytochrom_B561*Eukaryotic cytochrome b561*207-332*E:8.4e-06	0.026	2.218	0	3.778	0.002	2.768	0.118	1	0.099 B561J_ARATH	Cytochrome b561 and DOMON domain-containing protein At5g47530 (Protein b561A.tha10)	At5g47530 MNJ7.12	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Electron transport; Heme; Iron; Membrane; Metal-binding; Reference proteome; Signal; Transmembrane; Transmembrane helix; Transport
SRR1271858_TR51869_c0_g1_i1_len=1317	SGT1_ORYSJ	Q:119-395,H:5-367	66.85%ID	E1e-149	Protein SGT1 homolog (ECO:0000250|UniProtKB:Q08446)	PF13181.3*TPR_8*Tetratricopeptide repeat*37-69*E:0.00066*PF13432.3*TPR_16*Tetratricopeptide repeat*42-97*E:0.0004*PF13181.3*TPR_8*Tetratricopeptide repeat*71-101*E:0.0045*PF04969.13*CS*CS domain*167-242*E:2.3e-14*PF00502.12*SGS*SGS domain*282-362*E:4.4e-37	0.156	-0.572	0	1.927	0.758	0.159	0.139	0.604	1	0.668 SGT1_ORYSJ	Protein SGT1 homolog (OsSGT1) (Suppressor of G2 allele of SKP1 homolog)	SGT1 Os01g0624500 LOC_Os01g43540 Osj_02863	Oryza sativa subsp. japonica (Rice)		Complete proteome; Cytoplasm; Nucleus; Plant defense; Reference proteome; Repeat; TPR repeat; Ubl conjugation pathway
SRR1271858_TR53271_c0_g1_i1_len=1364	AOC4_ARATH	Q:798-388,H:111-248	71.74%ID	E6e-58	Allene oxide cyclase 4, chloroplastic		0.254	3.247	0	7.683	0.034	4.655	0.002	5.395	1	0.592 AOC4_ARATH	Allene oxide cyclase 4, chloroplastic (EC 5.3.99.6)	AOC4 At1g13280 T6J4.4 T6J4_23	Arabidopsis thaliana (Mouse-ear cress)		Chloroplast; Complete proteome; Isomerase; Plastid; Reference proteome; Transit peptide
SRR1271858_TR53253_c0_g1_i1_len=570	NA	NA	NA	NA	NA		NA	1	1.397	0	3.865	0.629	2.311	1	0.742	1	-0.347				
SRR1271858_TR53658_c0_g2_i1_len=949	NA	NA	NA	NA	NA		0.135	0.662	0	4.303	0.123	0.75	0.443	0.416	0.158	1.778					
SRR1271858_TR54040_c0_g1_i3_len=4108	AROF_ARATH	Q:3912-3115,H:1-269	68.4%ID	E6e-113	Phospho-2-dehydro-3-deoxyheptonate aldolase 1, chloroplastic	PF01474.13*DAHP_synth_2*Class-II DAHP synthetase family*137-331*E:9.5e-78	0.072	0.715	0	2.702	0.045	0.875	0.298	0.528	0.059	1.093 AROF_ARATH	Phospho-2-dehydro-3-deoxyheptonate aldolase 1, chloroplastic (EC 2.5.1.54) (3-deoxy-D-arabino-heptulosonate 7-phosphate synthase 1) (DAHP synthase 1) (Phospho-2-keto-3-deoxyheptonate aldolase 1)	DHS1 At4g39980 T5J17.150	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Metabolic intermediate biosynthesis; chorismate biosynthesis; chorismate from D-erythrose 4-phosphate and phosphoenolpyruvate: step 1/7.	Amino-acid biosynthesis; Aromatic amino acid biosynthesis; Chloroplast; Complete proteome; Plastid; Reference proteome; Transferase; Transit peptide
SRR1271858_TR54152_c0_g1_i2_len=1045	NAC68_ORYSJ	Q:226-803,H:1-216	30.62%ID	E4e-23	NAC domain-containing protein 68	PF02365.12*NAM*No apical meristem (NAM) protein*8-135*E:8e-21	1	1.52	0	6.119	0.066	3.313	0.254	2.739	1	0 NAC68_ORYSJ	NAC domain-containing protein 68 (ONAC068)	NAC68 NAC4 Os01g0816100 LOC_Os01g60020 B1148D12.1 OsJNBa0050074.44	Oryza sativa subsp. japonica (Rice)		Complete proteome; DNA-binding; Nucleus; Reference proteome; Transcription; Transcription regulation
SRR1271858_TR55679_c0_g2_i2_len=2894	SERB2_ARATH	Q:2705-1827,H:18-305	75.59%ID	E4e-153	Phosphoserine aminotransferase 2, chloroplastic	PF12146.5*Hydrolase_4*Serine aminopeptidase, S33*62-323*E:3.5e-13*PF00561.17*Abhydrolase_1*alpha/beta hydrolase fold*66-326*E:3.2e-13*PF12697.4*Abhydrolase_6*Alpha/beta hydrolase family*67-327*E:5.7e-15	0.555	0.258	0	2.367	0.832	0.174	0.545	0.418	0.025	3.089 SERB2_ARATH	Phosphoserine aminotransferase 2, chloroplastic (AtPSAT2) (EC 2.6.1.52)	PSAT2 At2g17630 T19E12.3	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Amino-acid biosynthesis; Lserine biosynthesis; Lserine from 3-phospho-D-glycerate: step 2/3.	Aminotransferase; Chloroplast; Complete proteome; Pyridoxal phosphate; Reference proteome; Serine biosynthesis; Transferase; Transit peptide
SRR1271858_TR56848_c0_g1_i1_len=1619	NA	NA	NA	NA	NA		0.9	0.139	0	2.488	0.057	1.291	0.028	1.419	0.518	0.385					
SRR1271858_TR57629_c1_g1_i1_len=1200	GEDH1_OCIBA	Q:7106-5,H:3-358	61.8%ID	E4e-153	Geraniol dehydrogenase 1	PF08240.9*ADH_N*Alcohol dehydrogenase GroES-like domain*38-147*E:3.5e-23*PF00107.23*ADH_zinc_N*Zinc-binding dehydrogenase*151-314*E:1.3e-15	0.034	5.007	0	7.7	1	0.506	1	-1.506	1	0 GEDH1_OCIBA	Geraniol dehydrogenase 1 (ObaGEDH1) (EC 1.1.1.183)	GEDH1	Ocimum basilicum (Sweet basil)		Metal-binding; NADP; Oxidoreductase; Zinc
SRR1271858_TR59296_c0_g1_i2_len=1962	MDAR_SOLLC	Q:187-484,H:1-433	80.82%ID	E0	Monodehydroascorbate reductase	PF07992.11*Pyr_redox_2*Pyridine nucleotide-disulphide oxidoreductase*10-201*E:3.6e-39 PF00070.24*Pyr_redox*Pyridine nucleotide-disulphide oxidoreductase*44-126*E:8.4e-14	0.398	0.41	0	1.963	0.006	1.926	0.045	1.554	0.088	1.507 MDAR_SOLLC	Monodehydroascorbate reductase (MDAR) (EC 1.6.5.4) (Ascorbate free radical reductase) (AFR reductase)	AFRR	Solanum lycopersicum (Tomato) (Lycopersicon esculentum)		Complete proteome; Cytoplasm; FAD; Flavoprotein; NAD; Oxidoreductase; Reductase; Reference proteome
SRR1271858_TR59410_c0_g1_i1_len=1630	C7352_ARATH	Q:1357-59,H:88-510	37.61%ID	E4e-79	Cytokinin hydroxylase	PF00067.19*p450*Cytochrome P450*15-426*E:4.9e-82	1	2.29	0	6.848	1	2.441	1	2.615	1	-1.098 C7352_ARATH	Cytokinin hydroxylase (EC 1.14.13.-) (Cytochrome P450 35A2)	CYP735A2 At1g67110 F5A8.3	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Cytochrome P450; Heme; Iron; Membrane; Metal-binding; Monooxygenase; NADP; Oxidoreductase; Reference proteome; Transmembrane; Transmembrane helix
SRR1271858_TR62188_c0_g1_i8_len=2292	SRPR_DROME	Q:1055-129,H:293-614	59.63%ID	E2e-119	Signal recognition particle receptor subunit alpha homolog	PF04086.10*SRP-alpha_N*Signal recognition particle, alpha subunit, N-terminal*28-302*E:4.8e-66*PF02881.16*SRP54_N*SRP54-type protein, helical bundle domain*319-386*E:1.2e-06*PF00448.19*SRP54*SRP54-type protein, GTPase domain*418-622*E:5.1e-55	0.324	0.376	0	1.434	0.014	0.901	0.13	0.581	0.389	0.36 SRPR_DROME	Signal recognition particle receptor subunit alpha homolog (DPalpha) (Docking protein alpha) (SR-alpha) (GTP-binding protein)	Glp-bp CG2522	Drosophila melanogaster (Fruit fly)		Complete proteome; Endoplasmic reticulum; GTP-binding; Membrane; Nucleotide-binding; Phosphoprotein; Reference proteome; Receptor; Reference proteome
SRR1271858_TR62488_c1_g3_i1_len=596	RS23_FRAAN	Q:445-44,H:1-134	98.51%ID	E8e-91	40S ribosomal protein S23	PF00164.22*Ribosom_S12_S23*Ribosomal protein S12/S23*9-135*E:5.3e-57	0.004	-1.225	0	1.751	0.03	-1.059	0.008	-1.343	1	0 RS23_FRAAN	40S ribosomal protein S23 (S12)	RPS23	Fragaria ananassa (Strawberry)		Hydroxylation; Ribonucleoprotein; Ribosomal protein
SRR1271858_TR65065_c0_g2_i2_len=1798	ACCH1_ARATH	Q:1063-203,H:80-365	48.96%ID	E2e-92	1-aminocyclopropane-1-carboxylate oxidase homolog 1	PF14226.3*DIOX_N*non-haem dioxygenase in morphine synthesis N-terminal*26-94*E:2.7e-07*PF03171.17*2OG-Fe(II)_Oxy*2OG-Fe(II) oxygenase superfamily*153-245*E:1.2e-21	0.129	4.66	0	7.266	0.254	4.459	1	3.124	1	0 ACCH1_ARATH	1-aminocyclopropane-1-carboxylate oxidase homolog 1	At1g06620 F12K11.24 F12K11.6	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Iron; Metal-binding; Oxidoreductase; Reference proteome
SRR1271858_TR66001_c0_g1_i2_len=2746	AIM1_ARATH	Q:1287-211,H:354-712	73.26%ID	E2e-176	Peroxisomal fatty acid beta-oxidation multifunctional protein AIM1	PF03786.17*ECH_1*Enoyl-CoA hydratase/isomerase*80-282*E:1.6e-37*PF16113.2*ECH_2*Enoyl-CoA hydratase/isomerase*85-281*E:1.9e-20 PF02737.15*3HCDH_N*3-hydroxyacyl-CoA dehydrogenase, NAD binding domain*377-420*E:1.9e-07	0.226	2.263	0	2.576	0.517	0.963	0.356	1.315	1	0.032 AIM1_ARATH	Peroxisomal fatty acid beta-oxidation multifunctional protein AIM1 (Protein ABNORMAL INFLORESCENCE MERISTEM 1) (AIAIM1) [Includes: Enoyl-CoA hydratase/3-2-trans-enoyl-CoA isomerase/3-hydroxybutyryl-CoA epimerase (EC 4.2.1.17) (EC 5.1.2.3) (EC 5.3.3.8); 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35)]	AIM1 At4g29010 F19B15.40	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Lipid metabolism; fatty acid beta-oxidation.	Complete proteome; Fatty acid metabolism; Isomerase; Lipid metabolism; Lyase; Multifunctional enzyme; NAD; Oxidoreductase; Peroxisome; Reference proteome
SRR1271858_TR66262_c2_g1_i19_len=3904	4CLL5_ARATH	Q:208-1839,H:3-542	70.77%ID	E0	4-coumarate--CoA ligase-like 5	PF00501.25*AMP-binding*AMP-binding enzyme*53-461*E:8.2e-103*PF13193.3*AMP-binding_C*AMP-binding enzyme C-terminal domain*470-545*E:1.3e-16	0.032	1.216	0	2.728	0.046	0.897	0.108	0.762	0.147	0.892 4CLL5_ARATH	4-coumarate--CoA ligase-like 5 (EC 6.2.1.-) (4-coumarate--CoA ligase isoform 9) (At4CL9) (Peroxisomal OPC-8:0-CoA ligase 1)	4CLL5 OPCL1 At1g20510 F5M15.17	Arabidopsis thaliana (Mouse-ear cress)		ATP-binding; Alternative splicing; Complete proteome; Ligase; Nucleotide-binding; Peroxisome; Reference proteome
SRR1271858_TR68514_c0_g1_i1_len=713	NA	NA	NA	NA	NA		0.73	0.983	0	3.03	0.759	0.01	0.821	0	-1.268						
SRR1271858_TR69965_c1_g1_i5_len=1187	CAMT4_ARATH	Q:139-981,H:15-259	79.72%ID	E8e-158	Caffeoyl-CoA O-methyltransferase 1	PF01596.14*Methyltransf_3*O-methyltransferase*10-150*E:2.2e-65	0.239	1.278	0	3.189	0.407	0.579	0.407	0.652	0.072	0.72 CAMT4_ARATH	Caffeoyl-CoA O-methyltransferase 1 (EC 2.1.1.104) (Trans-caffeoyl-CoA 3-O-methyltransferase) (CCoAMT) (CCoAOMT1)	CCOAOMT1 At4g34050 F28A23.190	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Aromatic compound metabolism; phenylpropanoid biosynthesis.	Acetylation; Alternative splicing; Complete proteome; Lignin biosynthesis; Metal-binding; Methyltransferase; Reference proteome; Sadenosyl-L-methionine; Transferase
SRR1271858_TR692_c0_g1_i1_len=3438	SND1_DANRE	Q:3210-1231,H:11-616	37.07%ID	E9e-106	Staphylococcal nuclease domain-containing protein 1	PF00565.14*SNase*Staphylococcal nuclease homologue*40-148*E:2.7e-11*PF00565.14*SNase*Staphylococcal nuclease homologue*270-382*E:3.3e-13*PF00565.14*SNase*Staphylococcal nuclease homologue*409-549*E:8.3e-07	0.788	0.157	0	2.82	1	0.13	1	0.183	1	0.009 SND1_DANRE	Staphylococcal nuclease domain-containing protein 1 (100 kDa coactivator) (45Nc-Tudor domain protein) (p100 co-activator)	snd1 sn4tdr	Danio rerio (Zebrafish) (Brachydanio rerio)		Alternative splicing; Complete proteome; Cytoplasm; Reference proteome; Repeat
SRR1271858_TR815_c0_g1_i2_len=1144	NA	NA	NA	NA	NA		0.026	0.548	0	1.113	0.144	0.367	0.45	0.197	0.009	0.608					
SRR1271858_TR1178_c0_g1_i1_len=1795	BZR1_ARATH	Q:448-1335,H:22-335	63.06%ID	E2e-78	Protein BRASSINAZOLE-RESISTANT 1	PF05687.10*BES1_N*BES1/BZR1 plant transcription factor, N-terminal*34-159*E:6.2e-61	0.581	0.335	0	2.423	0.043	1.352	0.195	1.01	1	-0.069 BZR1_ARATH	Protein BRASSINAZOLE-RESISTANT 1 (Protein BIN2 SUBSTRATE 2)	BZR1 BIS2 At1g75080 F9E10_7	Arabidopsis thaliana (Mouse-ear cress)		Brassinosteroid signaling pathway; Complete proteome; DNA-binding; Growth regulation; Nucleus; Phosphoprotein; Reference proteome; Transcription; Transcription regulation
SRR1271858_TR1593_c0_g1_i1_len=1501	TRL2_ORYSJ	Q:421-930,H:26-202	72.51%ID	E5e-83	Thioredoxin-like 2, chloroplastic	PF00085.17*Thioredoxin*Thioredoxin*96-182*E:2.7e-18	0.321	0.424	0	1.385	0.875	0.057	1	-0.02	0.389	0.398 TRL2_ORYSJ	Thioredoxin-like 2, chloroplastic (Lilium-type thioredoxin 2) (OsTrx19)	Os05g0200100 LOC_Os05g10190 OSJNBa0017006.11	Oryza sativa subsp. japonica (Rice)		Chloroplast; Complete proteome; Disulfide bond; Electron transport; Plastid; Redoxactive center; Reference proteome; Transit peptide; Transport
SRR1271859_TR2392_c0_g1_i1_len=1113	TCTP_ELAGV	Q:846-343,H:1-168	87.5%ID	E6e-83	Translationally-controlled tumor protein homolog	PF00838.14*TCTP*Translationally controlled tumour protein*1-164*E:9.4e-59	1	-0.005	0	2.838	0.09	1.03	0.152	0.877	1	-0.033 TCTP_ELAGV	Translationally-controlled tumor protein homolog (TCTP)	TCTP	Elaeis guineensis var. tenera (Oil palm)		Calcium; Cytoplasm
SRR1271859_TR3405_c0_g1_i11_len=2129	Y5707_ARATH	Q:557-1630,H:40-389	52.09%ID	E3e-117	Probable receptor-like protein kinase At5g47070	PF00069.22*Pkinase*Protein kinase domain*86-364*E:1.9e-47*PF07714.14*Pkinase_Tyr*Protein tyrosine kinase*88-365*E:2.8e-49	0.819	0.153	0	1.482	0.037	1.197	0.01	1.429	0.904	-0.108 Y5707_ARATH	Probable receptor-like protein kinase At5g47070 (EC 2.7.11.1)	At5g47070 K14A3.2	Arabidopsis thaliana (Mouse-ear cress)		ATP-binding; Cell membrane; Complete proteome; Kinase; Membrane; Nucleotide-binding; Phosphoprotein; Reference proteome; Serine/threonine-protein kinase; Transferase
SRR1271859_TR3793_c0_g4_i1_len=870	NA	NA	NA	NA	NA		0.043	1.256	0	2.542	0.044	2.224	0.027	2.357	1	0.948					
SRR1271859_TR4407_c1_g1_i2_len=2549	NA	NA	NA	NA	NA		0.267	0.4	0	1.356	0.004	0.936	0.004	0.928	0.381	0.824					
SRR1271859_TR5307_c0_g1_i2_len=2094	GSHRP_SPIOL	Q:1824-385,H:10-489	86.67%ID	E0	Glutathione reductase, chloroplastic	PF00676.9*HIPI*HIPI-like protein*21-94*E:9.6e-37 PF07992.11*Pyr_redox_2*Pyridine nucleotide-disulphide oxidoreductase*26-352*E:7.1e-67*PF13738.3*Pyr_redox_3*Pyridine nucleotide-disulphide oxidoreductase*157-336*E:4.6e-13*PF00070.24*Pyr_redox*Pyridine nucleotide-disulphide oxidoreductase*204-278*E:1.2e-17*PF02852.19*Pyr_redox_dim*Pyridine nucleotide-disulphide oxidoreductase, dimerisation domain*372-481*E:4.1e-30	0.606	-0.196	0	1.426	0.004	1.476	0.016	1.305	0.272	0.502 GSHRP_SPIOL	Glutathione reductase, chloroplastic (GR) (GRase) (EC 1.8.1.7) (Fragment)	Spinacia oleracea (Spinach)			Chloroplast; Disulfide bond; FAD; Flavoprotein; NADP; Oxidoreductase; Plastid; Redoxactive center; Transit peptide
SRR1271859_TR6013_c0_g1_i1_len=2112	NA	NA	NA	NA	NA		0.662	0.19	0	1.361	0.02	1.406	0.027	1.36	0.887	0.067					
SRR1271859_TR6020_c0_g2_i3_len=2090	PTR21_ARATH	Q:1188-157,H:274-617	52.74%ID	E8e-179	Protein NRT1/ PTR FAMILY 2.13	PF00854.18*PTR2*POT family*150-305*E:2.1e-29	1	1.144	0	4.079	0.003	1.921	0.021	1.543	1	0.558 PTR21_ARATH	Protein NRT1/ PTR FAMILY 2.13 (AINPF2.13) (Nitrate transporter 1.7)	NPF2.13 NRT1.7 At1g69870 T17F3.10	Arabidopsis thaliana (Mouse-ear cress)		Cell membrane; Complete proteome; Membrane; Nitrate assimilation; Reference proteome; Symport; Transmembrane; Transmembrane helix; Transport
SRR1271859_TR7382_c0_g1_i2_len=1349	NA	NA	NA	NA	NA		0.319	0.939	0	2.429	0.005	1.281	0.123	0.789	1	-0.06					
SRR1271859_TR7939_c0_g1_i1_len=1931	SNX1_ARATH	Q:418-1554,H:24-401	79.95%ID	E0	Sorting nexin 1	PF00787.21*PX*PX domain*24-137*E:2.7e-25*PF09325.7*Vps5*Vps5 C terminal like*169-394*E:5.2e-23	1	-0.031	0.001	1.885	0.239	1.325	0.158	1.44	1	0.011 SNX1_ARATH	Sorting nexin 1 (AtSNX1) (Vacuolar protein sorting-associated protein 5 homology)	SNX1 VPS5 At5g06140 K16F4.11 MBL20	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Cytoplasm; Endosome; Golgi apparatus; Lipid-binding; Membrane; Phosphoprotein; Protein transport; Reference proteome; Transport
SRR1271859_TR12007_c0_g1_i1_len=2551	CP74A_ARATH	Q:782-2203,H:43-517	70.32%ID	E0	Allene oxide synthase, chloroplastic	PF00067.19*p450*Cytochrome P450*37-518*E:1.7e-15	0.04	1.315	0	4.296	0.003	1.864	0.001	1.937	0.402	0.837 CP74A_ARATH	Allene oxide synthase, chloroplastic (EC 4.2.1.92) (Cytochrome P450 74A) (Hydroperoxide dehydrase)	CYP74A AOS At5g42650 MJB21.2	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Lipid metabolism; oxylipin biosynthesis. (ECO:0000305).	3D-structure; Complete proteome; Fatty acid biosynthesis;

SRR342017_TR18067_c0_g1_i3_len=1739	DNJH2_ALLPO	Q:1567-236,H:1-418	79.1%ID	E:0	DnaJ protein homolog 2	PF00226.28*DnaJ*DnaJ domain*13-71*E:3.9e-22*PF01556.15*DnaJ_C*DnaJ C terminal domain*121-369*E:1.3e-35*PF00684.16*DnaJ_CXXCXGXG*DnaJ central domain*147-213*E:5e-15	0,606	0,177	0	2,102	0,549	0,174	0,635	0,137	0,019	0,931	DNJH2_ALLPO	DnaJ protein homolog 2	LDJ2	Allium porrum (Leek) (Allium ampeloprasum var. porrum)		Chaperone; Lipoprotein; Membrane; Metal-binding; Methylation; Prenylation; Repeat; Zinc; Zinc-finger
SRR342017_TR19861_c0_g1_i1_len=1064	KCY4_ORYSJ	Q:232-837,H:1-208	78.85%ID	E:3e-112	UMP-CMP kinase 4 (ECO:0000255|HAMAP-Rule:MF_01172)	PF13671.3*AAA_33*AAA domain*23-156*E:3.4e-08*PF13238.3*AAA_18*AAA domain*24-150*E:7e-09*PF00406.19*ADK*Adenylate kinase*26-178*E:2e-08*PF13207.3*AAA_7*AAA domain*37-157*E:3.2e-37*PF13426.4*PAS_9*PAS domain*39-161*E:0.3	0,591	0,207	0	1,489	0,528	-0,272	0,528	-0,285	0,578	0,238	KCY4_ORYSJ	Probable UMP/CMP kinase 4 (EC 2.7.4.14)	Os02g0778400 LOC_Os02g53790 OJ1293_A01.3	Oryza sativa subsp. japonica (Rice)		ATP-binding; Complete proteome; Kinase; Nucleotide-binding; Pyrimidine biosynthesis; Reference proteome; Transferase
SRR342017_TR20576_c1_g5_i1_len=2757	THIK2_ARATH	Q:364-1701,H:1-449	78.32%ID	E:0	3-ketoacyl-CoA thiolase 2, peroxisomal	PF00108.20*Thiolase_N*Thiolase, N-terminal domain*49-304*E:3.3e-78*PF02803.15*Thiolase_C*Thiolase, C-terminal domain*313-435*E:4.5e-48	0,463	0,288	0	2,282	0,007	1,514	0,001	1,694	0,729	0,142	THIK2_ARATH	3-ketoacyl-CoA thiolase 2, peroxisomal (EC 2.3.1.16) (Acetyl-CoA acyltransferase 2) (Beta-ketothiolase 2) (Peroxisomal 3-oxoacyl-CoA thiolase 2) (Peroxisome defective protein 1)	PED1 KAT2 At2g33150 F25I18.11	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Lipid metabolism; fatty acid metabolism.	3-Ductructive; Acyltransferase; Complete proteome; Fatty acid biosynthesis; Fatty acid metabolism; Glycoxysome; Lipid biosynthesis; Lipid metabolism; Oxylipin biosynthesis; Peroxisome; Reference proteome; Transferase; Transit peptide
SRR342017_TR20662_c1_g1_i2_len=3177	NDHK_EUCGG	Q:1710-1033,H:1-224	95.58%ID	E:7e-139	NAD(P)H-quinone oxidoreductase subunit K, chloroplastic (ECO:0000255|HAMAP-Rule:MF_01356)	PF01058.19*Oxidored_q6*NADH ubiquinone oxidoreductase, 20 Kd subunit*44-153*E:1.6e-23	1	0,037	0,001	2,023	0,917	0,088	0,189	0,544	-1	-0,125	NDHK_EUCGG	NAD(P)H-quinone oxidoreductase subunit K, chloroplastic (EC 1.6.5-) (NAD(P)H dehydrogenase subunit K) (NADH-plastoquinone oxidoreductase subunit K)	ndhK	Eucalyptus globulus subsp. globulus (Tasmanian blue gum)		4Fe-4S; Chloroplast; Iron; Iron-sulfur; Membrane; Metal-binding; NAD; NADP; Oxidoreductase; Plastid; Plastoquinone; Quinone; Thylakoid; Transport
SRR342017_TR20766_c0_g1_i2_len=788	NIFU1_ARATH	Q:509-18,H:6-230	77.58%ID	E:2e-64	NifU-like protein 1, chloroplastic	PF01106.14*NifU*NifU-like domain*71-131*E:6.3e-23*PF01106.14*NifU*NifU-like domain*154-209*E:7.3e-05	0,058	0,653	0	1,000	0,003	0,913	0,01	0,812	0,381	2,348	NIFU1_ARATH	NifU-like protein 1, chloroplastic (AtCNfu1) (AtCnfU-Vb)	NIFU1 CNFU1 NFU1 At4g01940 TB11.20	Arabidopsis thaliana (Mouse-ear cress)		Chloroplast; Complete proteome; Disulfide bond; Plastid; Reference proteome; Transit peptide
SRR342017_TR20766_c0_g9_i1_len=839	DREB3_ARATH	Q:1250-957,H:38-135	80.61%ID	E:6e-48	Dehydration-responsive element-binding protein 3	PF00847.17*AP2*AP2 domain*74-124*E:6.6e-12	0,129	1,133	0	3,283	0,117	0,606	0,022	0,854	0,381	-0,779	DREB3_ARATH	Dehydration-responsive element-binding protein 3 (Protein TINY 2)	DREB3 ERF041 TINY2 At5g11590 F15N18.180	Arabidopsis thaliana (Mouse-ear cress)		Activator; Complete proteome; DNA-binding; Ethylene signaling pathway; Nucleus; Reference proteome; Transcription; Transcription regulation
SRR342017_TR20986_c1_g1_i2_len=1210	GEDH1_OCIBA	Q:1136-441,H:11-242	65.95%ID	E:1e-71	Geraniol dehydrogenase 1	PF00180.9*ADH_N*Alcohol dehydrogenase GroES-like domain*132-144*E:2.4e-27*PF02826.16*2-Hacid_dh_C*D-isomer specific 2-hydroxyacid dehydrogenase, NAD binding domain*167-721*E:6.4e-07	0,317	-0,509	0	2,591	0,798	-0,23	0,663	0,488	0,04	0,514	GEDH1_OCIBA	Geraniol dehydrogenase 1 (ObaGEDH1) (EC 1.1.1.183)	GEDH1	Ocimum basilicum (Sweet basil)		Metal-binding; NADP; Oxidoreductase; Zinc
SRR342017_TR21527_c1_g1_i6_len=1845	NA	NA	NA	NA	NA	PF00790.16*VHS*VHS domain*138-269*E:1.4e-22*PF03127.11*GAT*GAT domain*325-399*E:3.2e-16	0,925	0,064	0	1,625	0,051	1,028	0,051	1,063	-1	1,28	-	-	-	-		
SRR342017_TR22495_c0_g2_i1_len=2497	KPYC_SOYBN	Q:1869-1549,H:27-557	44.15%ID	E:2e-122	Pyruvate kinase, cytosolic isozyme	PF00224.18*PK*Pyruvate kinase, barrel domain*30-375*E:4.5e-93*PF02887.13*PK_C*Pyruvate kinase, alpha/beta domain*395-522*E:7.8e-25	0,713	0,141	0	1,719	0,877	0,06	0,356	0,285	0,377	0,573	KPYC_SOYBN	Pyruvate kinase, cytosolic isozyme (PK) (EC 2.7.1.40)	-	Glycine max (Soybean) (Glycine hispida)	PATHWAY: Carbohydrate degradation; glycolysis; pyruvate from D-glyceraldehyde 3-phosphate; step 5/5.	
SRR342017_TR23313_c2_g1_i3_len=2140	GLYK_ARATH	Q:443-1549,H:87-455	73.24%ID	E:0	D-glycerate 3-kinase, chloroplastic	PF02595.12*Glycerate_kinase_chloroplastic	0,451	0,328	0	4,222	0	-6,62	0	-6,674	0,099	-0,831	GLYK_ARATH	D-glycerate 3-kinase, chloroplastic (AtGLYK) (EC 2.7.1.31)	GLYK At1g80380 F5I6.13	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Photosynthesis; photorespiration; 3-phospho-D-glycerate from glycine; step 4/4.	ATP-binding; Alternative splicing; Chloroplast; Complete proteome; Glycolate pathway; Kinase; Nucleotide-binding; Photorespiration; Plastid; Reference proteome; Transferase; Transit peptide
SRR342017_TR23421_c1_g2_i7_len=1492	RSSA_DAUCA	Q:166-681,H:1-269	78.02%ID	E:1e-139	40S ribosomal protein SA (ECO:0000255|HAMAP-Rule:MF_03015)	PF03318.17*Ribosomal_S2*Ribosomal protein S2*18-112*E:1.3e-12*PF00318.17*Ribosomal_S2*Ribosomal protein S2*117-182*E:1.8e-12	0,09	-0,734	0	8,258	-1	0	0	0	0,009	-5,941	RSSA_DAUCA	40S ribosomal protein SA (p40)	17B	Daucus carota (Wild carrot)		Cytoplasm; Ribonucleoprotein; Ribosomal protein
SRR342017_TR24328_c0_g3_i3_len=574	NUS0B_ARATH	Q:396-572,H:320-378	72.88%ID	E:5e-22	Nuclear pore complex protein NUP50B (ECO:0000303|PubMed:21189294)	PF06638.15*Ran_BP1*RanBP1 domain*121-173*E:1e-07	0,163	-0,689	0,001	6,638	0	0	-6,728	0,196	0,517	NUS0B_ARATH	Nuclear pore complex protein NUP50B (Nucleoporin 50kDa)	NUP50B At3g15970 MSL1.1	Arabidopsis thaliana (Mouse-ear cress)		Acetylation; Complete proteome; Nuclear pore complex; Nucleus; Phosphoprotein; Protein transport; Reference proteome; Repeat; Translocation; Transport; mRNA transport
SRR342017_TR24386_c3_g1_i4_len=1596	LEUNG_ARATH	Q:1276-1539,H:1-88	98.86%ID	E:6e-50	Transcriptional corepressor LEUNIG (ECO:0000303|PubMed:11058164)	PF06232.8*ATS3*Embryo-specific protein 3, (ATS3)*30-132*E:4.1e-07*PF01477.20*PLAT*PLAT/LH2 domain*36-153*E:2.2e-14	0,187	1,035	0	4,17	0,001	3,204	0,003	3,059	0,111	-0,915	LEUNG_ARATH	Transcriptional corepressor LEUNIG (Protein ROTUNDA2)	LUG RON2 At4g32551 L23H3.30	Arabidopsis thaliana (Mouse-ear cress)		Alternative splicing; Complete proteome; Developmental protein; Differentiation; Flowering; Nucleus; Reference proteome; Repeat; Repressor; Transcription; Transcription regulation; WD repeat
SRR342017_TR24619_c3_g5_i1_len=2646	PAO4_ARATH	Q:691-2139,H:1-497	68.79%ID	E:0	Probable polyamine oxidase 4	PF00890.21*FAD_binding_2*FAD binding domain*33-76*E:3.6e-05*PF13450.3*NAD_binding_8*NAD(P)-binding Rossmann-like domain*35-101*E:8.6e-15*PF01593.21*Amino_oxidase*Flavin containing amine oxidoreductase*40-459*E:3.3e-88	0,704	0,186	0	2,2	0,319	1,051	0,228	1,083	0,188	-0,452	PAO4_ARATH	Probable polyamine oxidase 4 (AtPAO4) (EC 1.5.3.16) (Amine oxidase 2)	PAO4 At1g65840 F1E22.18	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; FAD; Flavoprotein; Oxidoreductase; Peroxisome; Reference proteome
SRR342017_TR24903_c0_g4_i1_len=3970	PSAA_EUCGG	Q:3431-1182,H:1-750	99.33%ID	E:0	Photosystem I P700 chlorophyll a apoprotein A1 (ECO:0000255|HAMAP-Rule:MF_00458)	PF00223.16*PsaA_PsaB*Photosystem I psaA/psaB protein*38-750*E:0	0,058	0,819	0	2,022	0	-1,767	0	-1,43	1	-0,304	PSAA_EUCGG	Photosystem I P700 chlorophyll a apoprotein A1 (EC 1.97.1.12) (PSI-A) (PsaA)	psaA	Eucalyptus globulus subsp. globulus (Tasmanian blue gum)		4Fe-4S; Chlorophyll; Chloroplast; Chromophore; Electron transport; Iron; Iron-sulfur; Magnesium; Membrane; Metal-binding; Oxidoreductase; Photosynthesis; Photosystem I; Plastid; Thylakoid; Transmembrane; Transmembrane helix; Transport
SRR342017_TR30377_c3_g5_i5_len=2173	RP45C_ARATH	Q:389-87,H:261-361	71.29%ID	E:3e-41	Polyadenylate-binding protein RBP45C	PF01490.15*Aa_trans*Transmembrane amino acid transporter protein*33-415*E:1.9e-75	1	0,017	0	2,075	0,517	0,922	0,732	0,678	1	0,032	RP45C_ARATH	Polyadenylate-binding protein RBP45C (Poly(A)-binding protein RBP45C) (RNA-binding protein 45C) (AtRBP45C)	RBP45C At4g27000 F10M23.340	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Nucleus; RNA-binding; Reference proteome; Repeat; mRNA processing
SRR342017_TR31799_c2_g4_i2_len=1294	CLC1_ARATH	Q:346-900,H:56-241	63.44%ID	E:1e-57	Clathrin light chain 1	PF01086.14*Clathrin_lg_ch*Clathrin light chain*131-271*E:4.4e-10	1	0,009	0	1,741	0,196	0,531	0,085	0,691	1	0,011	CLC1_ARATH	Clathrin light chain 1	At2g20760 F5H14.27	Arabidopsis thaliana (Mouse-ear cress)		Coated pit; Coiled coil; Complete proteome; Cytoplasmic vesicle; Membrane; Reference proteome
SRR342017_TR32897_c1_g10_i4_len=2602	TRP8_CAMAC	Q:1236-2600,H:1-451	83.99%ID	E:0	Tryptophan synthase beta chain 2, chloroplastic	PF00291.22*PALP*Pyridoxal-phosphate dependent enzyme*126-455*E:3.5e-94	0,154	0,522	0	3,095	0,895	-0,13	0,788	-0,159	0,011	0,663	TRP8_CAMAC	Tryptophan synthase beta chain 2, chloroplastic (EC 4.2.1.20)	TSB	Camptotheca acuminata (Happy tree)	PATHWAY: Amino-acid biosynthesis; L-tryptophan biosynthesis; L-tryptophan from chorismate; step 5/5.	Amino-acid biosynthesis; Aromatic amino acid biosynthesis; Chloroplast; Lyase; Plastid; Pyridoxal phosphate; Transit peptide; Tryptophan biosynthesis
SRR342017_TR33069_c2_g2_i1_len=3355	SPE1_PEA	Q:1075-326,H:1-727	70.79%ID	E:0	Arginine decarboxylase	PF02784.13*Orn_Arg_deC_N*Pyridoxal-dependent decarboxylase, pyridoxal binding domain*140-410*E:2.1e-40*PF02278.19*Orn_DAP_Arg_deC*Pyridoxal-dependent decarboxylase, C-terminal sheet domain*498-612*E:7.4e-19	1	-0,072	0	2,609	0,656	0,344	0,114	0,82	0,536	-0,184	SPE1_PEA	Arginine decarboxylase (ADC) (ARGDC) (EC 4.1.1.19)	-	Pisum sativum (Garden pea)	PATHWAY: Amino-acid biosynthesis; Arginine biosynthesis; Putrescine biosynthesis; Pyridoxal phosphate; Spermidine biosynthesis	Decarboxylase; Lyase; Magnesium; Putrescine biosynthesis; Pyridoxal phosphate; Spermidine biosynthesis
SRR342017_TR33314_c2_g1_i3_len=802	NA	NA	NA	NA	NA	NA	1	-0,132	0	4,2	1	0	1	0	0,528	-0,317	-	-	-	-		-
SRR342017_TR33422_c0_g1_i1_len=791	NA	NA	NA	NA	NA	PF04770.9*ZF-HD_dimer*ZF-HD protein dimerisation region*26-77*E:2.8e-28	1	0,238	0	4,093	0,597	0,368	1	-0,202	0,811	-0,317	-	-	-	-		-
SRR342019_TR881_c0_g5_i3_len=2314	WRK19_ARATH	Q:839-1309,H:91-297	56.52%ID	E:8e-60	Probable WRKY transcription factor 19	-	1	0,13	0,001	2,192	1	0,113	0,777	-0,186	0,874	0,198	WRK19_ARATH	Probable WRKY transcription factor 19 (WRKY DNA-binding protein 19)	WRKY19 At4g12020 F16J13.90	Arabidopsis thaliana (Mouse-ear cress)		ATP-binding; Alternative splicing; Complete proteome; DNA-binding; Kinase; Leucine-rich repeat; Nucleotide-binding; Nucleus; Plant defense; Reference proteome; Repeat; Serine/threonine-protein kinase; Transcription; Transcription regulation; Transferase
SRR342019_TR1150_c9_g1_i4_len=633	NA	NA	NA	NA	NA	-	0,934	-0,05	0	6,847	1	0	1	2,444	0,803	0,14	-	-	-	-		-
SRR342019_TR2208_c1_g2_i4_len=2113	ACOT8_MOUSE	Q:773-1633,H:24-310	44.18%ID	E:2e-62	Acyl-coenzyme A thioesterase 8	PF00027.26*cNMP_binding*Cyclic nucleotide-binding domain*34-112*E:9.2e-11*PF13622.3*4HBT_3*Thioesterase-like superfamily*161-434*E:5.4e-66*PF02551.12*Acyl_CoA_thio*Acyl-CoA thioesterase*307-414*E:2.2e-26	0,609	0,267	0	2,186	0,034	1,035	0,006	1,286	1	1,676	ACOT8_MOUSE	Acyl-coenzyme A thioesterase 8 (Acyl-CoA thioesterase 8) (EC 3.1.2.27) (Choloyl-coenzyme A thioesterase) (Peroxisomal acyl-CoA thioesterase 2) (PTE-2) (Peroxisomal acyl-coenzyme A thioester hydrolase 1) (PTE-1) (Peroxisomal long-chain acyl-CoA thioesterase 1)	Acot8 Pte1 Pte2	Mus musculus (Mouse)		Complete proteome; Hydrolase; Peroxisome; Peroxisome biogenesis; Reference proteome; Serine esterase
SRR342019_TR2813_c0_g4_i7_len=2773	MT8T8_ARATH	Q:1045-20,H:1-347	44.44%ID	E:6e-78	Probable S-adenosylmethionine-dependent methyltransferase At5g38780	PF03492.12*Methyltransf_7*SAM dependent carboxyl methyltransferase*69-350*E:4e-101	0,011	0,897	0	2,763	0,002	1,368	0,666	0,255	0,196	0,782	MT8T8_ARATH	Probable S-adenosylmethionine-dependent methyltransferase At5g38780 (EC 2.1.1.-)	At5g38780 MKD10.80	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Methyltransferase; Reference proteome; S-adenosyl-L-methionine; Transferase
SRR342019_TR2947_c0_g1_i3_len=584	NA	NA	NA	NA	NA	-	0,766	-0,153	0	4,794	1	0,31	1	-1,505	0,419	-0,476	-	-	-	-		-
SRR342019_TR2947_c2_g4_i3_len=521	NA	NA	NA	NA	NA	-	0,704	0,212	0	7,203	1	-1,628	1	-1,628	0,079	-0,87	-	-	-	-		-
SRR342019_TR3324_c3_g3_i2_len=3520	AGLU_SPIOL	Q:2071-3369,H:471-602	59.73%ID	E:2e-172	Alpha-glucosidase	PF01055.23*Glyco_hydro_31*Glycosyl hydrolases family 31*1-168*E:5.9e-59	0,364	0,475	0	1,626	0,517	0,817	1	0,353	0,254	4,494	AGLU_SPIOL	Alpha-glucosidase (EC 3.2.1.20) (Maltase)	-	Spinacia oleracea (Spinach)		Direct protein sequencing; Glycoprotein; Glycosidase; Hydrolase; Signal
SRR342019_TR3806_c0_g1_i3_len=4254	TRPX_ARATH	Q:3320-1599,H:26-607	74.4%ID	E:0	Anthranilate synthase alpha subunit 2, chloroplastic	PF04715.10*Anth_synt_I_N*Anthranilate synthase component I, N terminal region*104-258*E:1.9e-30*PF00425.15*Chorismate_bind*chorismate binding enzyme*319-590*E:3.9e-85	0,155	1,125	0	4,855	1	-0,404	0,381	-1,909	1	3,219	TRPX_ARATH	Anthranilate synthase alpha subunit 2, chloroplastic (EC 4.1.3.27) (Anthranilate synthase component I-2) (Anthranilate synthase component I-2)	ASA2 At2g29690 T27A16.21	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Amino-acid biosynthesis; L-tryptophan biosynthesis; L-tryptophan from chorismate; step 1/5.	Amino-acid biosynthesis; Aromatic amino acid biosynthesis; Chloroplast; Complete proteome; Lyase; Plastid; Reference proteome; Transit peptide; Tryptophan biosynthesis
SRR342019_TR5968_c2_g10_i4_len=2743	Y005_SYNY3	Q:539-1831,H:107-525	35.86%ID	E:2e-83	Uncharacterized protein sll0005	PF03109.13*ABC1*ABC1 family*124-241*E:3.1e-31	0,025	3,442	0	2,739	0,039	1,086	0,255	0,653	0,839	0,111	Y005_SYNY3	Uncharacterized protein sll0005	sll0005	Synechocystis sp. (strain PCC 6803 / Kazusa)		Complete proteome; Reference proteome
SRR342019_TR7099_c4_g2_i7_len=2073	GEDH1_OCIBA	Q:429-1293,H:68-242	62.86%ID	E:4e-48	Geraniol dehydrogenase 1	PF00180.9*ADH_N*Alcohol dehydrogenase GroES-like domain*48-82*E:4e-15*PF02826.16*2-Hacid_dh_C*D-isomer specific 2-hydroxyacid dehydrogenase, NAD binding domain*105-155*E:3.2e-07	0,254	4,397	0	6,832	0,001	-6,492	0,001	-6,492	0,005	-6,197	GEDH1_OCIBA	Geraniol dehydrogenase 1 (ObaGEDH1) (EC 1.1.1.183)	GEDH1	Ocimum basilicum (Sweet basil)		Metal-binding; NADP; Oxidoreductase; Zinc
SRR342019_TR7176_c0_g1_i1_len=1811	DDC_CATRO	Q:1360-194,H:112-500	98.46%ID	E:0	Aromatic-L-amino-acid decarboxylase	PF00282.16*Pyridoxal_deC*Pyridoxal-dependent decarboxylase conserved domain*4-333*E:5e-102	0,011	0,59	0	4,73	0,96	-1,39	1	0,323	DDC_CATRO	Aromatic-L-amino-acid decarboxylase (AADC) (EC 4.1.1.28) (DOPA decarboxylase) (Tryptophan decarboxylase)	TDC	Catharanthus roseus (Madagascar periwinkle) (Vinca rosea)		Decarboxylase; Lyase; Pyridoxal phosphate
SRR342019_TR8002_c0_g2_i1_len=1154	ARGE_ARATH	Q:1084-26,H:1-357	77.31%ID	E:0	Acetylornithine deacetylase	PF01546.25*Peptidase_M20*Peptidase family M20/M25/M40*94-282*E:5.8e-20*PF07687.11*M20_dimer*Peptidase dimerisation domain*202-315*E:2.3e-13	0,316	0,634	0	3,52	0,08	1,206	0,057	1,315	0,502	3,97	ARGE_ARATH	Acetylornithine deacetylase (EC 3.5.1.16) (N-acetylornithinase) (AO) (Acetylornithinase) (NAD)	At4g17830 dl4945w T6K21	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Amino-acid biosynthesis; L-arginine biosynthesis; L-ornithine from N(2)-acetyl-L-ornithine (linear); step 1/1.	Alternative splicing; Amino-acid biosynthesis; Arginine biosynthesis; Cobalt; Complete proteome; Hydrolase; Metal-binding; Reference proteome; Zinc
SRR342019_TR8266_c0_g2_i1_len=1510	MYR1_SOLTU	Q:1413-886,H:24-188	57.89%ID	E:9e-39	Transcription factor MYB1R1	PF00249.28*Myb_DNA-binding*Myb-like DNA-binding domain*107-151*E:4.6e-11	0,009	2,187	0	2,197	0,168	0,459	0,722	0,143	0,025	1,171	MYR1_SOLTU	Transcription factor MYB1R1 (Myb-related protein 1) (Protein TINY)	Solanum tuberosum (Potato)			Complete proteome; Cytoplasm; DNA-binding; Nucleus; Reference proteome; Stress response; Transcription; Transcription regulation
SRR342019_TR8733_c0_g1_i4_len=2110	ASPG1_ARATH	Q:1530-3177,H:500-698	28.64%ID	E:3e-26	Protein ASPARTIC PROTEASE IN GUARD CELL 1	PF15453.3*TAXI_N*Xylanase inhibitor N-terminal*83-265*E:3.6e-28*PF00026.20*Asp*Eukaryotic aspartyl proteases*90-490*E:6e-07*PF14541.3*TAXI_C*Xylanase inhibitor C-terminal*303-489*E:1.8e-28	0,004	2,399	0	4,149	0,002	1,894	0,057	1,293	1	-0,93	ASPG1_ARATH	Protein ASPARTIC PROTEASE IN GUARD CELL 1 (AtASPG1) (EC 3.4.23.-)	ASPG1 At3g18490 MYF24.22	Arabidopsis thaliana (Mouse-ear cress)		Aspartyl protease; Complete proteome; DNA-binding; Disulfide bond; Endoplasmic reticulum; Hydrolase; Reference proteome; Signal
SRR342019_TR8982_c2_g3_i3_len=977	MTDH_APIGR	Q:648-4,H:2-325	62.79%ID	E:7e-84	Mannitol dehydrogenase	PF00180.9*ADH_N*Alcohol dehydrogenase GroES-like domain*39-151*E:2.5e-22	0,587	0,575	0	6,872	0,066	5,362	0,009	5,984	1	-0,318	MTDH_APIGR	Mannitol dehydrogenase (EC 1.1.1.255) (NAD-dependent mannitol dehydrogenase)	MTD	Apium graveolens (Celery)		Cytoplasm; Metal-binding; NAD; Oxidoreductase; Zinc
SRR342019_TR9643_c2_g2_i3_len=2153	STSY_RAUMA	Q:1165-2031,H:35-322	43.34%ID	E:2e-72	Strictosidine synthase	PF02121.15*P_trans*Phosphatidylinositol transfer protein*418-628*E:2.4e-82	0,001	6,53	0	6,787	0,025	1,83	0,038	1,732	1	0	STSY_RAUMA	Strictosidine synthase (EC 4.3.3.2) (Fragment)	STR1	Rauvolfia mannii	PATHWAY: Alkaloid biosynthesis; 3alpha(S)-strictosidine biosynthesis; 3alpha(S)-strictosidine from secologanin and tryptamine; step 1/1.	Alkaloid metabolism; Glycoprotein; Lyase; Signal; Vacuole
SRR342019_TR9656_c0_g2_i1_len=712	PR1B4_ARATH	Q:253-708,H:8-159	64.05%ID	E:9e-49	PRA1 family protein B4	-	0,547	0,318	0	2,81	0,695	-0,174	0,878	-0,088	1	-0,004	PR1B4_ARATH	PRA1 family protein B4 (AtPRA1.B4)	PRA1B4 At2g38360 T19C21.15	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Endosome; Membrane; Reference proteome; Transmembrane; Transmembrane helix; Transport
SRR342019_TR10001_c1_g1_i1_len=984	NA	NA	NA	NA	NA	-	0,006	1,834	0	6,924	0,005	6,125	0,005	6,164	1	0	-	-	-	-		-
SRR342019_TR10238_c0_g2_i2_len=782	NA	NA	NA	NA	NA	-	1	-0,063	0	2,091	0,472	0,755	0,352	0,889	0,832	-0,291	-	-	-	-		-
SRR342019_TR11670_c0_g7_i1_len=2195	P2A13_ARATH	Q:950-114,H:1-245	61.89%ID	E:2e-120	F-box protein PP2-A13	PF00646.30*F-box*F-box domain*56-97*E:0.0054*PF14299.3*PP2*Phloem protein 2*152-310*E:1.3e-36	0,079	1,1	0	2,954	0,004	0,758	0,013	0,651	0,007	1,163	P2A13_ARATH	F-box protein PP2-A13 (Protein PHLOEM PROTEIN 2-LIKE A13) (AtPP2-A13) (SKP1-interacting partner 9)	PP2A13 SKIP9 At3g61060 T27I15.150	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Protein modification; protein ubiquitination.	Alternative splicing; Complete proteome; Nucleus; Reference proteome; Ubl conjugation pathway
SRR342019_TR13074_c0_g1_i1_len=2903	RFS_PEA	Q:2645-327,H:4-798	68.72%ID	E:0	Galactinol--sucrose galactosyltransferase	PF05691.9*Raffinose_syn*Raffinose synthase or seed imbibition protein Sip1*25-758*E:0	0,077	0,788	0	1,638	0,07	-0,504	0,016	-0,673	0,005	1,186	RFS_PEA	Galactinol--sucrose galactosyltransferase (EC 2.4.1.82) (Raffinose synthase)	RFS	Pisum sativum (Garden pea)		Carbohydrate metabolism; Glycosyltransferase; Transferase
SRR342019_TR13756_c1_g1_i1_len=1526	MOMT_CATRO	Q:311-1354,H:1-348	93.97%ID	E:0	Myricetin O-methyltransferase	PF08100.8*Dimerisation*Dimerisation domain*27-74*E:8.4e-20*PF00891.15*Methyltransf_2*O-methyltransferase*117-334*E:1.7e-58	1	-0,067	0	2,773	0,56	0,859	1	0,486	0,745	-0,179	MOMT_CATRO	Myricetin O-methyltransferase (EC 2.1.1.267) (CrOMT2) (Flavonoid O-methyltransferase)	-	Catharanthus roseus (Madagascar periwinkle) (Vinca rosea)		Acetylation; Direct protein sequencing; Methyltransferase; S-adenosyl-L-methionine; Transferase
SRR342019_TR15806_c0_g2_i1_len=1588	UBQ4_ARATH	Q:95-1240,H:1-382	100%ID	E:0	Polyubiquitin 4	PF11976.5*Rad60-SLD*Ubiquitin-2 like Rad60 SUMO-like*1-71*E:1.4e-15*PF00240.20*ubiquitin*Ubiquitin family*3-74*E:2.1e-33*PF14560.3*Ubiquitin_2*Ubiquitin-like domain*14-69*E:0.00098*PF11976.5*Rad60-SLD*Ubiquitin-2 like Rad60 SUMO-like*77-147*E:1.4e-15*PF00240.20*ubiquitin*Ubiquitin family*79-150*E:2.1e-33*PF14560.3*Ubiquitin_2*Ubiquitin-like domain*148-149*E:0.00088*PF11976.5*Rad60-SLD*Ubiquitin-2 like Rad60 SUMO-like*153-223*E:1.4e-15*PF00240.20*ubiquitin*Ubiquitin family*155-226*E:2.1e-33*PF14560.3*Ubiquitin_2*Ubiquitin-like domain*164-221*E:0.00088*PF11976.5*Rad60-SLD*Ubiquitin-2 like Rad60 SUMO-like*229-293*E:1.4e-15*PF00240.20*ubiquitin*Ubiquitin family*231-302*E:2.1e-33*PF14560.3*Ubiquitin_2*Ubiquitin-like domain*240-297*E:0.00088*PF11976.5*Rad60-SLD*Ubiquitin-2 like Rad60 SUMO-like*305-375*E:1.4e-15*PF00240.20*ubiquitin*Ubiquitin family*307-378*E:2.1e-33*PF14560.3*Ubiquitin_2*Ubiquitin-like domain*316-375*E:0.00088	0,788	0,092	0	1,385	0,025	0,81	0,001	1,114	0,269	0,308	UBQ4_ARATH	Polyubiquitin 4 [Cleaved into: Ubiquitin]	UBQ4 At5g20620 T1M15.20	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Cytoplasm; Isopeptide bond; Nucleus; Reference proteome; Repeat; Ubl conjugation; Ubl conjugation pathway
SRR342019_TR16674_c1_g1_i1_len=1211	NA	NA	NA	NA	NA	PF00010.23*HLH*Helix-loop-helix DNA-binding domain*14-60*E:5.1e-09	1	0,175	0,917	0	3,766	0,003	2,942	0,01	2,774	1	0,216	-	-	-		-
SRR342019_TR18903_c8_g2_i2_len=4370	ADS3_ARATH	Q:3244-4218,H:54-367	71.78%ID	E:1e-147	Palmitoyl-monogalactosyldiacylglycerol delta-7 desaturase, chloroplastic (ECO:0000303|PubMed:15579662)	PF04487.21*FA_desaturase*Fatty acid desaturase*142-354*E:4e-17	1	-0,002	0	3,337	1	-0,188	0,56	0,636	0,705	0,18	ADS3_ARATH	Palmitoyl-monogalactosyldiacylglycerol delta-7 desaturase, chloroplastic (EC 1.14.19.-) (FADS) (Monogalactosyldiacylglycerol-specific palmitic acid desaturase)	ADS3 At3g15850 MSJ11.25	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Lipid metabolism; oxylipin biosynthesis; PATHWAY: Lipid metabolism; polyunsaturated fatty acid biosynthesis.	Chloroplast; Complete proteome; Fatty acid biosynthesis; Fatty acid metabolism; Iron; Lipid biosynthesis; Lipid metabolism; Membrane; Oxidoreductase; Oxylipin biosynthesis; Plastid; Reference proteome; Transit peptide; Transmembrane; Transmembrane helix
SRR342019_TR20560_c4_g2_i7_len=2144	BAT1_ORYSJ	Q:1615-116,H:19-518	82.8%ID	E:0	Amino-acid permease BAT1 homolog	PF13520.3*AA_permease_2*Amino acid permease*43-499*E:2.4e-61*PF00324.18*AA_permease*Amino acid permease*67-518*E:2e-24	0,044	1,148	0	2,091	0,548	-0,277	0,13	-0,67	1	-0,136	BAT1_ORYSJ	Amino-acid permease BAT1 homolog	BAT1 Os01g0607200 LOC_Os01g42234 OsJ_02547	Oryza sativa subsp. japonica (Rice)		Amino-acid transport; Complete proteome; Membrane; Reference proteome; Transmemb

						258*E:1.7e-08																		
SRR342022_TR20398_c2_g1_i3_len=619	NA	NA	NA	NA	NA	-	0.187	1.108	0	3.01	0.034	1.063	0.142	0.793	1	0.057	-	-	-	-	-	-	-	-
SRR342022_TR20837_c4_g8_i1_len=644	SCE1_ARATH	Q:98-577,H:1-160	84.38%ID	E:6e-85	SUMO-conjugating enzyme SCE1	PF00179.23*UQ_con*Ubiquitin-conjugating enzyme*9-151*E:4.9e-44	0.821	0.079	0	1.649	0.001	1.026	0.031	0.716	0.07	0.583	SCE1_ARATH	SUMO-conjugating enzyme SCE1 (EC 6.3.2.-) (Protein EMBRYO DEFECTIVE 1637) (Protein hus5 homolog) (SUMO-conjugating enzyme 1) (AtSCE1)	SCE1 AHUS5 EMB1637 At3g57670 T10K17.80	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Protein modification; protein sumoylation.	ATP-binding; Acetylation; Complete proteome; Ligase; Nucleotide-binding; Reference proteome; Ubl conjugation pathway
SRR342022_TR20959_c3_g3_i6_len=508	Q3118-1822,H:1-753	60.16%ID	E:2e-170	Serine decarboxylase	PF00282.16*Pyridoxal_dec*Pyridoxal-dependent decarboxylase conserved domain*48-302*E:1.5e-23	0.052	1.5	0.001	6.607	0.007	2.193	0.025	1.956	0.112	1,113	SDC1_ARATH	Serine decarboxylase (AtSDC) (EC 4.1.1.-) (Protein EMBRYO DEFECTIVE 1075) (Serine decarboxylase 1) (AtSDC1)	SDC EMB1075 SDC1 At1g43710 F2J6.7	Arabidopsis thaliana (Mouse-ear cress)	-	Complete proteome; Cytoplasm; Decarboxylase; Lyase; Pyridoxal phosphate; Reference proteome
SRR342022_TR21029_c2_g2_i2_len=3334	MACP2_ARATH	Q:1199-2992,H:15-998	66.1%ID	E:0	MACPF domain-containing protein At4g24290	PF01823.16*MACPF*MAC/Perforin domain*110-311*E:2.1e-36	0.319	0.882	0	2.337	0.042	1.775	0.158	1.408	0.732	-0.853	MACP2_ARATH	MACPF domain-containing protein At4g24290	At4g24290 T22A6.120	Arabidopsis thaliana (Mouse-ear cress)	-	Alternative splicing; Complete proteome; Hypersensitive response; Immunity; Innate immunity; Plant defense; Reference proteome
SRR342022_TR21370_c4_g3_i1_len=2810	SPE1_PEA	Q:2286-9,H:1-727	70.79%ID	E:0	Arginine decarboxylase	PF02784.13*Orn_Arg_deC_N*Pyridoxal-dependent decarboxylase, pyridoxal binding domain*140-410*E:2.1e-40 PF00278.19*Orn_DAP_Arg_deC*Pyridoxal-dependent decarboxylase, C-terminal sheet domain*498-612*E:7.4e-19	0.723	0.123	0	3.17	0.664	0.122	0.017	0.614	1	0.176	SPE1_PEA	Arginine decarboxylase (ADC) (ARGDC) (EC 4.1.1.19)	Pisum sativum (Garden pea)	PATHWAY: Amine and polyamine biosynthesis; agmatine biosynthesis; agmatine from L-arginine; step 1/1.	Decarboxylase; Lyase; Magnesium; Putrescine biosynthesis; Pyridoxal phosphate; Spermidine biosynthesis
SRR342022_TR21436_c1_g5_i1_len=1437	VPS2A_ARATH	Q:429-1097,H:2-225	91.0%ID	E:3e-108	Vacuolar protein sorting-associated protein 2 homolog 1	PF03357.18*Snf7*Snf7*17-186*E:6.1e-45	0.419	0.368	0	1.701	0.017	1.252	0.012	1.278	1	1.2	VPS2A_ARATH	Vacuolar protein sorting-associated protein 2 homolog 1 (AtVPS2-1) (Charged multivesicular body protein 2 homolog 1) (ESCRT-III complex subunit VPS2 homolog 1) (SNF7-like protein)	VPS2.1 CHMP2-1 SLP At2g06530 T12H3.8	Arabidopsis thaliana (Mouse-ear cress)	-	Coiled coil; Complete proteome; Endosome; Protein transport; Reference proteome; Transport
SRR342022_TR22371_c0_g2_i4_len=796	NA	NA	NA	NA	NA	-	0.004	1.902	0	2.852	0.487	-0.323	0.541	0.244	1	-1.24	-	-	-	-	-	-	-	-
SRR342022_TR24124_c0_g1_i5_len=1744	10HGO_CATRO	Q:170-786,H:11-303	57.52%ID	E:5e-95	8-hydroxygeraniol dehydrogenase	PF08240.9*ADH_N*Alcohol dehydrogenase GroES-like domain*41-164*E:2.7e-23 PF02826.16*2-Hacid_dh_C*D-isomer specific 2-hydroxyacid dehydrogenase, NAD binding domain*195-244*E:3.2e-07 PF00107.23*ADH_zinc_N*Zinc-binding dehydrogenase*211-318*E:2.7e-12	0.034	0.489	0	1.198	0.016	0.659	0.787	0.096	0.007	0.639	10HGO_CATRO	8-hydroxygeraniol dehydrogenase (Cr10HGO) (EC 1.1.1.324)	10HGO	Catharanthus roseus (Madagascar periwinkle) (Vinca rosea)	-	Metal-binding; NADP; Oxidoreductase; Zinc
SRR342022_TR26056_c0_g2_i2_len=710	RL192_ARATH	Q:67-648,H:1-196	86.22%ID	E:7e-90	60S ribosomal protein L19-2	PF01280.17*Ribosomal_L19e*Ribosomal protein L19e*4-146*E:2.6e-68	0.009	-0.836	0	1.559	0.102	0.565	0.684	-0.155	0.13	0.493	RL192_ARATH	60S ribosomal protein L19-2	RPL19B At3g16780 MGL6.25	Arabidopsis thaliana (Mouse-ear cress)	-	Complete proteome; Reference proteome; Ribonucleoprotein; Ribosomal protein
SRR342022_TR26073_c3_g1_i13_len=567	NA	NA	NA	NA	NA	-	0	-1.521	0	1.794	0.21	1.787	1	-1.477	1	1.187	-	-	-	-	-	-	-	-
SRR342022_TR27588_c4_g1_i1_len=2560	PP11_ARATH	Q:305-1459,H:25-412	56.01%ID	E:6e-133	Proton pump-interactor 1	-	0.903	-0.051	0	1.611	0.61	0.186	0.654	0.17	0.674	0.126	PP11_ARATH	Proton pump-interactor 1	PP11 At4g27500 F27G19.100	Arabidopsis thaliana (Mouse-ear cress)	-	Cell membrane; Coiled coil; Complete proteome; Endoplasmic reticulum; Membrane; Phosphoprotein; Reference proteome; Transmembrane; Transmembrane helix
SRR342022_TR28482_c0_g2_i1_len=540	VATL_GOSHI	Q:422-39,H:1-128	96.88%ID	E:3e-43	V-type proton ATPase 16 kDa proteolipid subunit	PF00137.18*ATP-synt_C*ATP synthase subunit C*17-76*E:1.3e-13 PF00137.18*ATP-synt_C*ATP synthase subunit C*97-128*E:6.3e-08	0.448	-0.183	0	2.922	0.918	0.03	0.65	0.113	0.76	0.336	VATL_GOSHI	V-type proton ATPase 16 kDa proteolipid subunit (V-ATPase 16 kDa proteolipid subunit) (Vacuolar proton pump 16 kDa proteolipid subunit)	Gossypium hirsutum (Upland cotton) (Gossypium mexicanum)	Hydrogen ion transport; Ion transport; Membrane; Transmembrane; Transmembrane helix; Transport; Vacuole
SRR342022_TR28725_c0_g1_i2_len=1839	BEBT_TOBAC	Q:121-1452,H:7-445	77.25%ID	E:0	Benzyl alcohol O-benzoyltransferase	PF02458.12*Transferase*Transferase family*14-440*E:4.9e-81	0.402	1.223	0	2.705	0.003	1.335	0.002	1.372	0.094	1.43	BEBT_TOBAC	Benzyl alcohol O-benzoyltransferase (EC 2.3.1.196) (Benzoyl coenzyme A:benzyl alcohol benzoyl transferase)	HSR201	Nicotiana tabacum (Common tobacco)	-	Acyltransferase; Transferase
SRR342022_TR28792_c1_g1_i3_len=1799	PTR21_ARATH	Q:551-1429,H:322-611	92.03%ID	E:3e-106	Protein NRT1/ PTR FAMILY 2.13	PF00854.18*PTR2*POT family*1-161*E:1.1e-29	0.002	1.654	0	2.736	0.002	1.435	0.007	1.298	0.335	0.624	PTR21_ARATH	Protein NRT1/ PTR FAMILY 2.13 (AtNPF2.13) (Nitrate transporter 1.7)	NPF2.13 NRT1.7 Atlg69870 T17F3.10	Arabidopsis thaliana (Mouse-ear cress)	-	Cell membrane; Complete proteome; Membrane; Nitrate assimilation; Reference proteome; Symport; Transmembrane; Transmembrane helix; Transport
SRR342022_TR28792_c1_g1_i3_len=1186	PTR21_ARATH	Q:1368-2816,H:136-611	53.91%ID	E:4e-177	Protein NRT1/ PTR FAMILY 2.13	PF00854.18*PTR2*POT family*22-440*E:4.2e-80	0.108	1.708	0	2.282	1	1.147	0.319	1.09	PTR21_ARATH	Protein NRT1/ PTR FAMILY 2.13 (AtNPF2.13) (Nitrate transporter 1.7)	NPF2.13 NRT1.7 Atlg69870 T17F3.10	Arabidopsis thaliana (Mouse-ear cress)	-	Cell membrane; Complete proteome; Membrane; Nitrate assimilation; Reference proteome; Symport; Transmembrane; Transmembrane helix; Transport
SRR342022_TR29142_c3_g2_i2_len=2476	ATHB6_ARATH	Q:1134-1610,H:34-204	60.23%ID	E:3e-50	Homeobox+leucine zipper protein ATHB-6	PF00046.26*Homeobox*Homeobox domain*20-73*E:2.7e-16 PF02183.15*HALZ*Homeobox associated leucine zipper*75-117*E:1.2e-18	0.111	0.382	0	1.502	0.019	0.679	0.747	0.12	0.167	0.396	ATHB6_ARATH	Homeobox-leucine zipper protein ATHB-6 (HD-ZIP protein ATHB-6) (Homeodomain transcription factor ATHB-6)	ATHB-6 At2g22430 F14M13.17	Arabidopsis thaliana (Mouse-ear cress)	-	Abscisic acid signaling pathway; Complete proteome; DNA-binding; Homeobox; Nucleus; Reference proteome; Stress response; Transcription; Transcription regulation
SRR342022_TR29250_c1_g2_i1_len=3164	CIPK9_ARATH	Q:247-1551,H:6-445	78.44%ID	E:0	CBL-interacting serine/threonine-protein kinase 9	PF00069.22*Pkinase*Protein kinase domain*15-270*E:4.2e-73 PF07714.14*Pkinase_Tyr*Protein tyrosine kinase*16-266*E:3.4e-38*PF14531.3*Kinase-like*Kinase-like*110-220*E:2.3e-07 PF03822.11*NAP*NAF domain*309-369*E:2.1e-24	0.694	-0.427	0	2.542	1	-0.056	0.182	0.519	1	-0.555	CIPK9_ARATH	CBL-interacting serine/threonine-protein kinase 9 (EC 2.7.11.1) (SNF1-related kinase 3.12) (SOS2-like protein kinase PKS6)	CIPK9 PKS6 SnRK3.12 At1g01140 F6F3.28 T25K16.13	Arabidopsis thaliana (Mouse-ear cress)	-	ATP-binding; Alternative splicing; Complete proteome; Cytoplasm; Kinase; Manganese; Nucleotide-binding; Nucleus; Phosphoprotein; Reference proteome; Serine/threonine-protein kinase; Transferase
SRR342022_TR30274_c0_g1_i1_len=557	NA	NA	NA	NA	NA	-	0.517	0.867	0	7.671	0.066	5.342	1	0	0.407	0.482	-	-	-	-	-	-	-	-
SRR342022_TR30555_c0_g1_i1_len=2499	AROA_PETHY	Q:1858-3111,H:6-416	84.3%ID	E0	3-phosphoshikimate 1-carboxyvinyltransferase, chloroplastic	PF00275.17*EPSP_synthase*EPSP synthase (3-phosphoshikimate 1-carboxyvinyltransferase)*79-509*E:1.7e-149	0.911	0.049	0	1.187	0.28	0.295	0.098	0.444	1	0.789	AROA_PETHY	3-phosphoshikimate 1-carboxyvinyltransferase, chloroplastic (EC 2.5.1.19) (5-enolpyruvylshikimate-3-phosphate synthase) (EPSP synthase)	Petunia hybrida (Petunia)	PATHWAY: Metabolic intermediate biosynthesis; chorismate biosynthesis; chorismate from D-erythrose 4-phosphate and phosphoenolpyruvate; step 6/7.	Amino-acid biosynthesis; Aromatic amino acid biosynthesis; Chloroplast; Herbicide resistance; Plastid; Transferase; Transit peptide
SRR342022_TR30829_c0_g2_i1_len=1950	THCAS_CANSA	Q:270-1762,H:32-540	43.95%ID	E:3e-133	Tetrahydrocannabinolic acid synthase	PF01565.20*FAD_binding_4*FAD binding domain*74-210*E:5.6e-23 PF08031.9*BBE*Berberine and berberine like*486-521*E:1.1e-13	0.472	0.32	0	3.208	0.277	0.579	0.777	-0.176	0.203	0.555	THCAS_CANSA	Tetrahydrocannabinolic acid synthase (THCAS) (EC 1.21.3.7) (Delta(1)-tetrahydrocannabinolic acid synthase) (THCA synthase)	Cannabis sativa (Hemp) (Marijuana)	2D-structure; Apoplast; Direct protein sequencing; Disulfide bond; FAD; Flavoprotein; Glycoprotein; Oxidoreductase; Secreted; Signal	-
SRR342022_TR33557_c0_g1_i1_len=542	NA	NA	NA	NA	NA	-	0.593	0.794	0	3.37	0.026	1.983	0.004	2.392	1	0.365	-	-	-	-	-	-	-	-
SRR342022_TR34117_c0_g3_i2_len=900	TRXH_RICCO	Q:78-466,H:3-113	83.78%ID	E:4e-63	Thioredoxin H-type	PF00085.17*Thioredoxin*Thioredoxin*42-144*E:3.8e-33	1	0.277	0	6.041	0.502	4.048	0.502	3.763	1	0	TRXH_RICCO	Thioredoxin H-type (TrxH)	Ricinus communis (Castor bean)	-	Cytoplasm; Disulfide bond; Electron transport; Redox-active center; Transport
SRR342022_TR34371_c0_g3_i1_len=691	NA	NA	NA	NA	NA	-	0.058	0.986	0.001	1.547	0.003	1.448	0.365	0.529	0.129	3.921	-	-	-	-	-	-	-	-
SRR342022_TR34629_c0_g1_i1_len=857	NA	NA	NA	NA	NA	-	0.184	0.476	0	1.221	0.008	0.904	0.067	0.641	0.597	0.208	-	-	-	-	-	-	-	-
SRR342022_TR34968_c0_g1_i1_len=751	NA	NA	NA	NA	NA	-	0.56	0.874	0	2.774	0.008	1.64	0.663	0.521	1	-0.114	-	-	-	-	-	-	-	-
SRR342022_TR36961_c0_g1_i1_len=1290	NA	NA	NA	NA	NA	-	0.653	0.198	0.001	1.203	0.03	0.748	0.008	0.896	0.266	-0.519	-	-	-	-	-	-	-	-
SRR342022_TR417_c0_g2_i5_len=2137	NA	NA	NA	NA	NA	-	0.201	0.493	0	1.333	0.258	1.123	0.472	0.853	1	-0.094	-	-	-	-	-	-	-	-
SRR342022_TR623_c0_g2_i1_len=1317	TAF7_ARATH	Q:310-753,H:1-148	75%ID	E:4e-66	Transcription initiation factor TFIID subunit 7	PF04658.10*TAF155_N*TAF155 protein conserved region*1-139*E:1.5e-33	1	-0.001	0.001	6.63	1	-0.102	1	1	0.326	0.904	0.099	TAF7_ARATH	Transcription initiation factor TFIID subunit 7 (TBP-associated factor 7) (AtTAF7)	TAF7 At1g55300 F7A10.3	Arabidopsis thaliana (Mouse-ear cress)	-	Activator; Alternative splicing; Complete proteome; Nucleus; Reference proteome; Transcription; Transcription regulation
SRR342022_TR1754_c1_g5_i2_len=986	AB19I_ARATH	Q:886-47,H:1-292	77.5%ID	E:4e-147	ABC transporter I family member 19	PF00005.24*ABC_tran*ABC transporter*27-170*E:2.3e-13	0.712	-0.248	0	2.158	0.889	-0.118	0.793	0.187	0.017	5.848	AB19I_ARATH	ABC transporter I family member 19 (ABC transporter ABCI.19) (AtABCI19) (GCN-related protein 2) (Noninitimisic ABC protein 4)	ABCI19 NAP4 At1g03905 F21M11.17	Arabidopsis thaliana (Mouse-ear cress)	-	ATP-binding; Complete proteome; Cytoplasm; Nucleotide-binding; Reference proteome; Transport
SRR342022_TR2711_c0_g2_i1_len=2040	AOC4_ARATH	Q:1611-2039,H:111-254	72.22%ID	E:3e-60	Allene oxide cyclase 4, chloroplastic	PF12049.5*DUF3531*Protein of unknown function (DUF3531)*1-141*E:1.1e-55	0.004	1.393	0	3.161	0.01	1.758	0.035	1.528	0.212	-1.05	AOC4_ARATH	Allene oxide cyclase 4, chloroplastic (EC 5.3.99.6)	AOC4 At1g13280 T6J4.4 T6J4_23	Arabidopsis thaliana (Mouse-ear cress)	-	Chloroplast; Complete proteome; Isomerase; Plastid; Reference proteome; Transit peptide
SRR342022_TR3089_c0_g1_i1_len=783	STAD_OLEEU	Q:78-332,H:241-390	85.33%ID	E:1e-91	Stearoyl-[acyl-carrier-protein] 9-desaturase, chloroplastic	PF03405.11*FA_desaturase_2*Fatty acid desaturase*1-144*E:3.4e-62	1	0.014	0	1.421	0.156	0.6	0.915	0.09	1	1.141	STAD_OLEEU	Stearoyl-[acyl-carrier-protein] 9-desaturase, chloroplastic (Stearoyl-ACP desaturase) (EC 1.14.19.2) (Acyl-[acyl-carrier-protein] desaturase)	Olea europaea (Common olive)	PATHWAY: Lipid metabolism; fatty acid metabolism.	Chloroplast; Fatty acid biosynthesis; Fatty acid metabolism; Iron; Lipid biosynthesis; Lipid metabolism; Metal-binding; Oxidoreductase; Plastid; Transit peptide
SRR342022_TR3168_c2_g1_i1_len=1254	LOR12_ARATH	Q:883-281,H:19-220	64.85%ID	E:8e-88	Protein LURP-one-related 12	PF04525.9*LOR*LURP-one-related*6-183*E:5.5e-53	0.074	0.922	0	3.363	0.005	0.77	0.042	0.56	0.175	0.537	LOR12_ARATH	Protein LURP-one-related 12	At3g15810 MSJ11.21	Arabidopsis thaliana (Mouse-ear cress)	-	Complete proteome; Reference proteome
SRR342022_TR3544_c0_g2_i2_len=563	DCE_PETHY	Q:50-562,H:27-447	87.13%ID	E:8e-108	Glutamate decarboxylase	PF00282.16*Pyridoxal_dec*Pyridoxal-dependent decarboxylase conserved domain*5-109*E:2.4e-28	1	0	0	5.532	0.034	5.665	0.017	5.917	1	0.365	DCE_PETHY	Glutamate decarboxylase (GAD) (EC 4.1.1.15)	GAD	Petunia hybrida (Petunia)	-	3D-structure; Calmodulin-binding; Decarboxylase; Lyase; Pyridoxal phosphate
SRR342022_TR3587_c2_g1_i2_len=1204	INT1_ARATH	Q:597-49,H:3-186	80.43%ID	E:3e-60	Inositol transporter 1	PF00083.21*Sugar_tr*Sugar (and other) transporter*32-185*E:3.7e-41 PF07690.13*MFS_1*Major Facilitator Superfamily*37-182*E:5.4e-13	0.666	0.308	0	3.06	0.052	1.46	0.052	1.455	1	0.971	INT1_ARATH	Inositol transporter 1	INT1 At2g43330 T10C24.7	Arabidopsis thaliana (Mouse-ear cress)	-	Complete proteome; Membrane; Reference proteome; Transport; Transmembrane; Transmembrane helix; Transport; Vacuole
SRR342022_TR5798_c3_g3_i1_len=522	NA	NA	NA	NA	NA	-	0.185	-0.41	0	3.13	0.028	-0.85	0.814	-0.109	1	0	-	-	-	-	-	-	-	-
SRR342022_TR6044_c0_g1_i9_len=1904	P2C06_ORYSJ	Q:805-2,H:126-391	57.35%ID	E:2e-89	Probable protein phosphatase 2C 6	PF00481.18*PP2C*Protein phosphatase 2C*134-363*E:3.6e-49	0.319	0.947	0	1.98	1	-0.013	0.781	-0.475	0.004	2.322	P2C06_ORYSJ	Probable protein phosphatase 2C 6 (OsPP2C06) (EC 3.1.3.16)	Os01g0583100 LOC_Os01g40094	Oryza sativa subsp. japonica (Rice)	-	3D-structure; Complete proteome; Hydrolase; Magnesium; Manganese; Metal-binding; Protein phosphatase; Reference proteome
SRR342022_TR6962_c0_g6_i1_len=1484	SPSA4_ARATH	Q:1052-3,H:205-555	82.91%ID	E0	Probable sucrose-phosphate synthase 4	PF13579.3*Glyco_trans_4_4*Glycosyltransferase 4-like domain*10-203*E:1.5e-07 PF13439.3*Glyco_transf_4*Glycosyltransferase Family 4*10-159*E:1.5e-06 PF00862.16*Sucrose_synth*Sucrose synthase*68-214*E:8.1e-08	0.212	0.915	0	3.555	0.117	0.977	0.117	0.968	0.008	0.889	SPSA4_ARATH	Probable sucrose-phosphate synthase 4 (EC 2.4.1.14) (Sucrose phosphate synthase 4F) (AtSPS4F) (UDP-glucose:fructose-phosphate glucosyltransferase)	SPS4 SPSC At4g10120 F28M11.40	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Glycan biosynthesis; sucrose biosynthesis; sucrose from D-fructose 6-phosphate and UDP-alpha-D-glucose; step 1/2.	Complete proteome; Glycosyltransferase; Phosphoprotein; Reference proteome; Transferase
SRR342022_TR7033_c4_g6_i3_len=1039	FLS_PETHY	Q:91-96,H:11-279	74.73%ID	E:3e-138	Flavonol synthase/flavanone 3-hydroxylase	PF14226.3*DIOX_N*non-haem dioxygenase in morphine synthesis N-terminal*43-154*E:1e-25 PF03171.17*2OG-Fe(II)_Oxy*2OG-Fe(II) oxygenase superfamily*204-270*E:1.7e-16	0.945	-0.059	0	1.896	0.004	-0.713	0.009	-0.639	1	0.288	FLS_PETHY	Flavonol synthase/flavanone 3-hydroxylase (FLS) (EC 1.14.11.23) (EC 1.14.11.9)	FL	Petunia hybrida (Petunia)	PATHWAY: Secondary metabolite biosynthesis; flavonoid biosynthesis.	Cytoplasm; Dioxygenase; Flavonoid biosynthesis; Iron; Metal-binding; Oxidoreductase; Vitamin C
SRR342022_TR7067_c0_g1_i1_len=769	NA	NA	NA	NA	NA	-	0.035	0.661	0	1.6	0.001	0.743	0.002	0.703	0.874	-0.105	-	-	-	-	-	-	-	-
SRR342022_TR10321_c1_g2_i1_len=935	NA	NA	NA	NA	NA	-	0.921	0.072	0.001	1.536	0.486	0.237	0.169	0.439	1	1.053	-	-	-	-	-	-	-	-
SRR342022_TR10433_c1_g1_i2_len=2969	PSCS_ACTDE	Q:2486-345,H:1-713	86.69%ID	E0	Delta-1-pyrroline-5-carboxylate synthase	PF00696.25*AA_kinase*Amino acid kinase family*16-261*E:1.1e-38*PF00171.19*Aldedh*Aldehyde dehydrogenase family*294-559*E:6.4e-08	0.41	-0.324	0	2.252	0.511	0.204	0.256	-0.343	0.381	1.865	PSCS_ACTDE	Delta-1-pyrroline-5-carboxylate synthase (PSCS) [Includes: Glutamate 5-kinase (GK) (EC 2.7.2.11) (Gamma-glutamyl kinase); Gamma-glutamyl phosphate reductase (GPR) (EC 1.2.1.41) (Glutamate-5-semialdehyde dehydrogenase) (Glutamyl-gamma-semialdehyde dehydrogenase)]	Actinidia deliciosa (Kiwi)	PATHWAY: Amino-acid biosynthesis; L-proline biosynthesis; L-glutamate 5-semialdehyde from L-glutamate; step 1/2. PATHWAY: Amino-acid biosynthesis; L-proline biosynthesis; L-glutamate 5-semialdehyde from L-glutamate; step 2/2.	ATP-binding; Amino-acid biosynthesis; Kinase; Multifunctional enzyme; NADP; Nucleotide-binding; Oxidoreductase; Proline biosynthesis; Transferase
SRR342022_TR12131_c0_g3_i1_len=605	UBL5_ARATH	Q:494-276,H:1-73	98.63%ID	E:2e-43	Ubiquitin-like protein 5	PF10591.6*SPARC_Ca_bdg*Secreted protein acidic and rich in cysteine Ca binding region*20-82*E:0.00011 PF13833.3*EF-hand_8*EF-hand domain pair*22-49*E:0.00063 PF00036.29*EF-hand_1*EF hand*23-51*E:2.7e-08 PF13405.3*EF-hand_6*EF-hand domain*23-52*E:1.1e-06 PF13499.3*EF-hand_7*EF-hand domain pair*24-84*E:5e-14 PF13202.3*EF-hand_5*EF hand*25-47*E:5.3e-09 PF13833.3*EF-hand_8*EF-hand domain pair*55-82*E:0.00014 PF00036.29*EF-hand_1*EF hand*59-85*E:6.7e-08 PF13202.3*EF-hand_5*EF hand*61-83*E:9.2e-05 PF13499.3*EF-hand_7*EF-hand domain pair*101-163*E:3.5e-16 PF00036.29*EF-hand_1*EF hand*102-130*E:1.9e-07 PF13405.3*EF-hand_6*EF-hand domain*102-131*E:1.2e-07 PF13202.3*EF-hand_5*EF hand*104-126*E:7.5e-05 PF13833.3*EF-hand_8*EF-hand domain pair*114-164*E:5.5e-13 PF00036.29*EF-hand_1*EF hand*140-165*E:1.4e-07 PF13202.3*EF-hand_5*EF hand*145-163*E:7.5e-05	0.005	0.739	0	1.402	0.047	0.496	0.094	0.421	0.034	5.726	UBL5_ARATH	Ubiquitin-like protein 5	UBL5 At5g42330 K5J14.10	Arabidopsis thaliana (Mouse-ear cress)	-	Complete proteome; Cytoplasm; Reference proteome; Ubl conjugation pathway
SRR342022_TR12510_c1_g2_i1_len=1214	ALL8_OLEEU	Q:490-960,H:8-161	67.52%ID	E:2e-66	Calcium-binding allergen Ole e 8	PF04145.12*Ca*Chr copper transporter family*4-143*E:1.5e-24	0.679	0.408	0	3.026	1	0.006	0.011	0.733	0.044	-0.802	ALL8_OLEEU	Calcium-binding allergen Ole e 8 (PCA18/PCA23) (allergen Ole e 8)	Olea europaea (Common olive)	-	Allergen; Calcium; Metal-binding; Polymorphism; Repeat
SRR342022_TR12885_c0_g1_i1_len=1070	COPT5_ARATH	Q:844-365,H:1-146	53.42%ID	E:2e-34	Copper transporter 5	PF04145.12*Ca*Chr copper transporter family*4-143*E:1.5e-24	0.031	0.874	0	2.008	0.051	0.805	0.019	0.94	1	0.637	COPT5_ARATH	Copper transporter 5 (AtCOPT5)	COPT5 At5g20650 T1M15.50	Arabidopsis thaliana (Mouse-ear cress)	-	Complete proteome; Copper; Copper transport; Ion transport; Membrane; Reference proteome; Transmembrane; Transmembrane helix; Transport
SRR342022_TR14316_c0_g1_i5_len=1804	NA	NA	NA	NA	NA	-	0.005	1.039	0.001	1.078	1	0	-1.309	1	-1.56	0.156	0.591	-	-	-	-	-	-	-
SRR342022_TR14686_c0_g1_i2_len=2205	FAP2_ARATH	Q:729-1865,H:24-398	53.87%ID	E:9e-124	Fattyacid-binding protein 2	PF16035.2*Chalcone_2*Chalcone isomerase like*234-406*E:2.4e-16 PF16036.2*Chalcone_3*Chalcone isomerase-like*289-405*E:5.2e-07	0.822	0.296	0	2.702	0.088	1.349	0.001	2.237	1	-0.008	FAP2_ARATH	Fattyacid-binding protein 2 (AtFAP2) (Chalcone-flavanone isomerase family protein 2)	FAP2 At2g26310 T1D16.5	Arabidopsis thaliana (Mouse-ear cress)	-	Alternative splicing; Chloroplast; Complete proteome; Plastid; Reference proteome
SRR342022_TR15920_c0_g1_i1_len=818	IMP3_MOUSE	Q:85-621,H:2-181	57.78%ID	E:1e-72	U3 small nucleolar ribonucleoprotein protein IMP3	PF00183.16*Ribosomal_S4*Ribosomal protein S4/S9 N-terminal domain*3-62*E:3.1e-10 PF01479.22*S4*S4 domain*107-153*E:3e-10	0.226	2.335	0	6.978	0.066	3.352	0.129	3.079	0	-7.671	IMP3_MOUSE	U3 small nucleolar ribonucleoprotein protein IMP3 (U3 snoRNP protein IMP3)	Imp3	Mus musculus (Mouse)	-	Complete proteome; Nucleus; RNA-binding; Reference proteome; Ribonucleoprotein; Ribosome biogenesis; rRNA processing; rRNA-binding
SRR342023_TR15973_c0_g3_i1_len=3335	Y3475_ARATH	Q:318-185,H:46-998	35.92%ID	E:1e-180	Probable LRR receptor-like serine/threonine-protein kinase At3g47570	PF08263.9*LRRNT_2*Leucine rich repeat N-terminal domain*42-88*E:2.1e-07 PF13855.3*LRR_8*Leucine rich repeat*165-225*E:6.4e-08 PF13516.3*LRR_6*Leucine Rich repeat*385-400*E:0.42 PF00560.30*LRR_1*Leucine Rich Repeat*388-410*E:0.028 PF13516.3*LRR_6*Leucine Rich repeat*460-475*E:1.2e-03 PF00560.30*LRR_1*Leucine Rich Repeat*607-629*E:0.0034 PF13516.3*LRR_6*Leucine Rich repeat*607-620*E:1.1 PF00069.22*Pkinase*Protein kinase domain*750-950*E:1.5e-44 PF07714.14*Pkinase_Tyr*Protein tyrosine kinase*754-952*E:6.4e-42	0.004	0.989	0	1.7	0.195	1.149	0.004	2.026	0.245	-0.513	Y3475_ARATH	Probable LRR receptor-like serine/threonine-protein kinase At3g47570 (EC 2.7.11.1)	At3g47570 F1P2.120	Arabidopsis thaliana (Mouse-ear cress)	-	ATP-binding; Cell membrane; Complete proteome; Glycoprotein; Kinase; Leucine-rich repeat; Membrane; Nucleotide-binding; Phosphoprotein; Receptor; Reference proteome; Repeat; Serine/threonine-protein kinase; Signal; Transferase; Transmembrane; Transmembrane helix
SRR342023_TR16547_c0_g1_i1_len=1366	NA	NA	NA	NA	NA	-	0.126	0.633	0	1.457	0.52	0.147	0.945	-0.02	0.852	0.068	-	-	-	-	-	-	-	-
SRR342023_TR18138_c2_g3_i3_len=2780	DRP2A_ARATH	Q:1304-3,H:361-794	81.01%ID	E0	Dynamin-2A	PF02469.19*Fasciclin*Fasciclin domain*129-258*E:1.2e-13	0.071	0.549	0	1.631	0.005	0.902	0.004	0.928	1	0.701	DRP2A_ARATH	Dynamin-2A (EC 3.6.5.5) (Dynamin-like protein 6) (Dynamin-related protein 2A)	DRP2A ADL6 At1g10290 F14N23.17	Arabidopsis thaliana (Mouse-ear cress)	-	Acetylation; Coiled coil; Complete proteome; Cytoplasm; Cytoplasmic vesicle; Cytoskeleton; GTP-binding; Golgi apparatus; Hydrolase; Lipid-binding; Membrane; Microtubule; Motor protein; Nucleotide-binding; Reference proteome
SRR342023_TR19692_c2_g6_i1_len=2356	CAP10_ARATH	Q:1969-536,H:1-479	70.54%ID	E0	Putative clathrin assembly protein At5g35200	PF07651.13*ANTH*ANTH domain*34-301*E:7.9e-91	0.255	0.623	0	1.839	0.093	0.788	0.075	0.829	1	0.917	CAP10_ARATH	Putative clathrin assembly protein At5g35200	At5g35200 K3D20.4 T25C13.80	Arabidopsis thaliana (Mouse-ear cress)	-	Coated pit; Complete proteome; Cytoplasmic vesicle; Endocytosis; Golgi apparatus; Membrane; Phosphoprotein; Reference proteome
SRR342023_TR20699_c2_g3_i2_len=2023	AROF_SOLTU	Q:10-1720,H:1-536	83.27%ID	E0	Phospho-2-dehydro-3-deoxyheptonate aldolase 1, chloroplastic	PF1474.13*DAHP_synth_2*Class-II DAHP synthetase family*96-532*E:3.7e-197	0.455	0.23	0	1.349	0.003	-0.803	0.071	-0.485	1	-0.117	AROF_SOLTU	Phospho-2

SRR646596_T103649_c0_g1_i1_len=939	FER13_ARATH	513;H:180-303	60.97;40	E:1e-50	Ferredoxin membrane protein 13	0.0119	0.134	0	1.290	0.021	0.134	0.004	0.002	0.939	0.030	FER13_ARATH	(Pex13p) (Protein ABERRANT PEROXISOME MORPHOLOGY 2)	FER13 PF04 Ferredoxin 12;10;0;47	Arabidopsis thaliana (Mouse-ear cress)	-	-	-	-	-	-	-	-	-	-
SRR646596_T26527_c0_g2_i1_len=931	NA	NA	NA	NA	NA	0.175	0.942	0	2.208	0.017	2.36	0.001	2.794	1	-0.46	-	-	-	-	-	-	-	-	-	-	-	-	-	biogenesis; Protein transport; Reference proteome; Translocation; Transport
SRR646596_T27458_c0_g1_i1_len=881	NA	NA	NA	NA	NA	0.18	0.775	0	1.574	0.004	1.958	0.004	1.985	0.328	0.473	-	-	-	-	-	-	-	-	-	-	-	-	-	-
SRR646596_T28941_c0_g2_i4_len=2045	NA	NA	NA	NA	NA	0.45	0.598	0	2.728	0.043	2.5	0.003	3.125	0.189	-1.9	-	Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial (EC 2.3.1.168) (Branched-chain alpha-keto acid dehydrogenase complex component E2) (BCE2) (BCKAD-E2) (BCKADE2) (Dihydrolipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex) (Dihydrolipoamide branched chain transacylase) (Dihydrolipoyllysine-residue (2-methylpropanoyl)transferase) (Protein DARK INDUCIBLE 3)	BCE2 DIN3 LTA1 At3g06850 F3E22.1	Arabidopsis thaliana (Mouse-ear cress)	-	-	-	-	-	-	-	-	-	-	Acyltransferase; Complete proteome; Fatty acid biosynthesis; Fatty acid metabolism; Lipid biosynthesis; Lipid metabolism; Lipoyl; Mitochondrion; Reference proteome; Transferase; Transit peptide
SRR646596_T28962_c0_g1_i4_len=2457	CT2A1_CATRO	Q2338-770;H:1-523	99.24%;ID	E:0	Secologanin synthase	0.269	0.442	0	5.087	1	0.121	0.534	-0.425	0.732	0.779	CT2A1_CATRO	Secologanin synthase (SLS) (EC 1.3.3.9) (CYPLXXII) (Cytochrome P450 72A1)	CYP72A1 CYP72 P450CR3	Catharanthus roseus (Madagascar periwinkle) (Vinca rosea)	PATHWAY: Alkaloid biosynthesis; secologanin biosynthesis.	-	-	-	-	-	-	-	-	Alkaloid metabolism; Heme; Iron; Membrane; Metal-binding; Monooxygenase; NADP; Oxidoreductase; Transmembrane; Transmembrane helix; Vacuole
SRR646596_T28962_c0_g1_i5_len=2543	CT2A1_CATRO	Q1608-770;H:245-523	97.49%;ID	E:0	Secologanin synthase	0.034	0.826	0	3.226	0.059	1.192	0.257	0.831	0.129	2.867	CT2A1_CATRO	Secologanin synthase (SLS) (EC 1.3.3.9) (CYPLXXII) (Cytochrome P450 72A1)	CYP72A1 CYP72 P450CR3	Catharanthus roseus (Madagascar periwinkle) (Vinca rosea)	PATHWAY: Alkaloid biosynthesis; secologanin biosynthesis.	-	-	-	-	-	-	-	-	Alkaloid metabolism; Heme; Iron; Membrane; Metal-binding; Monooxygenase; NADP; Oxidoreductase; Transmembrane; Transmembrane helix; Vacuole
SRR646596_T29927_c0_g1_i1_len=1056	NA	NA	NA	NA	NA	0.031	1.299	0	1.632	0.001	1.757	0.043	1.233	1	-0.015	-	-	-	-	-	-	-	-	-	-	-	-	-	-
SRR646596_T30351_c0_g1_i1_len=1104	PER25_ARATH	Q1918-119;H:29-328	74.33%;ID	E:3e-164	Peroxidase 25	0.502	2.751	0	5.525	0.189	1.976	0.118	2.157	1	1.533	PER25_ARATH	Peroxidase 25 (Atperox P25) (EC 1.11.1.7)	PER25 P25 At2g41480 T26J13.7	Arabidopsis thaliana (Mouse-ear cress)	-	-	-	-	-	-	-	-	-	-
SRR646464_T8355_c0_g1_i1_len=1464	NA	NA	NA	NA	NA	1	-0.014	0	7.719	1	-1.927	1	-1.228	0.798	0.541	-	-	-	-	-	-	-	-	-	-	-	-	-	-
SRR646604_T8619_c0_g1_i1_len=1903	PHT17_ARATH	Q1902-727;H:130-507	78.32%;ID	E:0	Probable inorganic phosphate transporter 1-7	1	0.724	0	3.864	0.694	0.418	1	-0.082	0.76	0.612	PHT17_ARATH	Probable inorganic phosphate transporter 1-7 (AtPht1;7) (H(+)/Pi cotransporter)	PHT1-7 At3g54700 T5N23.60	Arabidopsis thaliana (Mouse-ear cress)	-	-	-	-	-	-	-	-	-	Complete proteome; Membrane; Phosphate transport; Phosphoprotein; Reference proteome; Symport; Transmembrane; Transmembrane helix; Transport
SRR646604_T20491_c0_g1_i3_len=2295	MATE4_ARATH	Q1933-1863;H:5-559	63.88%;ID	E:0	-	0.009	1.315	0	2.707	0.012	0.809	0.052	0.643	0.38	0.433	DTX46_ARATH	Protein DETOXIFICATION 46, chloroplactic (AtDTX46) (Multidrug and toxic compound extrusion protein 46) (MATE protein 46) (Protein EDS5 HOMOLOGUE)	DTX46 EDS5H At2g21340 F3K23.10	Arabidopsis thaliana (Mouse-ear cress)	-	-	-	-	-	-	-	-	-	Alternative splicing; Chloroplast; Complete proteome; Membrane; Plastid; Reference proteome; Transit peptide; Transmembrane; Transmembrane helix; Transport
SRR646604_T8166_c0_g2_i1_len=2140	TCMO_CATRO	Q235-1749;H:1-505	98.81%;ID	E:0	Trans-cinnamate 4-monooxygenase	0.774	0.143	0	2.841	0.684	0.124	0.041	0.553	0.204	0.551	TCMO_CATRO	Trans-cinnamate 4-monooxygenase (EC 1.14.13.11) (Cinnamic acid 4-hydroxylase) (C4H) (CA4H) (Cytochrome P450 73) (Cytochrome P450C4H)	CYP73A4	Catharanthus roseus (Madagascar periwinkle) (Vinca rosea)	PATHWAY: Phenylpropanoid metabolism; trans-4-coumarate biosynthesis; trans-4-coumarate from trans-cinnamate: step 1/1.	-	-	-	-	-	-	-	-	-	Heme; Iron; Metal-binding; Monooxygenase; NADP; Oxidoreductase
SRR646604_T8543_c0_g1_i2_len=2070	MGDG_TOBAC	Q1682-498;H:6-413	71.15%;ID	E:0	Probable monogalactosyldiacylglycerol synthase, chloroplastic	0.126	0.619	0	2.655	0.083	0.587	0.005	0.901	1	0.061	MGDG_TOBAC	Probable monogalactosyldiacylglycerol synthase, chloroplastic (NtMGD1) (EC 2.4.1.46) (MGDG synthase type A)	MGD A	Nicotiana tabacum (Common tobacco)	-	-	-	-	-	-	-	-	-	Chloroplast; Glycosyltransferase; Membrane; Plastid; Transferase; Transit peptide
SRR646604_T9361_c0_g1_i1_len=933	TCP10_ARATH	Q2166-787;H:14-87	91.89%;ID	E:7e-40	Transcription factor TCP10	0.848	0.232	0	3.165	0.043	1.335	0.001	1.858	0.282	0.91	TCP10_ARATH	Transcription factor TCP10	TCP10 At2g31070 T16B12.12	Arabidopsis thaliana (Mouse-ear cress)	-	-	-	-	-	-	-	-	-	Complete proteome; DNA-binding; Development protein; Nucleus; Reference proteome; Transcription; Transcription regulation
SRR646604_T11233_c0_g2_i1_len=1666	ACOX4_ARATH	Q1540-620;H:1-307	79.15%;ID	E:0	Acyl-coenzyme A oxidase 4, peroxisomal	0.038	0.987	0	2.527	0.166	0.83	0.034	1.204	1	0.076	ACOX4_ARATH	Acyl-coenzyme A oxidase 4, peroxisomal (AOX 4) (EC 1.3.3.6) (G6p) (Short-chain acyl-CoA oxidase) (ACX4) (AG6) (SACX)	ACX4 G6 At3g51840 ATEM1.9	Arabidopsis thaliana (Mouse-ear cress)	-	-	-	-	-	-	-	-	-	3D-structure; Acetylation; Complete proteome; FAD; Fatty acid metabolism; Flavoprotein; Glyoxysome; Lipid metabolism; Oxidoreductase; Peroxisome; Reference proteome
SRR646604_T11484_c0_g2_i1_len=1111	RS141_MAIZE	Q984-568;H:1-138	94.24%;ID	E:4e-77	40S ribosomal protein S14	0.502	-4.307	0	2.602	0.461	1.106	0.692	0.898	1	0.01	RS141_MAIZE	40S ribosomal protein S14 (Clone MCH1)	-	Zea mays (Maize)	-	-	-	-	-	-	-	-	-	Complete proteome; Reference proteome; Ribonucleoprotein; Ribosomal protein
SRR646604_T12699_c0_g1_i3_len=2823	GGAP1_ARATH	Q1935-715;H:1-940	74.69%;ID	E:0	GDP-L-galactose phosphorylase 1	0.292	0.307	0	1.704	0.653	0.107	0.875	-0.042	0.001	0.842	GGAP1_ARATH	GDP-L-galactose phosphorylase 1 (EC 2.7.7.69) (Protein VITAMIN C DEFECTIVE 2)	VTC2 At4g26850 F10M23.190	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Cofactor biosynthesis; L-ascorbate biosynthesis via GDP-alpha-D-mannose pathway; Reference proteome; Transferase	-	-	-	-	-	-	-	-	-	Ascorbate biosynthesis; Complete proteome; Cytoplasm; Guanine-nucleotide releasing factor; Hydrolase; Nucleotide-binding; Nucleotidyltransferase; Nucleus; Reference proteome; Transferase
SRR646604_T17922_c0_g1_i1_len=3216	SERB2_ARATH	Q1676-2902;H:18-421	79.81%;ID	E:0	Phosphoserine aminotransferase 2, chloroplastic	0.568	0.278	0	2.25	0.748	0.265	0.87	0.162	0.431	0.331	SERB2_ARATH	Phosphoserine aminotransferase 2, chloroplastic (AtPSAT2) (EC 2.6.1.52)	PSAT2 At2g17630 T19E12.3	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Amino-acid biosynthesis; L-serine biosynthesis; L-serine from 3-phospho-D-glycerate: step 2/3.	-	-	-	-	-	-	-	-	-	Acetylation; Amino-acid biosynthesis; Aminotransferase; Chloroplast; Complete proteome; Plastid; Pyridoxal phosphate; Reference proteome; Serine biosynthesis; Transferase; Transit peptide
SRR646604_T19937_c0_g3_i1_len=4044	YSL7_ARATH	Q3621-1543;H:1-687	77.06%;ID	E:0	Probable metal-nicotianamine transporter YSL7	0.129	1.098	0	3.304	0.044	2.291	0.692	1.018	0.732	-0.516	YSL7_ARATH	Probable metal-nicotianamine transporter YSL7 (Protein YELLOW STRIPE LIKE 7) (AtYSL7)	YSL7 At1g65730 F1E22.10	Arabidopsis thaliana (Mouse-ear cress)	-	-	-	-	-	-	-	-	-	Complete proteome; Membrane; Reference proteome; Transmembrane; Transmembrane helix; Transport
SRR646604_T21373_c0_g1_i1_len=1971	NA	NA	NA	NA	NA	0.643	0.477	0	3.292	0.76	0.532	1	0.404	1	0.032	-	-	-	-	-	-	-	-	-	-	-	-	-	-
SRR646604_T22664_c0_g1_i1_len=812	NA	NA	NA	NA	NA	0.581	0.47	0	3.4	0.073	1.889	0.002	2.656	0.337	-0.466	-	-	-	-	-	-	-	-	-	-	-	-	-	-
SRR646604_T27892_c0_g1_i7_len=4401	NES1_FRAAN	Q4081-2468;H:14-615	50.74%;ID	E:1e-157	(3S,6E)-nerolidol synthase 1	0.066	5.324	0.001	4.77	1	3.141	0.066	5.477	1	2.102	NES1_FRAAN	(3S,6E)-nerolidol synthase 1 (FaNES1) (EC 4.2.3.48)	-	Fragaria ananassa (Strawberry)	PATHWAY: Secondary metabolite biosynthesis; terpenoid biosynthesis.	-	-	-	-	-	-	-	-	-	Cytoplasm; Lyase; Magnesium; Manganese; Metal-binding
SRR646604_T27892_c0_g1_i8_len=4323	NES1_FRAAN	Q4003-2468;H:14-615	53.32%;ID	E:2e-161	(3S,6E)-nerolidol synthase 1	0.003	3.075	0	4.541	1	2.464	1	0	1	0.954	NES1_FRAAN	(3S,6E)-nerolidol synthase 1 (FaNES1) (EC 4.2.3.48)	-	Fragaria ananassa (Strawberry)	PATHWAY: Secondary metabolite biosynthesis; terpenoid biosynthesis.	-	-	-	-	-	-	-	-	-	Cytoplasm; Lyase; Magnesium; Manganese; Metal-binding
SRR646604_T28367_c0_g1_i1_len=2132	G6PD_SOLTU	Q471-1868;H:46-511	89.7%;ID	E:0	Glucose-6-phosphate 1-dehydrogenase, cytoplasmic isoform	0.594	0.258	0	1.957	0.183	0.659	0.6	0.273	0.389	0.38	G6PD_SOLTU	Glucose-6-phosphate 1-dehydrogenase, cytoplasmic isoform (G6PD) (EC 1.1.1.49)	G6PDH	Solanum tuberosum (Potato)	PATHWAY: Carbohydrate degradation; pentose phosphate pathway; D-ribulose 5-phosphate from D-glucose 6-phosphate (oxidative stage): step 1/3.	-	-	-	-	-	-	-	-	-	Carbohydrate metabolism; Complete proteome; Cytoplasm; Glucose metabolism; NADP; Oxidoreductase; Reference proteome
SRR646604_T28486_c1_g1_i1_len=1134	NA	NA	NA	NA	NA	0.429	0.52	0	1.68	0.015	0.711	0.125	1.015	1	-0.079	-	-	-	-	-	-	-	-	-	-	-	-	-	-
SRR646604_T29269_c0_g1_i1_len=1949	UFOG6_FRAAN	Q1611-220;H:6-475	55.77%;ID	E:7e-177	UDP-glucose flavonoid 3-O-glucosyltransferase 6 (ECO:0000303)(PubMed:18487633)	1	1.674	0	6.591	0.129	3.523	0.502	2.376	1	1.211	UFOG6_FRAAN	UDP-glucose flavonoid 3-O-glucosyltransferase 6 (EC 2.4.1.91) (Flavonol 3-O-glucosyltransferase 6) (FaGT6)	GT6	Fragaria ananassa (Strawberry)	-	-	-	-	-	-	-	-	-	Glycosyltransferase; Transferase
SRR646604_T29370_c2_g1_i3_len=3560	HMDH_CATRO	Q3405-2193;H:1-407	98.29%;ID	E:0	3-hydroxy-3-methylglutaryl-coenzyme A reductase	0.352	0.866	0.001	3.209	0.077	1.023	0.505	0.921	1	0.337	HMDH_CATRO	3-hydroxy-3-methylglutaryl-coenzyme A reductase (HMG-CoA reductase) (EC 1.1.1.34)	HMGR	Catharanthus roseus (Madagascar periwinkle) (Vinca rosea)	PATHWAY: Metabolic intermediate biosynthesis; (R)-mevalonate biosynthesis; (R)-mevalonate from acetyl-CoA: step 3/3.	-	-	-	-	-	-	-	-	-	Endoplasmic reticulum; Glycoprotein; Isoprene biosynthesis; Membrane; NADP; Oxidoreductase; Transmembrane; Transmembrane helix
SRR646604_T34575_c0_g2_i1_len=1237	NA	NA	NA	NA	NA	0.16	1.126	0.001	3.858	0.003	2.042	0.228	1.016	1	-1.707	-	-	-	-	-	-	-	-	-	-	-	-	-	-
SRR646604_T34583_c0_g1_i4_len=3032	SUSY_SOLLC	Q2812-398;H:1-805	91.06%;ID	E:0	Sucrose synthase	0.325	0.407	0	3.574	0.191	0.91	-0.062	0.785	0.094	0.717	SUSY_SOLLC	Sucrose synthase (EC 2.4.1.13) (Sucrose-UDP glucosyltransferase)	TAF10 SGT1 TAFII15 At4g31720 F28M20.90	Solanum lycopersicum (Tomato) (Lycopersicon esculentum)	-	-	-	-	-	-	-	-	-	Complete proteome; Glycosyltransferase; Transferase; Transit peptide
SRR646604_T34878_c0_g1_i1_len=1243	CSPL7_SOYBN	Q198-680;H:16-173	56.17%;ID	E:5e-42	CASP-like protein 1D2	0.006	4.543	0	5.86	0.129	5.152	0.502	3.733	1	-2.595	CSPL7_SOYBN	CASP-like protein 1D2 (GmCASPL1D2)	-	Glycine max (Soybean) (Glycine hispida)	-	-	-	-	-	-	-	-	-	-
SRR646705_TR567_c0_g1_i1_len=1422	NA	NA	NA	NA	NA	0.493	0.34	0.001	1.446	0.056	0.954	0.005	1.326	1	-0.159	-	-	-	-	-	-	-	-	-	-	-	-	-	-
SRR646705_TR1034_c0_g3_i1_len=1629	MTDH_FRAAN	Q1418-357;H:1-452	67.81%;ID	E:8e-152	Probable mannitol dehydrogenase	0.454	-0.407	0	2.99	0.016	2.376	0.044	2.219	0.692	1.001	MTDH_FRAAN	Probable mannitol dehydrogenase (EC 1.1.1.255) (NAD-dependent mannitol dehydrogenase)	CAD	Fragaria ananassa (Strawberry)	-	-	-	-	-	-	-	-	-	Metal-binding; NAD; Oxidoreductase; Zinc
SRR646705_TR3034_c0_g1_i3_len=4755	SERA1_ARATH	Q399-2066;H:42-603	84.52%;ID	E:0	D-3-phosphoglycerate dehydrogenase 1, chloroplastic	0.756	-0.242	0	2.15	0.505	-0.445	0.666	0.303	0.394	0.476	SERA1_ARATH	D-3-phosphoglycerate dehydrogenase 1, chloroplastic (EC 1.1.1.95) (Protein EMBRYO SAC DEVELOPMENT ARREST 9)	PGDH1 EDA9 At4g34200 F10M10.7	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Amino-acid biosynthesis; L-serine biosynthesis; L-serine from 3-phospho-D-glycerate: step 1/3.	-	-	-	-	-	-	-	-	-	Chloroplast; Complete proteome; NAD; Oxidoreductase; Plastid; Reference proteome; Transit peptide
SRR646705_TR4584_c0_g2_i1_len=742	MYB44_ARATH	Q408-719;H:3-106	80.77%;ID	E:3e-51	Transcription factor MYB44	0.004	3.104	0	4.038	0.002	5.601	0.017	5.201	1	-0.19	MYB44_ARATH	Transcription factor MYB44 (Myb-related protein 44) (AtMYB44) (Myb-related protein R1) (AtMYBR1)	MYB44 MYBR1 At5g67300 K8K14.2	Arabidopsis thaliana (Mouse-ear cress)	-	-	-	-	-	-	-	-	-	Abscisic acid signaling pathway; Complete proteome; DNA-binding; Nucleus; Reference proteome; Repeat; Transcription; Transcription regulation
SRR646705_TR4794_c0_g1_i4_len=1868	AGD9_ARATH	Q1542-337;H:1-402	67.64%;ID	E:2e-178	Probable ADP-ribosylation factor GTPase-activating protein AGD9	0.1	0.044	0	1.597	0.102	0.716	0.085	0.743	0.707	-0.3	AGD9_ARATH	Probable ADP-ribosylation factor GTPase-activating protein AGD9 (ARF GAP AGD9) (Protein ARF-GAP DOMAIN 9) (AAGD9)	AGD9 At5g46750 MZA15.17	Arabidopsis thaliana (Mouse-ear cress)	-	-	-	-	-	-	-	-	-	Acetylation; Complete proteome; GTPase activation; Metal-binding; Phosphoprotein; Reference proteome; Zinc; Zinc-finger
SRR646705_TR4868_c0_g1_i1_len=2051	NA	NA	NA	NA	NA	0.865	-0.135	0	3.357	0.593	-0.713	0.798	-0.48	1	0.016	-	-	-	-	-	-	-	-	-	-	-	-	-	-
SRR646705_TR6257_c0_g2_i1_len=1567	NIFU2_ARATH	Q1164-508;H:7-225	68.78%;ID	E:3e-88	NifU-like protein 2, chloroplastic	0.661	0.263	0	1.465	0.095	0.72	0.095	0.724	1	-0.122	NIFU2_ARATH	NifU-like protein 2, chloroplastic (AtCNfu2) (AtCnfU-V)	NIFU2 CNFU2 NFU2 At5g49940 K9P8.16	Arabidopsis thaliana (Mouse-ear cress)	-	-	-	-	-	-	-	-	-	2Fe-2S; 3D-structure; Alternative splicing; Chloroplast; Complete proteome; Disulfide bond; Iron; Iron-sulfur; Metal-binding; Plastid; Reference proteome; Transit peptide
SRR646705_TR7060_c0_g2_i1_len=6120	TPL_ARATH	Q222-3548;H:1-1109	82.69%;ID	E:0	Protein TOPLESS	0.568	0.251	0	3.571	1	0.06	1	0.327	0.34	0.535	TPL_ARATH	Protein TOPLESS (WUS-interacting protein 1)	TOPLESS WSIP1 At1g15750 F7H2.9	Arabidopsis thaliana (Mouse-ear cress)	-	-	-	-	-	-	-	-	-	Complete proteome; Developmental protein; Jasmonic acid signaling pathway; Nucleus; Phosphoprotein; Reference proteome; Repeat; Repressor; Transcription; Transcription regulation; WD repeat
SRR646705_TR8110_c0_g1_i1_len=1031	IAA17_ARATH	Q245-820;H:3-218	51.15%;ID	E:1e-59	Auxin-responsive protein IAA17	1	0.038	0	7.058	0	-7.593	0	-9.345	0.786	0.1	IAA17_ARATH	Auxin-responsive protein IAA17 (Auxin response 3) (Indoleacetic acid-induced protein 17)	IAA17 AXR3 At1g04250 F19P19.31	Arabidopsis thaliana (Mouse-ear cress)	-	-	-	-	-	-	-	-	-	Alternative splicing; Complete proteome; ER-Golgi transport; Endoplasmic reticulum; Golgi apparatus; Membrane; Reference proteome; Transmembrane; Transmembrane helix; Transport
SRR646705_TR8125_c0_g2_i2_len=2472	2AAB_ARATH	Q363-2123;H:1-687	89.44%;ID	E:0	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform	0.547	0.335	0	1.833	0.777	0.26	0.777	0.204	0.419	0.391	2AAB_ARATH	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform (AtA beta) (PP2A, subunit A, beta isoform)	PP2AA2 DF1 At3g25800 K13N2.14	Arabidopsis thaliana (Mouse-ear cress)	-	-	-	-	-	-	-	-	-	3D-structure; Auxin signaling pathway; Complete proteome; Nucleus; Phosphoprotein; Reference proteome; Repeat; Transcription; Transcription regulation
SRR646705_TR8541_c2_g1_i3_len=1354	RS5A_DAUCA	Q153-978;H:1-269	76.92%;ID	E:2e-138	40S ribosomal protein S5 (ECO:0000255)(HAMAP-Rule:MF_03015)	0	-1.173	0	10.892	1	0	1	0	0.353	-0.229	RS5A_DAUCA	40S ribosomal protein S5 (p40)	17B	Daucus carota (Wild carrot)	-	-	-	-	-	-	-	-	-	Cytoplasm; Ribonucleoprotein; Ribosomal protein
SRR646705_TR9327_c0_g1_i1_len=2293	MLO6_ARATH	Q1732-257;H:1-539	44.22%;ID	E:4e-144	MLO-like protein 6	0.517	1.091	0	4.131	0.073	2.338	0.027	2.538	1	-0.188	MLO6_ARATH	MLO-like protein 6 (AtMlo6)	MLO6 At1g61560 T25B24.9	Arabidopsis thaliana (Mouse-ear cress)	-	-	-	-	-	-	-	-	-	Alternative splicing; Calmodulin-binding; Complete proteome; Membrane; Pathogenesis-related protein; Plant defense; Reference proteome; Transmembrane; Transmembrane helix
SRR646705_TR9782_c1_g4_i1_len=2063	WTR18_ARATH	Q816-1886;H:14-365	60.55%;ID	E:1e-121	WAT1-related protein At3g28050	0.025	1.887	0	4.117	0.025	2.634	0.076	2.191	0.629	-1.428	WTR18_ARATH	WAT1-related protein At3g28050	At3g28050 MMG15.6	Arabidopsis thaliana (Mouse-ear cress)	-	-	-	-	-	-	-	-	-	Complete proteome; Membrane; Reference proteome; Repeat; Transmembrane; Transmembrane helix
SRR646705_TR10167_c1_g1_i1_len=1637	MOMT_CATRO	Q1318-275;H:1-348	100%;ID	E:0	Myricetin O-methyltransferase	0.341	0.402	0	2.197	0.01	1.436	0.093	1.059	0.798	-0.412	MOMT_CATRO	Myricetin O-methyltransferase (EC 2.1.1.267) (CrOMT2) (Flavonoid O-methyltransferase)	-	Catharanthus roseus (Madagascar periwinkle) (Vinca rosea)	-	-	-	-	-	-	-	-	-	Acetylation; Direct protein sequencing; Methyltransferase; S-adenosyl-L-methionine; Transferase
SRR646705_TR10690_c0_g2_i1_len=1030	NA	NA	NA	NA	NA	1	0.224	0	3.362	0.076	2.373	0.076	2.313	0.822	-0.421	-	-	-	-	-	-	-	-	-	-	-	-	-	-
SRR646705_TR11339_c0_g2_i1_len=2032	PAT_PETHY	Q482-1711;H:70-479	89.02%;ID	E:0	Bifunctional aspartate aminotransferase and glutamate/aspartate-prephenate aminotransferase	0.68	0.185	0	1.838	0.108	0.673	0.187	0.594	0.58	0.26	PAT_PETHY	Bifunctional aspartate aminotransferase and glutamate/aspartate-prephenate aminotransferase (PhPPA-AT) (EC 2.6.1.1) (EC 2.6.1.78) (EC 2.6.1.79)	-	Petunia hybrida (Petunia)	PATHWAY: Amino-acid biosynthesis; L-phenylalanine biosynthesis; L-arogenate from prephenate (L-Asp route): step 1/1.; PATHWAY: Amino-acid biosynthesis; L-phenylalanine biosynthesis; L-arogenate from prephenate (L-Glu route): step 1/1.	-	-	-	-	-	-	-	-	-	Amino-acid biosynthesis; Aminotransferase; Chloroplast; Plastid; Pyridoxal phosphate; Transferase; Transit peptide
SRR646705_TR11458_c2_g2_i2_len=1353	NA	NA	NA	NA	NA	0.002	-6.299	0	7.041	1	0	1	3.582	0.111	-0.499	-	-	-	-	-	-	-	-	-	-	-	-	-	-
SRR646705_TR12335_c0_g1_i2_len=2429	KPYC_SOLTU	Q1935-406;H:1-510	90.78%;ID	E:0	Pyruvate kinase, cytosolic isozyme	0.566	0.197	0.001	1.22	0.004	1.156	0.009	1.066	0.64	0.172	KPYC_SOLTU	Pyruvate kinase, cytosolic isozyme (PK) (EC 2.7.1.40)	-	Solanum tuberosum (Potato)	PATHWAY: Carbohydrate degradation; glycolysis; pyruvate from D-glyceraldehyde 3-phosphate: step 5/5.	-	-	-	-	-	-	-	-	-	ATP-binding; Complete proteome; Cytoplasm; Glycolysis; Kinase; Magnesium; Metal-binding; Nucleotide-binding; Potassium; Pyruvate; Reference proteome; Transferase
SRR646705_TR13569_c0_g2_i6_len=2015	EF1A_TOBAC	Q1791-844;H:1-436	97.94%;ID	E:0	Elongation factor 1-alpha	0.002	-0.75	0	1.406	0.676	0.123	0.932	0.04	0.066	-4.445	EF1A_TOBAC	Elongation factor 1-alpha (EF-1-alpha) (Vitronectin-like adhesion protein 1) (PVN1)	-	Nicotiana tabacum (Common tobacco)	-	-	-	-	-	-	-	-	-	Cytoplasm; Elongation factor; GTP-binding; Nucleotide-binding; Phosphoprotein; Protein biosynthesis
SRR646705_TR13752_c1_g1_i1_len=2469	HEMH_CUCSA	Q328-1812;H:1-491	68.01%;ID	E:0	Ferrochelatase-2, chloroplastic	0.2	0.655	0	2.29	0.109	1.135	0.257	0.841	0.623	0.299	HEMH_CUCSA	Ferrochelatase-2, chloroplastic (EC 4.99.1.1) (Ferrochelatase II) (Heme synthase 2) (Protoheme ferro-lyase 2)	HEMH	Cucumis sativus (Cucumber)	PATHWAY: Porphyrin-containing compound metabolism; protoheme biosynthesis; protoheme from protoporphyrin-IX: step 1/1.	-	-	-	-	-	-	-	-	-	Chloroplast; Heme biosynthesis; Iron; Lyase; Plastid; Porphyrin biosynthesis; Transit peptide
SRR646705_TR14391_c0_g2_i6_len=2536	NEK6_ARATH	Q309-1139;H:1-276	75.45%;ID	E:1e-134	Serine/threonine-protein kinase Nek6	0.132	0.751	0	2.47	0.047	1.147	1.028	0.257	0.847	0.906	-0.121	NEK6_ARATH	Serine/threonine-protein kinase Nek6 (EC 2.7.11.1) (NimA-related protein kinase 6) (AtNek6)	NEK6 At3g20860 MOE17.17	Arabidopsis thaliana (Mouse-ear cress)	-	-	-	-	-	-	-	-	-	ATP-binding; Complete proteome; Kinase; Nucleotide-binding; Reference proteome; Serine/threonine-protein kinase; Transferase
SRR646705_TR14643_c0_g1_i1_len=571	NA	NA	NA	NA	NA	0.623	0.308	0	2.452	0.195	1.326	0.003	2.361	0.781	-0.352	-	-	-	-	-	-	-	-	-	-	-	-	-	-
SRR646705_TR15040_c0_g1_i1_len=3233	SDL5A_SOYBN	Q531-2357;H:1-610	85.25%;ID	E:0	Dynamin-related protein 5A	1	0.045	0.001	1.852	0.683	0.269	0.591	0.351	0.705	0.275	SDL5A_SOYBN	Dynamin-related protein 5A (Soybean dynamin-like protein 5A) (SDL5A)	-	Glycine max (Soybean) (Glycine hispida)	-	-	-	-	-	-	-	-	-	Cell cycle; Cell division; Complete proteome; Cytoplasm; Cytoskeleton; GTP-binding; Hydrolase; Microtubule; Motor protein; Nucleotide-binding; Reference proteome
SRR646705_TR17092_c0_g4_i1_len=1630	ADK2_ARATH	Q148-456;H:3-344	80.99%;ID	E:0	Adenosine kinase 2	0.338	-0.223	0	3.106	0.321	-0.249	0.65	-0.117	0.848	-0.174	ADK2_ARATH	Adenosine kinase 2 (AK 2) (EC 2.7.1.20) (Adenosine 5'-phosphotransferase 2)	ADK2 At5g03300 F12E4.30 MOK16.21	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Purine metabolism; AMP biosynthesis via salvage pathway; AMP from adenosine: step 1/1.	-	-	-	-	-	-	-	-	-	ATP-binding; Complete proteome; Hostvirus interaction; Kinase; Magnesium; Nucleotide-binding; Purine salvage; Reference proteome; Transferase
SRR646705_TR17142_c0_g2_i1_len=4604	PAP14_ARATH	Q648-2441;H:72-666	66.94%;ID	E:0	Probable plastid-lipid-associated protein 14, chloroplastic	0.073	2.372	0	7.007	0.502	4.11	0.254	4.457	0.001	6.532	PAP14_ARATH	Probable plastid-lipid-associated protein 14, chloroplastic (AtPap14) (Fibrillin-11) (OBP3-responsive protein 1)	PAP14 FBN11 FIB11 ORG1 At5g53450	Arabidopsis thaliana (Mouse-ear cress)	-	-	-	-	-	-	-	-	-	Alternative splicing; Chloroplast; Complete proteome; Plastid; Reference proteome; Transit peptide
SRR646705_TR1281_c0_g1_i2_len=2445	RD21A_ARATH	Q2176-923;H:42-458	63.18%;ID	E:2e-171	Cysteine proteinase RD21a	0.076	2.82	0.001	5.82	0.502	2.73	0.502	2.605	0.84	0.308	RD21A_ARATH	Cysteine proteinase RD21a (RD21) (EC 3.4.22.-)	RD21A At1g47128 F2G19.31	Arabidopsis thaliana (Mouse-ear cress)	-	-	-	-	-	-	-	-	-	Complete proteome; Disulfide bond; Glycosylation; Hydrolase; Protease; Reference proteome; Signal; Thiol protease; Zymogen
SRR646705_TR18288_c0_g1_i1_len=1412	NA	NA	NA	NA	NA	0.129	3.37	0	7.5

SRR6488707_TR5635_c2_g3_i8_len=1332	GEDH1_OCIBA	Q:225-1097;H:1-299	54.64%ID	E:1e-89	Geraniol dehydrogenase 1	PF08240.9^ADH_N^Alcohol dehydrogenase GroES-like domain^39-152^E:2.1e-27^PF00107.23^ADH_zinc_N^Zinc-binding dehydrogenase^196-299^E:6.1e-10	1	-0.102	0	5.775	0.629	0.868	1	-0.229	0.718	0.217	GEDH1_OCIBA	Geraniol dehydrogenase 1 (ObaGEDH1) (EC 1.1.1.183)	GEDH1	Ocimum basilicum (Sweet basil)		Metal-binding; NADP; Oxidoreductase; Zinc
SRR6488707_TR5814_c0_g2_i4_len=1929	BZW2_CHICK	Q:258-1484;H:1-411	32.77%ID	E:8e-72	Basic leucine zipper and W2 domain-containing protein 2	PF00200.15^W2^eIF4-gamma/eIF5/eIF2-epsilon^337-410^E:2.1e-19	0.456	0.246	0	1.445	0.034	1.145	0.1	0.937	0.908	0.04	BZW2_CHICK	Basic leucine zipper and W2 domain-containing protein 2	BZW2 RCJMB04_7o12	Gallus gallus (Chicken)		Complete proteome; Developmental protein; Differentiation; Neurogenesis; Reference proteome
SRR6488707_TR6209_c0_g1_i1_len=1737	GST23_MAIZE	Q:366-1028;H:1-222	49.55%ID	E:8e-71	Glutathione transferase GST 23	PF02798.17^GST_N^Glutathione S-transferase, N-terminal domain^5-77^E:2.4e-19^PF13417.3^GST_N_3^Glutathione S-transferase, N-terminal domain^8-79^E:2.8e-16^PF13409.3^GST_N_2^Glutathione S-transferase, N-terminal domain^13-77^E:1.4e-12	1	0	0.001	6.643	0.25	4.734	1	3.215	1	2.871	GST23_MAIZE	Glutathione transferase GST 23 (EC 2.5.1.18) (Glutathione transferase GST 36)	Zea mays (Maize)			Complete proteome; Plant defense; Reference proteome; Transferase
SRR6488707_TR6306_c0_g1_i1_len=1846	METK1_CATRO	Q:1729-651;H:1-349	99.75%ID	E0	S-adenosylmethionine synthase 1	PF00438.17^S-AdoMet_synt_N^S-adenosylmethionine synthetase, N-terminal domain^4-101^E:8.4e-43^PF02772.13^S-AdoMet_synt_M^S-adenosylmethionine synthetase, central domain^112-238^E:1.7e-46^PF02773.13^S-AdoMet_synt_C^S-adenosylmethionine synthetase, C-terminal domain^240-381^E:2e-62	0.018	0.506	0	1.914	0.045	0.445	0.014	0.547	0.507	-0.388	METK1_CATRO	S-adenosylmethionine synthase 1 (AdoMet synthase 1) (EC 2.5.1.6) (Methionine adenosyltransferase 1) (MAT 1)	SAMS1	Catharanthus roseus (Madagascar periwinkle) (Vinca rosea)	PATHWAY: Amino-acid biosynthesis; S-adenosyl-L-methionine biosynthesis; S-adenosyl-L-methionine from L-methionine: step 1/1.	ATP-binding; Cobalt; Cytoplasm; Magnesium; Manganese; Metal-binding; Nucleotide-binding; One-carbon metabolism; Potassium; Transferase
SRR6488707_TR7957_c0_g2_i1_len=2226	DHQS_SOLLC	Q:1873-992;H:40-339	85.33%ID	E:7e-179	3-dehydroquinate synthase, chloroplastic	PF13685.3^Fe-ADH_2^Iron-containing alcohol dehydrogenase^98-318^E:1.2e-11^PF01761.17^DHQ_synthase^3-dehydroquinate synthase^150-335^E:3.3e-62	0.089	0.73	0	1.511	0.573	0.235	0.349	0.358	0.043	2.606	DHQS_SOLLC	3-dehydroquinate synthase, chloroplastic (EC 4.2.3.4)	DHQS ARDB Solyc02g083590 LOC544273	Solanum lycopersicum (Tomato) (Lycopersicon esculentum)	PATHWAY: Metabolic intermediate biosynthesis; chorismate biosynthesis; chorismate from D-erythrose 4-phosphate and phosphoenolpyruvate: step 2/7.	Amino-acid biosynthesis; Aromatic amino acid biosynthesis; Chloroplast; Complete proteome; Lyase; Metal-binding; NAD; Plastid; Reference proteome; Transit peptide
SRR6488707_TR8248_c0_g2_i1_len=1563	TT12_ARATH	Q:275-1468;H:107-503	48.99%ID	E:5e-118	-	PF01554.15^MatE^MatE^-121^E:1.8e-25^PF01554.15^MatE^MatE^183-344^E:1.2e-30	0.239	1.225	0	3.88	0.132	1.94	0.381	1.317	0.27	0.296	DTX41_ARATH	Protein DETOXIFICATION 41 (AtDTX41) (Multidrug and toxic compound extrusion protein 41) (MATE protein 41) (Protein TANNIN-DEFICIENT SEED 3) (Protein TRANSPARENT TESTA 12)	DTX41 TDS3 TT12 At3g59030 F17J16_80	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Secondary metabolite biosynthesis; flavonoid biosynthesis.	Antiport; Complete proteome; Flavonoid biosynthesis; Membrane; Reference proteome; Transmembrane; Transmembrane helix; Transport; Vacuole
SRR6488707_TR8391_c0_g1_i1_len=2404	SGRW_PEA	Q:2106-1384;H:1-236	71.07%ID	E:4e-112	Protein STAY-GREEN, chloroplastic	PF06688.9^Put_Phosphatase^Putative Phosphatase^5-237^E:9.6e-97^PF12710.4^HAD^haloacid dehalogenase-like hydrolase^1-165^E:4.8e-09	1	0.985	0.001	4.573	0.76	2.808	0.014	3.301	1	-1.584	SGRW_PEA	Protein STAY-GREEN, chloroplastic (Protein STAYGREEN)	SGR	Pisum sativum (Garden pea)		Chloroplast; Plastid; Transit peptide
SRR6488707_TR8550_c0_g1_i1_len=1443	PPSP2_ARATH	Q:193-366;H:7-274	65.22%ID	E:1e-127	Inorganic pyrophosphatase 2	PF00719.14^Pyrophosphatase^Inorganic pyrophosphatase^3-215^E:3.8e-121^PF01175.15^Mal3h_synt_2^Cobalamin-independent synthase, Catalytic domain^432-755^E:1e-157^PF08267.9^Mal3h_synt_1^Cobalamin-independent synthase, N-terminal domain^551-690^E:0.00019	0.502	4.157	0	7.512	0.011	1.502	0.016	1.436	0.629	1.898	PPSP2_ARATH	Inorganic pyrophosphatase 2 (AtPPaPase2) (PPi phosphatase 2) (Pyrophosphate-specific phosphatase 2) (EC 3.6.1.1)	At1g17710 F11A6.5	Arabidopsis thaliana (Mouse-ear cress)		Alternative splicing; Complete proteome; Hydrolase; Magnesium; Metal-binding; Reference proteome
SRR6488707_TR8559_c2_g1_i1_len=2840	METE_CATRO	Q:2685-3991;H:1-765	99.22%ID	E0	5-methyltetrahydropteroyltriglutamate–homocysteine methyltransferase	PF08267.9^Mal3h_synt_1^Cobalamin-independent synthase, N-terminal domain^3-315^E:3.8e-121^PF01175.15^Mal3h_synt_2^Cobalamin-independent synthase, Catalytic domain^432-755^E:1e-157^PF08267.9^Mal3h_synt_1^Cobalamin-independent synthase, N-terminal domain^551-690^E:0.00019	0.138	0.318	0	2.233	0.002	0.526	0.176	-0.409	METE_CATRO	5-methyltetrahydropteroyltriglutamate–homocysteine methyltransferase (EC 2.1.1.14) (Cobalamin-independent methionine synthase (isozyme) (Vitamin-B12-independent methionine synthase isozyme)	METE	Catharanthus roseus (Madagascar periwinkle) (Vinca rosea)	PATHWAY: Amino-acid biosynthesis; L-methionine biosynthesis via de novo pathway; Methylfuranose; Transferase; Zinc	Amino-acid biosynthesis; Cytoplasm; Metal-binding; Methionine biosynthesis; Reference proteome; Transferase; Zinc
SRR6488707_TR9041_c1_g1_i2_len=279	CUL1_ARATH	Q:270-3117;H:4-732	79.29%ID	E0	Cullin-1	PF00888.19^Cullin^Cullin family^24-644^E:1.7e-178^PF10557.4^Cullin_Nedd8^Cullin protein neddylation domain^671-733^E:5.4e-26	0.178	-0.598	0	7.685	0.057	1.241	0.04	1.325	1	0	CUL1_ARATH	Cullin-1	CUL1 At4g02570 T10P11.26	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Protein modification; protein ubiquitination.	Auxin signaling pathway; Cell cycle; Complete proteome; Cytoplasm; Cytoskeleton; Development protein; Ethylene signaling pathway; Isopeptide bond; Nucleus; Reference proteome; Ubl conjugation; Ubl conjugation pathway
SRR6488707_TR10329_c0_g1_i1_len=2485	KPRS2_SPIOL	Q:1824-763;H:39-395	84.87%ID	E0	Ribose-phosphate pyrophosphokinase 2, chloroplastic	PF13793.3^Phosphoribosyltransferase^Phosphoribosyl transferase domain^133-229^E:1.7e-45^PF14572.3^Pribosyl_synth^Phosphoribosyl synthetase-associated domain^184-291^E:2.1e-23	1	-0.06	0	3.27	0.035	1.74	0.023	1.819	1	-0.109	KPRS2_SPIOL	Ribose-phosphate pyrophosphokinase 2, chloroplastic (EC 2.7.6.1) (Phosphoribosyl pyrophosphate synthase 2)	PRS2	Spinacia oleracea (Spinach)		ATP-binding; Chloroplast; Kinase; Magnesium; Metal-binding; Nucleotide biosynthesis; Nucleotide-binding; Plastid; Transferase; Transit peptide
SRR6488707_TR11016_c0_g3_i1_len=1459	GSTXC_TOBAC	Q:1070-398;H:1-221	53.1%ID	E6e-70	Probable glutathione S-transferase parC	PF13417.3^GST_N_3^Glutathione S-transferase, N-terminal domain^11-87^E:1.3e-14^PF02798.13^GST_N^Glutathione S-transferase, N-terminal domain^16-82^E:1.9e-10^PF00043.22^GST_C^Glutathione S-transferase, C-terminal domain^123-191^E:5.9e-10^PF13410.3^GST_C_2^Glutathione S-transferase, C-terminal domain^128-194^E:1.7e-09	0.356	1.292	0	3.531	0.002	1.803	0.109	1.101	1	0.419	GSTXC_TOBAC	Probable glutathione S-transferase parC (EC 2.5.1.18) (Auxin-regulated protein parC)	PARC	Nicotiana tabacum (Common tobacco)		Auxin signaling pathway; Transferase
SRR6488707_TR11446_c0_g2_i1_len=1674	C7D55_HYOMU	Q:1437-462;H:47-495	45.58%ID	E:1e-149	Premnaspirodiene oxygenase	PF00067.19^p450^Cytochrome P450^66-511^E:4.5e-90	0.629	2.092	0	6.027	1	0.562	1	1.461	1	-0.075	C7D55_HYOMU	Premnaspirodiene oxygenase (HPO) (EC 1.14.13.121) (Cytochrome P450 7ID55)	CYP71D55	Hyoscyamus muticus (Egyptian henbane)		Complete proteome; Heme; Iron; Membrane; Metal-binding; Monooxygenase; NADP; Oxidoreductase; Transmembrane; Transmembrane helix
SRR6488707_TR11517_c0_g1_i1_len=1879	VINSY_RAUSE	Q:1568-366;H:1-401	70.79%ID	E0	Vinorine synthase	PF02458.12^Transferase^Transferase family^6-411^E:5.8e-92	0.61	0.184	0.001	1.501	0.206	-0.464	0.176	-0.506	0.121	0.795	VINSY_RAUSE	Vinorine synthase (EC 2.3.1.160)	SCT	Rauvolfia serpentina (Serpentine wood) (Ophiorhiza serpentinum)		3D-structure; Acyltransferase; Alkaloid metabolism; Direct protein sequencing; Transferase
SRR6488707_TR11691_c0_g1_i1_len=1632	CLC1_ARATH	Q:494-1000;H:1-169	63.44%ID	E:1e-56	Clathrin light chain 1	PF10186.14^Clathrin_lg_ch^Clathrin light chain^131-271^E:4.4e-10	1	0.048	0	1.795	1	0.044	0.86	-0.204	1	-0.018	CLC1_ARATH	Clathrin light chain 1	At2g20760 F5H14.27	Arabidopsis thaliana (Mouse-ear cress)		Coated pit; Coiled coil; Complete proteome; Cytoplasmic vesicle; Membrane; Reference proteome
SRR6488707_TR11691_c2_g3_i9_len=1871	MTDH_APIGR	Q:281-1345;H:3-357	63.66%ID	E:4e-151	Mannitol dehydrogenase	PF08240.9^ADH_N^Alcohol dehydrogenase GroES-like domain^39-151^E:8.1e-22^PF00107.23^ADH_zinc_N^Zinc-binding dehydrogenase^195-318^E:1.8e-15	0.798	0.154	0	1.969	0.006	1.857	0.003	1.991	0.317	-0.469	MTDH_APIGR	Mannitol dehydrogenase (EC 1.1.1.255) (NAD-dependent mannitol dehydrogenase)	MTD	Apium graveolens (Celery)		Cytoplasm; Metal-binding; NAD; Oxidoreductase; Zinc
SRR6488707_TR12055_c0_g1_i1_len=3210	AGLU_SPIOL	Q:302-2848;H:43-902	63.21%ID	E0	Alpha-glucosidase	PF16863.2^NtCIMGAM_N^N-terminal barrel of NtMGAM and CtMGAM, maltase-glucoamylase^70-203^E:2.9e-35^PF13892.3^Glycosyl_hydrolase_2^Glycosyl hydrolases family 31^293-760^E:1.4e-156	0.175	1.074	0	8.685	1	-3.198	1	0.666	0.44	-0.83	AGLU_SPIOL	Alpha-glucosidase (EC 3.2.1.20) (Maltase)		Spinacia oleracea (Spinach)		Direct protein sequencing; Glycoprotein; Glycosidase; Hydrolase; Signal
SRR6488707_TR13003_c0_g1_i1_len=2774	Y5262_ARATH	Q:915-2483;H:5-524	51.5%ID	E:4e-152	Ankyrin repeat-containing protein At5g02620	PF12796.4^Ank_2^Ankyrin repeats (3 copies)^70-140^E:1.9e-08^PF12796.4^Ank_2^Ankyrin repeats (3 copies)^101-176^E:8.4e-09^PF13637.3^Ank_4^Ankyrin repeats (many copies)^151-203^E:5.3e-06^PF12796.4^Ank_2^Ankyrin repeats (3 copies)^153-240^E:8.7e-18^PF13637.3^Ank_4^Ankyrin repeats (many copies)^184-236^E:9.8e-11^PF00023.27^Ank^Ankyrin repeat^185-209^E:0.025^PF00023.27^Ank^Ankyrin repeat^216-242^E:0.0007^PF13637.3^Ank_4^Ankyrin repeats (many copies)^219-271^E:2.1e-11^PF12796.4^Ank_2^Ankyrin repeats (3 copies)^248-314^E:9.5e-13^PF00023.27^Ank^Ankyrin repeat^251-271^E:0.017^PF13637.3^Ank_5^Ankyrin repeats (many copies)^278-326^E:1.4e-09^PF00023.27^Ank^Ankyrin repeat^285-317^E:8.7e-06^PF13962.3^PGG^Domain of unknown function^399-509^E:1.6e-24	0.183	0.68	0001	1.871	0.547	0.421	0.547	0.43	1	0.076	Y5262_ARATH	Ankyrin repeat-containing protein At5g02620	At5g02620 T22P11.210	Arabidopsis thaliana (Mouse-ear cress)		ANK repeat; Complete proteome; Membrane; Phosphoprotein; Reference proteome; Repeat; Transmembrane; Transmembrane helix
SRR6488707_TR13703_c0_g2_i1_len=1723	C94C1_ARATH	Q:1564-185;H:31-493	62.5%ID	E0	Cytochrome P450 94C1	PF00067.19^p450^Cytochrome P450^89-488^E:1e-66	0.002	5.898	0	8.53	0.129	2.82	0.129	2.608	1	1.198	C94C1_ARATH	Cytochrome P450 94C1 (EC 1.14.--)	CYP94C1 At2g27690 F15K20.21	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Heme; Iron; Jasmonic acid signaling pathway; Membrane; Metal-binding; Monooxygenase; Oxidoreductase; Reference proteome; Transmembrane; Transmembrane helix
SRR6488707_TR17560_c0_g2_i1_len=1994	DHEB_NICPL	Q:1624-392;H:1-411	90.51%ID	E0	Glutamate dehydrogenase B	PF02812.15^ELFV_dehydrog_N^Glu/Leu/Phe/Val dehydrogenase, dimerisation domain^33-159^E:6e-49^PF00208.18^ELFV_dehydrog^Glutamate/Leucine/Phenylalanine/Valine dehydrogenase^176-408^E:1.1e-72	0.08	1.347	0	1.7	1	-0.28	0.822	-0.355	1	-0.069	DHEB_NICPL	Glutamate dehydrogenase B (GDH B) (EC 1.4.1.3)	GDHB	Nicotiana plumbaginifolia (Leadwort-leaved tobacco) (TexMex tobacco)		NAD; Oxidoreductase
SRR6488707_TR17598_c0_g1_i1_len=1129	NA	NA	NA	NA	NA		0.381	1.738	0	3.153	0.006	1.876	0.004	1.91	1	-0.045	-	-	-	-	-	-
SRR6488707_TR19071_c1_g2_i1_len=965	NA	NA	NA	NA	NA		0.581	0.385	0	1.461	1	0	0	0	0.059	1.224	-	-	-	-	-	-
SRR6488707_TR19558_c0_g2_i2_len=1965	C72A1_CATRO	Q:1888-317;H:1-624	99.05%ID	E0	Secologanin synthase	PF00067.19^p450^Cytochrome P450^93-497^E:1.6e-87	0.131	0.464	0	2.337	0.844	0.077	0.1	-0.765	0.01	0.957	C72A1_CATRO	Secologanin synthase (SLS) (EC 1.3.3.9) (CYPLXXII) (Cytochrome P450 72A1)	CYP72A1 CYP72 P450CR3	Catharanthus roseus (Madagascar periwinkle) (Vinca rosea)	PATHWAY: Alkaloid biosynthesis; secologanin biosynthesis.	Alkaloid metabolism; Heme; Iron; Membrane; Metal-binding; Monooxygenase; NADP; Oxidoreductase; Transmembrane; Transmembrane helix; Vacuole
SRR6488707_TR19720_c0_g1_i1_len=1244	DNJ19_ARATH	Q:935-39;H:22-322	76.82%ID	E:2e-164	DnaJ protein ERDJ3B	PF00226.28^DnaJ^DnaJ domain^27-88^E:5e-29^PF01556.15^DnaJ_C^DnaJ C terminal domain^137-284^E:5.2e-22	0.194	-0.496	0	1.855	0.093	0.805	0.093	0.805	0.043	0.606	DNJ19_ARATH	DnaJ protein ERDJ3B (Chaperone protein dnaJ 19) (AtDjB19) (AtJ19) (Endoplasmic reticulum dnaJ domain-containing protein 3B) (AtERdj3B) (Protein SCJ1 homolog ERDJ3B)	ERDJ3B B19 At3g62600 F26K9.30	Arabidopsis thaliana (Mouse-ear cress)		Chaperone; Complete proteome; Endoplasmic reticulum; Glycoprotein; Reference proteome; Signal; Stress response
SRR6488707_TR20275_c1_g1_i1_len=2708	S38A6_XENTR	Q:548-1687;H:14-405	27.98%ID	E:4e-22	Probable sodium-coupled neutral amino acid transporter 6	PF01490.15^Aa_trans^Transmembrane amino acid transporter protein^45-447^E:3.3e-58^PF03222.10^Trp_Tyr_perm^Tryptophan/tyrosine permease family^46-447^E:1.8e-11	0.211	0.792	0	3.523	0.043	1.179	0.031	1.277	1	0.332	S38A6_XENTR	Probable sodium-coupled neutral amino acid transporter 6 (Na(+)-coupled neutral amino acid transporter 6) (Solute carrier family 38 member 6)	slc38a6 TEgg038h13.1	Xenopus tropicalis (Western clawed frog) (Silurana tropicalis)		Amino-acid transport; Cell membrane; Complete proteome; Glycoprotein; Ion transport; Membrane; Reference proteome; Sodium; Sodium transport; Transmembrane; Transmembrane helix; Transport
SRR6488707_TR20795_c0_g1_i1_len=3296	ZADH2_MOUSE	Q:1070-2113;H:29-377	45.79%ID	E:2e-79	Zinc-binding alcohol dehydrogenase domain-containing protein 2	PF00106.22^adh_short^short chain dehydrogenase^9-209^E:2.7e-39^PF13561.3^adh_short_C2^Enoyl-(Acyl carrier protein) reductase^13-221^E:1.2e-31^PF08240.9^ADH_N^Alcohol dehydrogenase GroES-like domain^320-385^E:1.1e-08^PF00107.23^ADH_zinc_N^Zinc-binding dehydrogenase^444-575^E:5.6e-29^PF13602.3^ADH_zinc_N_2^Zinc-binding dehydrogenase^476-621^E:4.2e-21	0.91	0.122	0	2.396	0.019	1.514	0.112	1.089	0.36	0.434	ZADH2_MOUSE	Zinc-binding alcohol dehydrogenase domain-containing protein 2 (EC 1.-.-.-)	Zadh2	Mus musculus (Mouse)		Acetylation; Complete proteome; NADP; Oxidoreductase; Peroxisome; Reference proteome
SRR6488707_TR21122_c0_g3_i1_len=1311	RAD2A_ARATH	Q:260-868;H:1-203	90.15%ID	E:3e-133	Ras-related protein RABD2a	PF03106.12^WRKY^WRKY DNA-binding domain^109-166^E:1.2e-26	0.374	0.286	0	1.457	0.069	0.51	0.042	0.565	0.828	-0.079	RAD2A_ARATH	Ras-related protein RABD2a (ARABD2a) (Ras-related protein Ara-8) (Ras-related protein Rab1B) (AtRab1B)	RABD2A ARA-5 RAB1B At1g02130 T7G3.6	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; ER-Golgi transport; GTP-binding; Golgi apparatus; Lipoprotein; Membrane; Nucleotide-binding; Prenylation; Protein transport; Reference proteome; Transport
SRR6488707_TR22512_c0_g3_i1_len=1245	RS12_HORVU	Q:965-594;H:20-143	82.26%ID	E:6e-59	40S ribosomal protein S12	PF01248.23^Ribosomal_L7Ae^Ribosomal protein L7Ae/L30e/S12e/Gad045 family^27-120^E:4.8e-26	0.04	-1.36	0	4.449	0.254	-4.413	0.629	-0.975	1	0.197	RS12_HORVU	40S ribosomal protein S12	RPS12	Hordeum vulgare (Barley)		Ribonucleoprotein; Ribosomal protein
SRR6488707_TR22679_c0_g1_i1_len=1138	PROF1_RICCO	Q:281-1131	88.55%ID	E:4e-79	Profilin-1	PF00235.16^Profilin^Profilin^1-130^E:2.3e-44	0.677	-0.119	0	1.043	0.121	0.391	0.087	0.429	0.466	0.207	PROF1_RICCO	Profilin-1	PRO1	Ricinus communis (Castor bean)		Actin-binding; Cytoplasm; Cytoskeleton
SRR6488707_TR24099_c1_g2_i1_len=2134	EF1A_TOBAC	Q:1860-556;H:1-435	97.93%ID	E0	Elongation factor 1-alpha	PF00009.24^GTP_EFTU^Elongation factor Tu GTP binding domain^6-221^E:1e-52^PF03144.22^GTP_EFTU_D2^Elongation factor Tu domain 2^248-313^E:7.3e-15^PF03143.14^GTP_EFTU_D3^Elongation factor Tu C-terminal domain^322-429^E:3.9e-38	0	-0.894	0	0.911	0.689	-0.103	0.316	-0.253	1	0.022	EF1A_TOBAC	Elongation factor 1-alpha (EF-1-alpha) (Vitronectin-like adhesion protein 1) (PVN1)		Nicotiana tabacum (Common tobacco)		Complete proteome; Cytoplasm; Direct protein sequencing; Iron; Metal-binding; Oxidoreductase; Vitamin C
SRR6488707_TR24774_c0_g3_i1_len=1552	DV4H_CATRO	Q:1444-308;H:23-400	66.14%ID	E:9e-170	Deacetoxyvindoline 4-hydroxylase	PF14226.2^DOX_N^non-haem dioxygenase in morphine synthesis N-terminal^59-162^E:1.1e-20^PF03171.17^2OG-Fe(II)_Oxy^2OG-Fe(II) oxygenase superfamily^216-309^E:6.1e-23	1	0	0	6.852	1	1	0	2.351	1	0	DV4H_CATRO	Deacetoxyvindoline 4-hydroxylase (EC 1.14.11.20)	D4H	Catharanthus roseus (Madagascar periwinkle) (Vinca rosea)	PATHWAY: Alkaloid biosynthesis; vindoline biosynthesis; vindoline from tabersonine: step 5/6.	Cytoplasm; Dioxygenase; Direct protein sequencing; Iron; Metal-binding; Reference proteome; Vitamin C
SRR6488707_TR25271_c0_g2_i1_len=1919	RA212_ARATH	Q:305-1507;H:1-358	42.26%ID	E:9e-63	Ethylene-responsive transcription factor RAP2-12	PF00847.17^AP2^AP2 domain^127-174^E:3.2e-11	0.883	0.073	0	1.745	0.009	0.913	0.085	0.628	0.107	0.602	RA212_ARATH	Ethylene-responsive transcription factor RAP2-12 (Protein RELATED TO APETALA2 12)	RAP2-12 ERF074 At1g53910 T18A20.14	Arabidopsis thaliana (Mouse-ear cress)		Activator; Alternative splicing; Cell membrane; Complete proteome; DNA-binding; Ethylene signaling pathway; Membrane; Nucleus; Reference proteome; Transcription; Transcription regulation
SRR6488707_TR25398_c0_g1_i1_len=2477	METK2_CATRO	Q:1710-532;H:1-393	100%ID	E0	S-adenosylmethionine synthase 2	PF00438.17^S-AdoMet_synt_N^S-adenosylmethionine synthetase, N-terminal domain^16-113^E:6.8e-43^PF02772.13^S-AdoMet_synt_M^S-adenosylmethionine synthetase, central domain^129-250^E:4.8e-46^PF02773.13^S-AdoMet_synt_C^S-adenosylmethionine synthetase, C-terminal domain^252-393^E:1.4e-62	0.004	0.866	0	2.635	0.359	-0.288	0.055	-0.591	0.912	-0.087	METK2_CATRO	S-adenosylmethionine synthase 2 (AdoMet synthase 2) (EC 2.5.1.6) (Methionine adenosyltransferase 2) (MAT 2)	SAMS2	Catharanthus roseus (Madagascar periwinkle) (Vinca rosea)	PATHWAY: Amino-acid biosynthesis; S-adenosyl-L-methionine biosynthesis; S-adenosyl-L-methionine from L-methionine: step 1/1.	ATP-binding; Cobalt; Cytoplasm; Magnesium; Manganese; Metal-binding; Nucleotide-binding; One-carbon metabolism; Potassium; Transferase
SRR6488707_TR25740_c0_g1_i3_len=846	NA	NA	NA	NA	NA		0.002	-1.261	0	7.548	1	-0.849	1	-1.551	0.001	-1.079	-	-	-	-	-	-
SRR6488707_TR26428_c1_g2_i5_len=1903	GCL1_ARATH	Q:1678-395;H:1-433	63.86%ID	E0	LanC-like protein GCL1	PF05147.10^LANC_like^Lanthionine synthetase C-like protein^71-427^E:1.2e-85	0.076	2.889	0	6.683	1	3.354	0.502	4.006	0.001	-4.472	GCL1_ARATH	LanC-like protein GCL1 (G protein-coupled receptor 2-like protein 1) (Protein GCR2-like 1)	GCL1 At5g65280 MQN23.23	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Reference proteome
SRR6488707_TR26579_c0_g2_i2_len=3527	PMA4_NICPL	Q:1966-2402;H:3-690	91.28%ID	E0	Plasma membrane ATPase 4	PF00690.23^Cation_ATPase_N^Cation transporter/ATPase, N-terminus^21-84^E:1.7e-14^PF00122.17^E1-E2_ATPase^E1-E2 ATPase^103-323^E:6.1e-61^PF00702.29^Hydrolase^haloacid dehalogenase-like hydrolase^328-605^E:1.2e-18	0.219	0.396	0	1.284	0.59	-0.153	0.085	-0.465	0.139	-0.575	PMA4_NICPL	Plasma membrane ATPase 4 (EC 3.6.3.6) (Proton pump 4)	PMA4	Nicotiana plumbaginifolia (Leadwort-leaved tobacco) (TexMex tobacco)		Complete proteome; Hydrolase; Ion transport; Magnesium; Membrane; Metal-binding; Phosphoprotein; Transmembrane; Transmembrane helix; Transport
SRR6488707_TR27191_c0_g1_i1_len=1699	CSD11_ARATH	Q:720-1307;H:304-497	55.84%ID	E:3e-70	Cytochrome P450 81D11	PF00067.19^p450^Cytochrome P450^14-191^E:1.5e-62	0.002	2.482	0.001	2.813	0.254	2.681	0.254	2.395	0.76	-0.574	CSD11_ARATH	Cytochrome P450 81D11 (EC 1.14.--)	CYP81D11 At3g28740 T19N8.3	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Heme; Iron; Membrane; Metal-binding; Monooxygenase; Oxidoreductase; Reference proteome; Transmembrane; Transmembrane helix
SRR6488707_TR27191_c0_g1_i2_len=1985	CS11D_ARATH	Q:166-1617;H:25-502	41.75%ID	E:2e-128	Cytochrome P450 81D1	PF00067.19^p450^Cytochrome P450^31-479^E:8.9e-98	0.015	0.931	0	3.529	0.132	0.751	0.675	0.32	0.287	-0.355	CS11D_ARATH	Cytochrome P450 81D1 (EC 1.14.--)	CYP81D1 CYP91A1 At5g36220 T30G6.3	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Heme; Iron; Membrane; Metal-binding; Monooxygenase; Oxidoreductase; Reference proteome; Transmembrane; Transmembrane helix
SRR6488707_TR28453_c0_g1_i2_len=1993	PYRD_ARATH	Q:478-1642;H:48-458	84.32%ID	E0	Dihydroorotate dehydrogenase (quinone), mitochondrial	PF01180.18^DHO_dh^Dihydroorotate dehydrogenase^124-442^E:2.5e-99	0.472	-0.741	0	6.784	0.381	1.379	1	0.017	0.189	-0.209	PYRD_ARATH	Dihydroorotate dehydrogenase (quinone), mitochondrial (DHOdehase) (EC 1.3.5.2) (Dihydroorotate oxidase)	PYRD At5g23300 MKD15.16	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Pyrimidine metabolism; UMP biosynthesis via de novo pathway; orotate from (S)-dihydroorotate (quinone route): step 1/1.	Complete proteome; FMN; Flavoprotein; Membrane; Mitochondrion; Mitochondrion inner membrane; Reference proteome; Repeat; Stress response; Transmembrane; Transmembrane helix; Transport
SRR6488707_TR28521_c0_g2_i3_len=1909	GUAA_HELHP	Q:1103-1483;H:846-979	42.52%ID	E:5e-37	Probable GMP synthase [glutamine-hydrolyzing]	PF03352.10^Adenine_glycosy^Methylpadenine glycosylase^179-228^E:9.9e-17	1	0.078	0	7.253	1	0	1	0	0.698	0.222	GUAA_HELHP	Probable GMP synthase [glutamine-hydrolyzing] (EC 6.3.5.2) (GMP synthetase) (Glutamine amidotransferase)	guaA HH_1444	Helicobacter hepaticus (strain ATCC 51449 / 3B1)	PATHWAY: Purine metabolism; GMP biosynthesis; GMP from XMP (L-Gln route): step 1/1.	ATP-binding; Complete proteome; GMP biosynthesis; Glutamine amidotransferase; Ligase; Nucleotide-binding; Purine biosynthesis; Reference proteome; Repeat
SRR6488707_TR28569_c0_g2_i2_len=667	NA	NA	NA	NA	NA		0.189	1.685	0	4.815	0.001	3.909	0.629	1.695	1	-0.23	-	-	-	-	-	-
SRR6488707_TR28758_c0_g2_i1_len=1680	CDA1_ARATH	Q:371-1369;H:3-298	53.29%ID	E:2e-103	Cytidine deaminase 1	PF00383.20^dCMP_cyt_deam_1^Cytidine and deoxycitidylate deaminase zinc-binding region^38-117^E:9.3e-11^PF08211.9^dCMP_cyt_deam_2^Cytidine and deoxycitidylate deaminase zinc-binding region^153-319^E:2.4e-48	0.5	0.599	0	2.372	1	-0.504	0.692	-0.898	1	-0.329	CDA1_ARATH	Cytidine deaminase 1 (AtCDA1) (EC 3.5.4.5)	CDA1 CDD DESZ At2g19570 F3P11	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Hydrolase; Metal-binding; Reference proteome; Zinc
SRR6488707_TR30433_c0_g1_i2_len=1559	10HGO_CATRO	Q:138-1229;H:10-360	59.89%ID	E:3e-130	8-hydroxygeraniol dehydrogenase	PF08240.9^ADH_N^Alcohol dehydrogenase GroES-like domain^74-197^E:4e-23^PF00107.23^ADH_zinc_N^Zinc-binding dehydrogenase^244-368^E:1.1e-17	0.049	0.575	0	1.556	0.065	0.708	0.918	0.091	0.003	0.822	10HGO_CATRO	8-hydroxygeraniol dehydrogenase (Cr10HGO) (EC 1.1.1.324)	10HGO	Catharanthus roseus (Madagascar periwinkle) (Vinca rosea)		Metal-binding; NADP; Oxidoreductase; Zinc
SRR6488707_TR30984_c0_g2_i1_len=710	NA	NA	NA	NA	NA		0.357	0.694	0	2.927	0.5	0.609	1	0.201	0.01	1.735	-	-	-	-	-	-
SRR6488707_TR31917_c0_

SRR924148_TR4911_c1_g2_i3_len=1404	UBQ14_ARATH	Q:201-1115,H:1-305	100%ID	E:0	Polyubiquitin 14	2 like Rad60 SUMO-like*89-147*E:0.15 PF11976.5*Rad60-SLD*Ubiquitin-2 like Rad60 SUMO-like*153-223*E:9.9e-16 PF00240.20*ubiquitin*Ubiquitin family*155-226*E:1.5e-33 PF14560.3*Ubiquitin_2*Ubiquitin-like domain*164-221*E:0.00061 PF13881.3*Rad60-SLD_2*Ubiquitin-2 like Rad60 SUMO-like*165-223*E:0.15 PF11976.5*Rad60-SLD*Ubiquitin-2 like Rad60 SUMO-like*229-299*E:9.9e-16 PF00240.20*ubiquitin*Ubiquitin family*231-302*E:1.5e-33 PF14560.3*Ubiquitin_2*Ubiquitin-like domain*240-297*E:0.00061 PF13881.3*Rad60-SLD_2*Ubiquitin-2 like Rad60 SUMO-like*241-299*E:0.15	0,774	0,072	0	0,984	0,003	0,701	0,089	0,416	0,118	0,413	UBQ14_ARATH	Polyubiquitin 14 [Cleaved into: Ubiquitin]	UBQ14 AtMg02890 T5J8.21	Arabidopsis thaliana (Mouse-ear cress)	-	Alternative splicing; Complete proteome; Cytoplasm; Isopeptide bond; Nucleus; Reference proteome; Repeat; Ubl conjugation; Ubl conjugation pathway
SRR924148_TR7529_c0_g1_i4_len=1635	MTDH_FRAAN	Q:193-1251,H:4-356	70.25%ID	E:1e-156	Probable mannitol dehydrogenase	PR09240.9*ADH_NAlcohol dehydrogenase GroES-like domain*39-152*E:1.2e-27 PF00107.23*ADH_zinc_N*Zinc-binding dehydrogenase*195-317*E:2e-18	0,448	0,182	0	3,707	0,852	0,064	0,122	-0,472	0,012	0,605	MTDH_FRAAN	Probable mannitol dehydrogenase (EC 1.1.1.255) (NAD-dependent mannitol dehydrogenase)	CAD	Fragaria ananassa (Strawberry)	-	Metal-binding; NAD; Oxidoreductase; Zinc
SRR924148_TR12807_c0_g2_i1_len=994	NA	NA	NA	NA	NA	-	0,257	0,346	0	2,851	0,003	1,165	0,135	0,62	0,552	-0,146	-	-	-	-	-	-
SRR924148_TR13374_c0_g2_i3_len=2798	TCMO_CATRO	Q:2157-1645,H:137-503	98.25%ID	E:8e-166	Trans-cinnamate 4-monooxygenase	PF00067.19*p450*Cytochrome P450*34-137*E:5.6e-24	1	-0,144	0	3,974	0,431	0,322	0,139	0,574	1	0,122	TCMO_CATRO	Trans-cinnamate 4-monooxygenase (EC 1.14.13.11) (Cinnamic acid 4-hydroxylase) (CA4H) (Cytochrome P450 73) (Cytochrome P450C4H)	CYP73A4	Catharanthus roseus (Madagascar periwinkle) (Vinca rosea)	PATHWAY: Phenylpropanoid metabolism; trans-4-coumarate biosynthesis; trans-4-coumarate from trans-cinnamate: step 1/1.	Heme; Iron; Metal-binding; Monooxygenase; NADP; Oxidoreductase
SRR924148_TR14715_c0_g1_i2_len=1791	MOMT_CATRO	Q:1303-263,H:1-348	73.85%ID	E:1e-178	Myricetin O-methyltransferase	PF08100.8*Dimerisation*Dimerisation domain*27-74*E:8.4e-20 PF00891.15*Methyltransf_2*O-methyltransferase*116-333*E:5.1e-56	0,431	0,409	0	2,323	0,402	1,059	0,56	0,997	1	-0,139	MOMT_CATRO	Myricetin O-methyltransferase (EC 2.1.1.267) (CrOMT2) (Flavonoid O-methyltransferase)	-	Catharanthus roseus (Madagascar periwinkle) (Vinca rosea)	-	Acetylation; Direct protein sequencing; Methyltransferase; S-adenosyl-L-methionine; Transferase
SRR924148_TR15049_c0_g2_i1_len=1789	WTR18_ARATH	Q:690-1607,H:64-365	58.6%ID	E:7e-109	WAT1-related protein At3g28050	PF08892.17*EamA*EamA-like transporter family*137-260*E:5.3e-08	0,027	2,315	0	2,941	0,014	3,386	0,132	2,734	1	0,025	WTR18_ARATH	WAT1-related protein At3g28050	At3g28050 MMG15.6	Arabidopsis thaliana (Mouse-ear cress)	-	Complete proteome; Membrane; Reference proteome; Repeat; Transmembrane; Transmembrane helix
SRR924148_TR15095_c0_g2_i1_len=1072	NCPR_CATRO	Q:860-1,H:450-714	99.62%ID	E:0	NADPH--cytochrome P450 reductase [ECO:0000255]HAMAP-Rule:MF_03212]	PF00667.17*FAD_binding_1*FAD binding domain*1-64*E:4.7e-19 PF00175.18*NAD_binding_1*Oxidoreductase NAD-binding domain*101-211*E:2.2e-17	0,111	0,843	0	1,519	0,001	0,959	1	0,022	0,008	-0,836	NCPR_CATRO	NADPH--cytochrome P450 reductase (CPR) (P450R) (EC 1.6.2.4)	CPR	Catharanthus roseus (Madagascar periwinkle) (Vinca rosea)	-	Endoplasmic reticulum; FAD; FMN; Flavoprotein; Membrane; NADP; Oxidoreductase
SRR924148_TR15241_c0_g1_i1_len=1429	ARR3_ARATH	Q:1050-514,H:1-175	66.67%ID	E:9e-67	Two-component response regulator ARR3	PF00072.21*Response_reg*Response regulator receiver domain*34-154*E:1.6e-21	0,729	0,242	0,001	1,648	0,798	-0,2	0,904	0,121	1	-0,208	ARR3_ARATH	Two-component response regulator ARR3	ARR3 At1g59940 F23H11.25	Arabidopsis thaliana (Mouse-ear cress)	-	Complete proteome; Cytokinin signaling pathway; Nucleus; Phosphoprotein; Reference proteome; Transcription; Transcription regulation; Two-component regulatory system
SRR924148_TR16153_c1_g1_i1_len=3622	COB22_ARATH	Q:3333-562,H:1-926	84.02%ID	E:0	Coatomer subunit beta'-2	PF00400.29*WD40*WD domain, G-beta repeat*91-127*E:8e-06 PF00400.29*WD40*WD domain, G-beta repeat*133-171*E:0.00013 PF00400.29*WD40*WD domain, G-beta repeat*177-215*E:5.6e-06 PF00400.29*WD40*WD domain, G-beta repeat*220-256*E:6.6e-09 PF04053.11*Coatomer_WDAD*Coatomer WD associated region*319-763*E:7.2e-167 PF00400.29*WD40*WD domain, G-beta repeat*91-127*E:8e-06 PF00400.29*WD40*WD domain, G-beta repeat*133-171*E:0.00013 PF00400.29*WD40*WD domain, G-beta repeat*177-215*E:5.6e-06 PF00400.29*WD40*WD domain, G-beta repeat*220-256*E:6.6e-09 PF04053.11*Coatomer_WDAD*Coatomer WD associated region*319-763*E:7.2e-167	1	0,006	0	2,883	0	-2,642	0	-2,99	0,547	-0,414	COB22_ARATH	Coatomer subunit beta'-2 (Beta'-coat protein 2) (Beta'-COP 2)	At1g52360 F19K6.16	Arabidopsis thaliana (Mouse-ear cress)	-	Alternative splicing; Complete proteome; Cytoplasm; Cytoplasmic vesicle; ER-Golgi transport; Golgi apparatus; Membrane; Protein transport; Reference proteome; Repeat; Transport; WD repeat
SRR924148_TR16153_c1_g1_i4_len=3587	COB22_ARATH	Q:3298-527,H:1-926	84.02%ID	E:0	Coatomer subunit beta'-2	PF00400.29*WD40*WD domain, G-beta repeat*91-127*E:8e-06 PF00400.29*WD40*WD domain, G-beta repeat*133-171*E:0.00013 PF00400.29*WD40*WD domain, G-beta repeat*177-215*E:5.6e-06 PF00400.29*WD40*WD domain, G-beta repeat*220-256*E:6.6e-09 PF04053.11*Coatomer_WDAD*Coatomer WD associated region*319-763*E:7.2e-167 PF00676.17*E1_Dh*Dehydrogenase E1 component*139-434*E:4.4e-122 PF02775.18*TPP_enzyme_C*Thiamine pyrophosphate enzyme_C-terminal TPP binding domain*225-340*E:3.8e-05 PF13292.3*DXP_synthase_N*1-deoxy-D-xylulose-5-phosphate synthase*237-301*E:7.1e-05	0,724	-0,203	0,001	5,566	0	-5,874	0	-4,508	0,679	-0,432	COB22_ARATH	Coatomer subunit beta'-2 (Beta'-coat protein 2) (Beta'-COP 2)	At1g52360 F19K6.16	Arabidopsis thaliana (Mouse-ear cress)	-	Alternative splicing; Complete proteome; Cytoplasm; Cytoplasmic vesicle; ER-Golgi transport; Golgi apparatus; Membrane; Protein transport; Reference proteome; Repeat; Transport; WD repeat
SRR924148_TR17798_c0_g1_i1_len=2057	ODPA1_ARATH	Q:207-1139,H:1-389	81.27%ID	E:0	Pyruvate dehydrogenase E1 component subunit alpha-1, mitochondrial	PF00676.17*E1_Dh*Dehydrogenase E1 component*139-434*E:4.4e-122 PF02775.18*TPP_enzyme_C*Thiamine pyrophosphate enzyme_C-terminal TPP binding domain*225-340*E:3.8e-05 PF13292.3*DXP_synthase_N*1-deoxy-D-xylulose-5-phosphate synthase*237-301*E:7.1e-05	0,79	0,15	0	1,951	0,739	0,143	0,802	0,117	0,317	0,534	ODPA1_ARATH	Pyruvate dehydrogenase E1 component subunit alpha-1, mitochondrial (PDHE1-A) (EC 1.2.4.1)	E1 ALPHA At1g59900 F23H11.21	Arabidopsis thaliana (Mouse-ear cress)	-	Complete proteome; Glycolysis; Mitochondrion; Oxidoreductase; Pyruvate; Reference proteome; Thiamine pyrophosphate; Transit peptide
SRR924148_TR19161_c0_g1_i2_len=3665	MACP2_ARATH	Q:643-2346,H:15-598	66.1%ID	E:0	MACPF domain-containing protein At4g24290	PF10823.16*MACPF*MACPerforin domain*110-311*E:2.1e-36	0,87	0,163	0	3,923	0,038	1,698	0,038	1,619	0,025	3,307	MACP2_ARATH	MACPF domain-containing protein At4g24290	At4g24290 T22A6.120	Arabidopsis thaliana (Mouse-ear cress)	-	Complete proteome; Cytoplasm; Hypersensitive response; Immunity; Innate immunity; Plant defense; Reference proteome
SRR924148_TR20718_c0_g2_i1_len=2035	COBRA_ARATH	Q:1784-588,H:35-435	83.29%ID	E:0	Protein COBRA	PF04833.12*COBRA*COBRA-like protein*56-219*E:1.1e-73	0,099	0,473	0	1,211	0,847	0,06	0,881	-0,066	0,781	-0,541	COBRA_ARATH	Protein COBRA (Cell expansion protein)	COB At5g60920 MSL3.40	Arabidopsis thaliana (Mouse-ear cress)	-	Cell membrane; Complete proteome; GPI-anchor; Glycoprotein; Lipoprotein; Membrane; Reference proteome; Signal
SRR924148_TR21272_c0_g1_i2_len=1671	UPTG2_SOLTU	Q:1388-348,H:2-348	93.37%ID	E:0	Alpha-1,4-glucan-protein synthase [UDP-forming] 2	PF03214.10*RGP*Reversibly glycosylated polypeptide*13-347*E:4.4e-180	0,522	0,274	0	2,007	0,019	1,277	0,505	0,45	1	-0,47	UPTG2_SOLTU	Alpha-1,4-glucan-protein synthase [UDP-forming] 2 (EC 2.4.1.-) (Reversibly glycosylated polypeptide 2) (RGP2) (UDP-glucose protein transglucosylase 2) (UPTG 2)	UPTG2	Solanum tuberosum (Potato)	-	Cell junction; Cell wall; Cell wall biogenesis/degradation; Cellulose biosynthesis; Complete proteome; Direct protein sequencing; Glycoprotein; Glycosyltransferase; Golgi apparatus; Reference proteome; Secreted; Transferase
SRR924148_TR21806_c0_g1_i1_len=1148	RNLE_SOLLC	Q:324-983,H:11-230	63.8%ID	E:8e-101	Extracellular ribonuclease LE	PF00445.15*Ribonuclease_T2*Ribonuclease T2 family*28-202*E:1.1e-59	0,066	5,267	0	8,773	0,099	1	0,168	3,173	1	-0,543	RNLE_SOLLC	Extracellular ribonuclease LE (RNase LE) (EC 3.1.27.1)	-	Solanum lycopersicum (Tomato) (Lycopersicon esculentum)	-	3D-structure; Cell wall; Complete proteome; Direct protein sequencing; Disulfide bond; Endonuclease; Hydrolase; Nuclease; Reference proteome; Secreted; Signal; Stress response
SRR924148_TR25216_c0_g1_i1_len=2005	6GPD3_ARATH	Q:1829-384,H:5-486	89.42%ID	E:0	6-phosphogluconate dehydrogenase, decarboxylating 3	PF03446.12*NAD_binding_2*NAD binding domain of 6-phosphogluconate dehydrogenase*6-178*E:9.7e-47 PF00393.18*PGD*6-phosphogluconate dehydrogenase, C-terminal domain*183-476*E:3.1e-126	0,771	0,081	0	1,216	0,052	0,566	0,018	0,679	0,511	0,264	6GPD3_ARATH	6-phosphogluconate dehydrogenase, decarboxylating 3 (EC 1.1.1.44)	At3g02360 F11A12.5	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Carbohydrate degradation; pentose phosphate pathway; D-ribulose 5-phosphate from D-glucose 6-phosphate (oxidative stage): step 3/3.	Complete proteome; Cytoplasm; Gluconate utilization; NADP; Oxidoreductase; Pentose shunt; Reference proteome
SRR924148_TR25216_c0_g2_i2_len=2009	6GPD3_ARATH	Q:1829-384,H:5-486	89.42%ID	E:0	6-phosphogluconate dehydrogenase, decarboxylating 3	PF03446.12*NAD_binding_2*NAD binding domain of 6-phosphogluconate dehydrogenase*6-178*E:9.7e-47 PF00393.18*PGD*6-phosphogluconate dehydrogenase, C-terminal domain*183-476*E:3.1e-126	0,76	0,599	0	5,792	0,129	3,912	0,034	4,336	0,132	-2,569	6GPD3_ARATH	6-phosphogluconate dehydrogenase, decarboxylating 3 (EC 1.1.1.44)	At3g02360 F11A12.5	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Carbohydrate degradation; pentose phosphate pathway; D-ribulose 5-phosphate from D-glucose 6-phosphate (oxidative stage): step 3/3.	Complete proteome; Cytoplasm; Gluconate utilization; NADP; Oxidoreductase; Pentose shunt; Reference proteome
SRR924148_TR26351_c1_g1_i1_len=2411	HSP7C_PETHY	Q:165-211,H:1-651	92.2%ID	E:0	Heat shock cognate 70 kDa protein	PF00012.17*HSP70*Hsp70 protein*9-618*E:7.6e-209 PF06723.10*MreB_Mbl*MreB/Mbl protein*142-380*E:4.4e-14	0,065	1,441	0	4,376	0,006	1,045	0,003	1,116	0,001	1,974	HSP7C_PETHY	Heat shock cognate 70 kDa protein	HSP70	Petunia hybrida (Petunia)	-	ATP-binding; Nucleotide-binding; Stress response
SRR924148_TR27417_c0_g3_i1_len=1194	YKT61_ARATH	Q:828-229,H:1-199	86.5%ID	E:3e-126	VAMP-like protein YKT61	PF13774.3*Longin*Regulated-SNARE-like domain*49-112*E:1.3e-10 PF00957.18*Synaptobrevin*Synaptobrevin*138-195*E:2.5e-15	0,211	0,757	0	1,986	0,268	0,419	0,337	0,369	0,679	0,383	YKT61_ARATH	VAMP-like protein YKT61 (AtYKT61) (Geranylgeranylated protein 1) (AtGP1)	YKT61 At5g58060 K21L19.5 K21L19_40	Arabidopsis thaliana (Mouse-ear cress)	-	Alternative splicing; Cell membrane; Coiled coil; Complete proteome; Lipoprotein; Membrane; Methylation; Palmitate; Prenylation; Protein transport; Reference proteome; Transport
SRR924148_TR27519_c0_g2_i1_len=1047	PXG4_ARATH	Q:1-288	68.36%ID	E:6e-83	Probable peroxygenase 4	PF05042.10*Caleosin*Caleosin related protein*23-195*E:1.5e-66	0,832	0,327	0	3,164	0,402	1,177	0,402	1,091	0,317	0,519	PXG4_ARATH	Probable peroxygenase 4 (AtPXG4) (EC 1.11.2.3) (Caleosin-4)	PXG4 CLO4 At1g70670 F5A18.15	Arabidopsis thaliana (Mouse-ear cress)	-	Calcium; Complete proteome; Iron; Lipid droplet; Metal-binding; Oxidoreductase; Phosphoprotein; Reference proteome
SRR924148_TR28419_c0_g3_i1_len=1569	PIP11_ORYSJ	Q:353-1207,H:1-289	85.42%ID	E:1e-178	Aquaporin PIP1-1	PF00230.17*MIP*Major intrinsic protein*45-274*E:8.8e-84	0,889	0,116	0	9,664	0,18	0,801	0,032	1,166	0,254	-3,804	PIP11_ORYSJ	Aquaporin PIP1-1 (OsPIP1;1) (Plasma membrane intrinsic protein 1-1) (Plasma membrane intrinsic protein 1a) (PIP1a) (Water channel protein RWC1) (RWC-1)	PIP1-1 PIP1A RWC1 Os02g0666200 LOC_Os02g44630 OJ1486_E07.10 OsJ_00759 P0461B08.25	Oryza sativa subsp. japonica (Rice)	-	Cell membrane; Complete proteome; Membrane; Reference proteome; Repeat; Transmembrane; Transmembrane helix; Transport
SRR924148_TR30000_c0_g1_i1_len=1212	PGR5_ARATH	Q:30-377,H:1-133	69.17%ID	E:4e-53	Protein PROTON GRADIENT REGULATION 5, chloroplastic	-	0,268	0,39	0	1,164	0,915	0,027	0,57	0,129	0,622	0,124	PGR5_ARATH	Protein PROTON GRADIENT REGULATION 5, chloroplastic	PGR5 At2g05620 T20G20.3	Arabidopsis thaliana (Mouse-ear cress)	-	Chloroplast; Complete proteome; Disulfide bond; Electron transport; Membrane; Plastid; Reference proteome; Thylakoid; Transit peptide; Transport
SRR924148_TR30106_c0_g1_i1_len=1893	NA	NA	NA	NA	NA	PF05542.8*DUF760*Protein of unknown function (DUF760)*148-273*E:9.7e-23 PF05542.8*DUF760*Protein of unknown function (DUF760)*337-418*E:0.00052	0,337	0,286	0	1,397	0,1	0,449	0,075	0,484	0,418	0,249	-	-	-	-	-	-
SRR924148_TR30611_c0_g1_i1_len=1898	NA	NA	NA	NA	NA	-	0,025	1,172	0	2,042	0,028	1,567	0,212	1,084	0,377	0,599	-	-	-	-	-	-
SRR924148_TR31965_c0_g1_i1_len=2718	EDR2L_ARATH	Q:390-2510,H:6-712	29.48%ID	E:4e-99	Protein ENHANCED DISEASE RESISTANCE 2-like	PF01852.16*START*START domain*251-416*E:4e-09 PF07059.9*DUF1336*Protein of unknown function (DUF1336)*538-743*E:8e-69	0,438	0,363	0	2,463	0,021	0,973	0,026	0,929	0,419	0,43	EDR2L_ARATH	Protein ENHANCED DISEASE RESISTANCE 2-like	EDR2L At5g45560 MFC19.23	Arabidopsis thaliana (Mouse-ear cress)	-	Cell membrane; Complete proteome; Endoplasmic reticulum; Endosome; Membrane; Plant defense; Reference proteome; Transmembrane; Transmembrane helix
SRR924148_TR33510_c0_g1_i4_len=1434	QKIL5_ARATH	Q:257-1120,H:11-296	60%ID	E:8e-95	KH domain-containing protein At1g09660/At1g09670	PF16544.2*STAR_dimer*Homodimerisation region of STAR domain protein*34-68*E:2.9e-09	0,038	0,956	0,001	2,095	0,663	0,462	0,049	1,248	0,129	-5,106	QKIL5_ARATH	KH domain-containing protein At1g09660/At1g09670 (Quaking-like protein 5)	At1g09660 F12M12.5 F12M12.6	Arabidopsis thaliana (Mouse-ear cress)	-	Alternative splicing; Complete proteome; Nucleus; Phosphoprotein; RNA-binding; Reference proteome
SRR924148_TR35505_c0_g1_i1_len=3045	NA	NA	NA	NA	NA	-	0,013	0,784	0	1,261	0,136	0,511	0,046	0,678	1	1,755	-	-	-	-	-	-
SRR924148_TR35571_c0_g1_i1_len=2095	UGDH1_SOYBN	Q:286-1725,H:1-480	92.29%ID	E:0	UDP-glucose 6-dehydrogenase 1	PF03721.11*UDPG_MGDP_dh_N*UDP-glucose/GDP-mannose dehydrogenase family, NAD binding domain*3-184*E:5.3e-66 PF00984.16*UDPG_MGDP_dh*UDP-glucose/GDP-mannose dehydrogenase family, central domain*210-304*E:8.8e-32 PF03720.12*UDPG_MGDP_dh_C*UDP-glucose/GDP-mannose dehydrogenase family, UDP binding domain*328-451*E:1.4e-37	0,265	0,314	0	1,704	0,267	-0,307	0,322	-0,277	0,004	-0,848	UGDH1_SOYBN	UDP-glucose 6-dehydrogenase 1 (UDP-Glc dehydrogenase 1) (UDP-GlcDH 1) (UDPGDH 1) (EC 1.1.1.22) (Gm-UGD1)	UGD1	Glycine max (Soybean) (Glycine hispida)	PATHWAY: Nucleotide-sugar biosynthesis; UDP-alpha-D-glucuronate biosynthesis; UDP-alpha-D-glucuronate from UDP-alpha-D-glucose: step 1/1.	Complete proteome; NAD; Oxidoreductase; Phosphoprotein; Reference proteome
SRR924148_TR37769_c0_g1_i6_len=2562	AGT23_ARATH	Q:228-1733,H:20-481	69.72%ID	E:0	Alanine--glyoxylate aminotransferase 2 homolog 3, mitochondrial	PF00202.18*Aminotran_3*Aminotransferase class-III*3-321*E:2.5e-75	0,189	1,826	0	5,652	0,254	2,918	1	1,843	0,228	1,024	AGT23_ARATH	Alanine--glyoxylate aminotransferase 2 homolog 3, mitochondrial (EC 2.6.1.44) (Beta-alanine-pyruvate aminotransferase 3)	At3g08860 T16O11.21	Arabidopsis thaliana (Mouse-ear cress)	-	Aminotransferase; Complete proteome; Mitochondrion; Photorespiration; Pyridoxal phosphate; Reference proteome; Transferase; Transit peptide
SRR924148_TR37788_c0_g1_i3_len=1429	NDK4_ARATH	Q:1108-404,H:1-235	76.37%ID	E:2e-123	Nucleoside diphosphate kinase IV, chloroplastic/mitochondrial	PF00334.16*NDK*Nucleoside diphosphate kinase*88-221*E:3.1e-52	0,364	0,272	0	1,475	0,144	0,41	0,213	0,347	0,449	0,225	NDK4_ARATH	Nucleoside diphosphate kinase IV, chloroplastic/mitochondrial (NDK IV) (NDP kinase IV) (NDPK IV) (EC 2.7.4.6) (Nucleoside diphosphate kinase 4)	NDK4 At4g23900 T32A16.70	Arabidopsis thaliana (Mouse-ear cress)	-	ATP-binding; Chloroplast; Complete proteome; Direct protein sequencing; Kinase; Magnesium; Metal-binding; Mitochondrion; Nucleotide metabolism; Nucleotide-binding; Plastid; Reference proteome; Thylakoid; Transferase; Transit peptide
SRR924148_TR38585_c0_g1_i2_len=2773	NA	NA	NA	NA	NA	-	0,346	0,425	0	1,503	0,429	0,246	0,627	0,161	0,692	1,17	-	-	-	-	-	-
SRR924148_TR39344_c1_g1_i1_len=1978	CALM_LILLO	Q:209-655,H:1-149	100%ID	E:2e-96	Calmodulin	PF00036.29*EF-hand_1*EF hand*12-40*E:2.4e-09 PF13499.3*EF-hand_7*EF-hand domain pair*12-73*E:1.9e-15 PF13405.3*EF-hand_6*EF-hand domain*12-41*E:1e-09 PF13202.3*EF-hand_2*EF hand*14-37*E:6.2e-05 PF13833.3*EF-hand_8*EF-hand domain pair*25-75*E:4.2e-14 PF00036.29*EF-hand_1*EF hand*48-75*E:1.7e-08 PF13202.3*EF-hand_5*EF hand*49-75*E:0.00014 PF13499.3*EF-hand_7*EF-hand domain pair*83-146*E:4.6e-18 PF00036.29*EF-hand_1*EF hand*85-112*E:2e-09 PF13405.3*EF-hand_6*EF-hand domain*85-114*E:1.9e-08 PF12763.4*EF-hand_4*Cytoskeletal-regulatory complex EF hand*85-146*E:4.6e-05 PF13202.3*EF-hand_2*EF hand*116-110*E:1.4e-06 PF13833.3*EF-hand_8*EF-hand domain pair*98-146*E:9.8e-15 PF00036.29*EF-hand_1*EF hand*121-148*E:3.3e-10 PF13202.3*EF-hand_5*EF hand*124-146*E:5.3e-05	0,315	-0,286	0	0,983	0,542	0,164	0,221	0,315	0,541	-0,146	CALM_LILLO	Calmodulin (CaM)	-	Lilium longiflorum (Trumpet lily)	-	Acetylation; Calcium; Metal-binding; Methylation; Repeat

MsDamaged24h

Transcript (CDF97)	Uniprot homolog	BLASTX Position	BLASTX %identity	BLASTX evalue	Uniprot descr	Pfam	PValue_Ms6h	logFC_Ms6h	PValue_Ms8h	logFC_Ms8h	PValue_MsDamaged24h	logFC_MsDamaged24h	PValue_MsIntact24h	logFC_MsIntact24h	PValue_Ms1wk	logFC_Ms1wk	Entry.name	Protein names	Gene names	Organism	Pathway	Keywords
SRR114633_TR4555_c1_g1_i1_len=968	LOR6_ARATH	Q:841-263,H:4-191	54.64%ID	E:4e-65	Protein LURP-one-related 6	PF04525.9*LUR*Uncharacterized protein*15-196*E:4.2e-44	1	0,254	1	-1,093	0	6,715	0,129	5,118	1	0	LOR6_ARATH	Protein LURP-one-related 6	At2g05910 T6P5.11	Arabidopsis thaliana (Mouse-ear cress)	-	Complete proteome; Reference proteome
SRR114633_TR5319_c0_g2_i1_len=1495	PER12_ARATH	Q:246-1187,H:26-339	63.38%ID	E:3e-147	Peroxidase 12	PF00141.20*peroxidase*Peroxidase*62-303*E:9.4e-70	0,064	0,425	0,002	0,725	0	2,162	0,001	1,296	1	-0,991	PER12_ARATH	Peroxidase 12 (Atperox P12) (EC 1.11.1.7) (ATP4a) (PRXR6)	PER12 P12 At1g71695 F14O23.6 F26A9.5	Arabidopsis thaliana (Mouse-ear cress)	-	Calcium; Complete proteome; Disulfide bond; Glycoprotein; Heme; Hydrogen peroxide; Iron; Metal-binding; Oxidoreductase; Peroxidase; Reference proteome; Secreted; Signal; Vacuole
SRR114633_TR18843_c0_g1_i1_len=769	RL361_ARATH	Q:203-484,H:8-101	88.3%ID	E:4e-50	60S ribosomal protein L36-1	-	0,064	0,583	0,393	0,218	0	1,486	0,006	0,995	0,399	-0,275	RL361_ARATH	60S ribosomal protein L36-1	RPL36A At2g37600 F13M22.10	Arabidopsis thaliana (Mouse-ear cress)	-	Complete proteome; Reference proteome; Ribonucleoprotein; Ribosomal protein
SRR114633_TR23923_c0_g1_i2_len=991	QCR7_SOLTU	Q:24-592,H:1-122	82.93%ID	E:3e-55	Cytochrome b-c1 complex subunit 7	PF02271.13*UCR_14kD*Ubiquinol-cytochrome C reductase complex 14kD subunit*17-110*E:2.1e-26	0,472	0,64	0,042	1,699	0	1,475	0,021	0,927	1	1,879	QCR7_SOLTU	Cytochrome b-c1 complex subunit 7 (CR14) (Complex III subunit 7) (Complex III subunit VII) (Ubiquinol-cytochrome c reductase complex 14 kDa protein)	-	Solanum tuberosum (Potato)	-	Complete proteome; Direct protein sequencing; Electron transport; Membrane; Mitochondrion; Mitochondrion inner membrane; Reference proteome; Respiratory chain; Transport
SRR114633_TR24183_c0_g1_i1_len=1194	E13A_MAIZE	Q:983-486,H:58-219	37.95%ID	E:2e-30	Endo-1,3	PF01738.15*DLH*Dienelactone hydrolase family*19-227*E:1.3e-28	0,946	0,045	0,319	0,377	0,001	1,221	0,001	1,17	1	-0,614	E13A_MAIZE	Endo-1,3;1,4-beta-D-glucanase (EC 3.2.1.-)	-	Zea mays (Maize)	-	Complete proteome; Direct protein sequencing; Glycoprotein; Hydrolase; Reference proteome; Secreted; Signal
SRR114633_TR27508_c1_g2_i1_len=1881	CASL2_CANSA	Q:375-1608,H:127-540	51.44%ID	E:1e-132	Cannabidiolic acid synthase-like 2	PF01565.20*FAD_binding_4*FAD binding domain*16-104*E:1.6e-16 PF08031.9*BBE*Berberine and berberine like*365-423*E:2.2e-21	0,781	0,586	0,066	1,721	0	3,745	0,299	1,772	1	0,362	CASL2_CANSA	Cannabidiolic acid synthase-like 2	CBDAS3	Cannabis sativa (Hemp) (Marijuana)	-	Disulfide bond; FAD; Flavoprotein; Glycoprotein; Secreted; Signal
SRR114634_TR3033_c0_g2_i1_len=975	FB237_ARATH	Q:963-484,H:223-380	90.62%ID	E:2e-95	F-box protein At4g18380	-	1	0,147	0,707	0,267	0	7,133	0,001	6,462	0,643	-0,415	FB237_ARATH	F-box protein At4g18380	At4g18380 F28J12.40	Arabidopsis thaliana (Mouse-ear cress)	-	Complete proteome; Reference proteome
SRR114634_TR3385_c0_g1_i1_len=875	NA	NA	NA	NA	NA	PF04554.10*Extensin_2*Extensin-like region*126-174*E:0.00016	0,502	2,687	1	2,807	0	3,646	0,001	3,307	1	0	-	-	-	-	-	-
SRR114634_TR10120_c0_g1_i2_len=950	NA	NA	NA	NA	NA	PF00582.23*Usp*Universal stress protein family*29-174*E:2.1e-26	1	0	0,502	3,788	0	7,095	0,017	5,879	0,412	-0,506	-	-	-	-	-	-
SRR114634_TR23319_c0_g1_i1_len=2062	APA1_ARATH	Q:268-1806,H:1-506	75.49%ID	E:0	Aspartic proteinase A1	PF00026.20*Asp*Eukaryotic aspartyl protease*131-554*E:4e-136 PF14543.3*TAXI_N*Xylanase inhibitor N-terminal*132-290*E:3.1e-13 PF03489.14*SapB_2*Saposin-like type B, region 2*365-398*E:8.4e-13 PF05184.12*SapB_1*Saposin-like type B, region 1*428-464*E:1.2e-14	0,054	0,584	0,501	0,218	0	1,107	0,022	0,696	0,062	0,608	APA1_ARATH	Aspartic proteinase A1 (EC 3.4.23.-)	APA1 PRA1 At1g11910 F12F1.24	Arabidopsis thaliana (Mouse-ear cress)	-	Aspartyl protease; Complete proteome; Disulfide bond; Glycoprotein; Hydrolase; Protease; Reference proteome; Repeat; Signal; Vacuole; Zymogen
SRR114634_TR27168_c0_g1_i1_len=1196	TPRL3_ERYCB	Q:327-1073,H:10-258	80.32%ID	E:1e-138	Tropinone reductase-like 3	PF00106.22*adh_short*adh short chain dehydrogenase*15-203*E:5.1e-42 PF08659.7*KR*KR domain*18-182*E:7.5e-09 PF13561.3*adh_short_C2*Enoyl-(Acyl carrier protein) reductase*24-253*E:6.1e-09	0,834	0,098	0,001	1,042	0	1,409	0,002	1,165	0,423	-0,373	TPRL3_ERYCB	Tropinone reductase-like 3 (EC 1.1.1.-)	-	Erythroxylum coca (Coca plant)	-	Oxidoreductase
SRR114634_TR38172_c0_g2_i1_len=1307	PUP3_ARATH	Q:111-1052,H:15-331	44.48%ID	E:5e-62	Purine permease 3	PF16913.2*PUNUT*Purine nucleobase transmembrane transport*14-333*E:4.8e-91 PF00892.17*EamA*EamA-like transporter family*69-156*E:2.4e-07	0,022	0,787	0,043	0,687	0	1,393	0,039	0,688	1	0,971	PUP3_ARATH	Purine permease 3 (AtPUP3)	PUP3 At1g28220 F3H9.12	Arabidopsis thaliana (Mouse-ear cress)	-	Complete proteome; Membrane; Reference proteome; Transmembrane; Transmembrane helix; Transport
SRR122236_TR13132_c1_g1_i1_len=1818	COMT1_CATRO	Q:1220-197,H:19-360	100%ID	E:0	Caffeic acid 3-O-methyltransferase	PF00891.15*Methyltransf_2*O-methyltransferase*135-351*E:8.2e-90	1	0	0,002	6,365	0	7,382	0,001	0,49	1	0	COMT1

SRR3271858_TR34960_c0_g2_i1_len=1074	XTH28_ARATH	Q:139-867;H:66-308	69.55%ID	E:1e-129	Probable xyloglucan endotransglucosylase/hydrolase protein 28	PF00722.18*Glyco_hydro_16*Glycosyl hydrolases family 16*2-120*E:1.1e-39 PF06955.9*XET_C*Xyloglucan endo-transglycosylase (XET) C-terminus*160-195*E:1.4e-13	1	0.248	1	0.031	0	1.612	0.013	1.176	0.024	-0.97	XTH28_ARATH	Probable xyloglucan endotransglucosylase/hydrolase protein 28 (At-XTH28) (XTH-28) (EC 2.4.1.207)	XTH28 EXGT-A2 XTR2 At1g14720 F10B6.12 F10B6.29	Arabidopsis thaliana (Mouse-ear cress)		Apoplast; Cell wall; Cell wall biogenesis/degradation; Complete proteome; Disulfide bond; Glycoprotein; Glycosidase; Hydrolase; Reference proteome; Secreted; Signal; Transferase
SRR3271858_TR35881_c1_g1_i1_len=707	NA	NA	NA	NA	NA	NA	1	2.839	1	1.414	0	9.008	0.001	6.475	0.502	-3.533	.	Gamma-interferon-inducible lysosomal thiol reductase (EC 1.8.--.-) (Gamma-interferon-inducible protein IP-30) (Legumatrain)	IFI30 GILT IP30	Homo sapiens (Human)				Complete proteome; Direct protein sequencing; Disulfide bond; Glycoprotein; Immunity; Lysosome; Oxidoreductase; Redox-active center; Reference proteome; Secreted; Signal
SRR3271858_TR38866_c0_g1_i1_len=1447	GILT_HUMAN	Q:927-379;H:62-243	37.23%ID	E:4e-29	Gamma-interferon-inducible lysosomal thiol reductase	PF03227.13*GILT*Gamma interferon inducible lysosomal thiol reductase (GILT)*41-143*E:4e-29	0.507	0.237	0.507	-0.248	0	1.232	0.028	0.789	1	0.219	GILT_HUMAN	1-aminocyclopropane-1-carboxylate oxidase 5 (ACC oxidase 5) (AtACO5) (EC 1.14.17.4)	At1g77330 F2P24.4	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Alkene biosynthesis; ethylene biosynthesis via S-adenosyl-L-methionine; ethylene from S-adenosyl-L-methionine: step 2/2.	Coiled coil; Complete proteome; Ethylene biosynthesis; Iron; Metal-binding; Oxidoreductase; Plant defense; Reference proteome; Vitamin C
SRR3271858_TR40126_c0_g3_i1_len=1150	ACCO5_ARATH	Q:240-746;H:109-285	43.5%ID	E:8e-42	1-aminocyclopropane-1-carboxylate oxidase 5	PF03171.17*2OG-Fe(II_Oxy*2OG-Fe(II) oxygenase superfamily*6-104*E:8.5e-30	0.034	3.582	0.017	3.974	0	3.697	0.003	3.239	0.034	-3.347	ACCO5_ARATH	1-aminocyclopropane-1-carboxylate oxidase 5 (ACC oxidase 5) (AtACO5) (EC 1.14.17.4)	At1g77330 F2P24.4	Arabidopsis thaliana (Mouse-ear cress)			
SRR3271858_TR47901_c0_g1_i1_len=790	NA	NA	NA	NA	NA	PF04398.9*DUF538*Protein of unknown function, DUF538*29-140*E:2.9e-29	1	0.521	0.034	5.649	0	7.351	0.254	4.732	1	-0.787	.	.	.	.				
SRR3271858_TR61015_c1_g3_i3_len=5104	AB36G_ARATH	Q:634-5019;H:34-1469	73.53%ID	E:0	ABC transporter G family member 36	PF14510.3*ABC_trans_N*ABC-transporter extracellular N-terminal*95-155*E:9.2e-12*PF00005.24*ABC_tran*ABC transporter*180-362*E:9.5e-14 PF01061.21*ABC2_membrane*ABC-2 type transporter*516-722*E:2.6e-45*PF08370.8*PDR_assoc*Plant PDR ABC transporter associated*733-796*E:1.1e-25 PF00005.24*ABC_tran*ABC transporter*913-1065*E:1.6e-20 PF01061.21*ABC2_membrane*ABC-2 type transporter*1211-1424*E:1.8e-57	0.502	2.716	0.502	3.91	0	3.753	0.027	2.694	1	-0.75	AB36G_ARATH	ABC transporter G family member 36 (ABC transporter ABCG.36) (AtABCG36) (Pleiotropic drug resistance protein 8) (Protein PENETRATION 3)	ABCG36 PDR8 PEN3 At1g59870 F23H11.19	Arabidopsis thaliana (Mouse-ear cress)		ATP-binding; Acetylation; Cell membrane; Complete proteome; Membrane; Nucleotide-binding; Phosphoprotein; Plant defense; Reference proteome; Repeat; Transmembrane; Transmembrane helix; Transport
SRR3271859_TR2892_c1_g1_i4_len=1308	ULT1_ARATH	Q:315-989;H:14-237	75.11%ID	E:2e-121	Protein ULTRAPETALA 1	PF01342.18*SAND*SAND domain*65-192*E:3.3e-05	0.692	-1.131	0.103	1.56	0	3.465	0.132	2.155	1	0	ULT1_ARATH	Protein ULTRAPETALA 1	ULT1 At4g28190 F26K10.70	Arabidopsis thaliana (Mouse-ear cress)				Alternative splicing; Complete proteome; Cytoplasm; DNA-binding; Developmental protein; Nucleus; Reference proteome; Transcription; Transcription regulation
SRR3271859_TR4140_c0_g2_i1_len=1050	NA	NA	NA	NA	NA	.	0.629	1.16	0.014	2.842	0	3.379	0.073	2.005	1	0.198	.	.	.	.				
SRR3271859_TR4946_c0_g3_i5_len=638	CB2D_SOLLC	Q:608-276;H:6-116	93.69%ID	E:4e-70	Chlorophyll a-b binding protein 1D	PF00011.16*PSP*Plant and cyanobacteria specific photosystem II protein PsbY family*	0.458	0.155	0	-2.667	0	1.036	0.004	0.613	0	-3.844	CB2D_SOLLC	Chlorophyll a-b binding protein 1D (LHCII type I CAB-1D) (LHCP) (Fragment)	CAB1D	Solanum lycopersicum (Tomato) (Lycopersicon esculentum)				Chlorophyll; Chloroplast; Chromophore; Complete proteome; Magnesium; Membrane; Metal-binding; Phosphoprotein; Photosynthesis; Photosystem I; Photosystem II; Plastid; Reference proteome; Thylakoid; Transmembrane; Transmembrane helix
SRR3271859_TR6881_c0_g2_i2_len=3130	FPP3_ARATH	Q:446-2428;H:1-615	43.79%ID	E:4e-92	Filamentlike plant protein 3	PF05911.8*FPP*Filamentlike plant protein, long coiled-coil*83-189*E:1.2e-36 PF05911.8*FPP*Filamentlike plant protein, long coiled-coil*198-267*E:8e-20 PF05911.8*FPP*Filamentlike plant protein, long coiled-coil*319-371*E:3.1e-13 PF05911.8*FPP*Filamentlike plant protein, long coiled-coil*480-655*E:1.9e-23	1	-0.015	0.096	0.674	0	2.694	0.132	1.495	0.708	0.176	FPP3_ARATH	Filamentlike plant protein 3 (AtFPP3)	FPP3 At3g05270 T12H1.24	Arabidopsis thaliana (Mouse-ear cress)		Coiled coil; Complete proteome; Reference proteome	
SRR3271859_TR12278_c0_g1_i1_len=2171	PTR3_ARATH	Q:2043-328;H:9-579	66.43%ID	E:0	Protein NRT1/ PTR FAMILY 5.2	PF00854.18*PTR2*POT family*101-530*E:1.8e-99	0.263	0.359	0.356	0.34	0	1.35	0.012	0.917	0.037	0.914	PTR3_ARATH	Protein NRT1/ PTR FAMILY 5.2 (AtNPF5.2) (Peptide transporter PTR3-A) (AtPTR3)	NPF5.2 PTR3-A At5g46050 MCL19.10	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Membrane; Reference proteome; Transmembrane; Transmembrane helix	
SRR3271859_TR13981_c0_g2_i1_len=608	HSP12_MEDSA	Q:1-441;H:12-158	85.71%ID	E:1e-67	18.2 kDa class I heat shock protein	PF04969.13*CS*CS domain*41-132*E:0.0089 PF00011.18*HSP20*Hsp20/alpha crystallin family*43-146*E:7.5e-33	0.086	-0.855	0.017	-1.025	0	2.181	0.034	1.103	0.901	-0.049	HSP12_MEDSA	18.2 kDa class I heat shock protein	HSP18.2	Medicago sativa (Alfalfa)				Cytoplasm; Stress response
SRR3271859_TR15741_c0_g3_i1_len=861	NA	NA	NA	NA	NA	.	1	0.019	1	3.345	0.001	5.61	0.066	4.263	1	-0.874	.	.	.	.				
SRR3271859_TR16572_c0_g1_i3_len=2193	GSTF6_ARATH	Q:316-936;H:1-207	62.8%ID	E:1e-88	Glutathione S-transferase F10	PF02798.17*GST_N*Glutathione S-transferase, N-terminal domain*2-75*E:3.7e-16 PF13417.3*GST_N_3*Glutathione S-transferase, N-terminal domain*13-78*E:1.5e-14 PF13409.3*GST_N_2*Glutathione S-transferase, N-terminal domain*14-75*E:8.7e-12 PF00043.22*GST_C*Glutathione S-transferase, C-terminal domain*127-202*E:1e-16 PF14497.3*GST_C_3*Glutathione S-transferase, C-terminal domain*134-203*E:6.5e-07	0.189	-0.521	0.522	-0.298	0.001	2.021	0.006	1.703	0.568	0.27	GSTF6_ARATH	Glutathione S-transferase F10 (AtGSTF10) (EC 2.5.1.18) (AtGSTF4) (GST class-phi member 10) (Protein EARLY RESPONSE TO DEHYDRATION 13)	GSTF10 ERD13 GSTF4 At2g30870 F7F1.8	Arabidopsis thaliana (Mouse-ear cress)				Complete proteome; Cytoplasm; Detoxification; Direct protein sequencing; Reference proteome; Stress response; Transferase
SRR3271859_TR21191_c0_g1_i1_len=1093	NA	NA	NA	NA	NA	.	1	1.694	0.502	4.346	0	8.377	0.017	5.885	1	-3.571	.	.	.	.				
SRR3271859_TR21383_c0_g2_i1_len=683	CSPL2_RICCO	Q:7-549;H:12-163	59.87%ID	E:3e-41	CASP-like protein 1C2	PF04535.9*DUF588*Domain of unknown function (DUF588)*7-141*E:1.8e-37	0.502	3.225	0.009	5.325	0.001	4.425	0.629	2.294	0.502	-2.716	CSPL2_RICCO	CASP-like protein 1C2 (RcCASPL1C2)	RCOM_0936380	Ricinus communis (Castor bean)				Cell membrane; Complete proteome; Glycoprotein; Membrane; Reference proteome; Transmembrane; Transmembrane helix
SRR3271859_TR22448_c0_g1_i1_len=717	H2B_GOSHI	Q:232-540;H:45-147	96.12%ID	E:5e-58	Histone H2B	PF00125.21*Histone*Core histone H2A/H2B/H3/H4*9-124*E:9.9e-23 PF00808.20*CBFD_NFYB_HMF*Histone-like transcription factor (CBF/NF-Y) and archaeal histone*66-122*E:4.4e-05	0	-0.953	0.205	-0.355	0	1.025	0.003	0.883	1	-2.277	H2B_GOSHI	Histone H2B	HIS2B	Gossypium hirsutum (Upland cotton) (Gossypium mexicanum)				Acetylation; Chromosome; DNA-binding; Isopeptide bond; Nucleosome core; Nucleus; Ubl conjugation
SRR3271859_TR25424_c0_g4_i1_len=1358	NA	NA	NA	NA	NA	PF09032.8*Slah-Interact_N*Slah interacting protein, N terminal*3-63*E:5.7e-08 PF04969.13*CS*CS domain*73-149*E:1.9e-15	0.226	-0.511	0.389	-0.41	0	1.27	0.023	0.809	1	0.015	.	.	.	.				
SRR3271859_TR26970_c0_g2_i1_len=1951	NA	NA	NA	NA	NA	.	0.129	3.623	0.005	4.182	0	3.496	0.025	2.733	0.732	0.891	.	.	.	.				
SRR3271859_TR43498_c0_g1_i4_len=2228	INT2_ARATH	Q:194-1951;H:1-579	67.63%ID	E:0	Probable inositol transporter 2	PF00083.21*Sugar_tr*Sugar (and other) transporter*30-379*E:1.9e-94 PF07690.13*MFS_1*Major Facilitator Superfamily*35-368*E:2e-33 PF06609.10*TRI12*Fungal trichothecene efflux pump (TRI12)*74-228*E:4.2e-07 PF00083.21*Sugar_tr*Sugar (and other) transporter*461-563*E:4.4e-28	0.073	1.898	0.132	2.964	0	7.051	0.034	5.66	1	0.127	INT2_ARATH	Probable inositol transporter 2	INT2 At1g30220 F12P21.2	Arabidopsis thaliana (Mouse-ear cress)		Cell membrane; Complete proteome; Membrane; Reference proteome; Symport; Transmembrane; Transmembrane helix; Transport
SRR3271859_TR45268_c0_g1_i1_len=685	NA	NA	NA	NA	NA	.	0.254	4.534	0.129	5.148	0	7.344	0.129	4.865	1	0	.	.	.	.				
SRR3271859_TR47365_c0_g3_i1_len=2084	APA1_ARATH	Q:1765-332;H:27-506	67.36%ID	E:0	Aspartic proteinase A1	PF00026.20*Asp*Eukaryotic aspartyl protease*121-544*E:6.3e-134 PF14543.3*TAXI_N*Xylanase inhibitor N-terminal*122-279*E:2.8e-14 PF03489.14*SapB_2*Saposin-like type B, region 2*354-387*E:1.5e-12 PF05184.12*SapB_1*Saposin-like type B, region 1*418-454*E:1e-10	0.934	0.03	0.935	-0.026	0.001	1.1	0.014	0.829	0.08	0.547	APA1_ARATH	Aspartic proteinase A1 (EC 3.4.23.-)	APA1 PRA1 At1g11910 F12F1.24	Arabidopsis thaliana (Mouse-ear cress)		Aspartyl protease; Complete proteome; Disulfide bond; Glycoprotein; Hydrolase; Protease; Reference proteome; Repeat; Signal; Vacuole; Zymogen
SRR3420117_TR987_c0_g9_i1_len=1009	ABB9_ARATH	Q:2697;H:994-1225	81.9%ID	E:7e-124	ABC transporter B family member 9	PF00005.24*ABC_tran*ABC transporter*19-168*E:2.5e-35	0.781	0.504	0.316	0.633	0	6.797	0.034	5.534	0.175	-0.966	ABB9_ARATH	ABC transporter B family member 9 (ABC transporter ABCB.9) (AtABCB9) (Multidrug resistance protein 9) (P-glycoprotein 9)	ABCB9 MDR9 PGP9 At4g18050 F15J5.20	Arabidopsis thaliana (Mouse-ear cress)		ATP-binding; Complete proteome; Glycoprotein; Membrane; Nucleotide-binding; Reference proteome; Repeat; Transmembrane; Transmembrane helix; Transport
SRR3420117_TR1512_c0_g3_i1_len=960	CH10C_ARATH	Q:6-474;H:31-253	77.58%ID	E:7e-119	20 kDa chaperonin, chloroplastic	PF00166.18*Cpn10*Chaperonin 10 Kd subunit*33-122*E:5.6e-28 PF00166.18*Cpn10*Chaperonin 10 Kd subunit*131-222*E:3.9e-28	0	-0.33	-1.4	0	0	4.284	0.004	3.434	0	-0.897	CH10C_ARATH	20 kDa chaperonin, chloroplastic (Chaperonin 10) (Ch-CPN10) (Cpn10) (Chaperonin 20) (Protein cpn21)	CPN21 CHCPN10 CPN20 At5g20720 T1M15.120	Arabidopsis thaliana (Mouse-ear cress)		Chaperone; Chloroplast; Complete proteome; Phosphoprotein; Plastid; Reference proteome; Repeat; Transit peptide
SRR3420117_TR2746_c0_g1_i2_len=3059	SUBL_ARATH	Q:2585-378;H:31-757	58.63%ID	E:0	.	PF05922.13*Inhibitor_I9*Peptidase inhibitor I9*29-107*E:1.4e-17 PF00082.19*Peptidase_S8*Subtilase family*137-568*E:1.3e-49 PF02225.19*PA*PA domain*403-463*E:2.4e-09	0	-1.437	0.357	0.649	0	1.743	0.739	0.338	1	0.022	SBT17_ARATH	Subtilisin-like protease SBT1.7 (EC 3.4.21.-) (Cucumisin-like serine protease) (Subtilase subfamily 1 member 7) (AtSBT1.7) (Subtilisin-like serine protease 1) (At-SLP1)	SBT1.7 ARA12 ASP48 SLP1 At5g67360 K8K14.8	Arabidopsis thaliana (Mouse-ear cress)		Calcium; Cell wall; Complete proteome; Direct protein sequencing; Glycoprotein; Hydrolase; Protease; Reference proteome; Secreted; Serine protease; Signal; Zymogen
SRR3420117_TR3159_c0_g5_i1_len=1156	NA	NA	NA	NA	NA	.	0.365	0.568	0	-1.631	0.001	6.552	1	0	0	-1.919	.	.	.	.				
SRR3420117_TR4266_c1_g9_i1_len=1532	PDI_DATGL	Q:22-1086;H:138-492	68.07%ID	E:1e-159	Protein disulfide-isomerase	PF13848.3*Thioredoxin_6*Thioredoxin-like domain*44-226*E:6.6e-20 PF00085.17*Thioredoxin*Thioredoxin*249-352*E:4e-26	0.01	-2.201	0.005	-0.937	0	2.809	0.282	1.209	0.004	-0.889	PDI_DATGL	Protein disulfide-isomerase (PDI) (EC 5.3.4.1)	PDI	Dalisca glomerata (Durango root)				Disulfide bond; Endoplasmic reticulum; Glycoprotein; Isomerase; Redox-active center; Repeat; Signal
SRR3420117_TR4309_c0_g2_i1_len=809	NA	NA	NA	NA	NA	.	0.102	-0.422	0.15	-0.387	0	2.973	0.042	1.842	0.009	-0.698	.	.	.	.				
SRR3420117_TR7232_c0_g1_i1_len=525	CID9_ARATH	Q:525-355;h:267-323	75.44%ID	E:2e-21	Polyadenylate-binding protein-interacting protein 9	.	0.017	5.772	0.105	-1.013	0	7.451	1	0	1	0	CID9_ARATH	Polyadenylate-binding protein-interacting protein 9 (PABP-interacting protein 9) (PolyA)-binding protein-interacting protein 9) (PAM2-containing protein CID9) (Protein CTC-INTERACTING DOMAIN 9)	CID9 At3g14450 MOA2.5	Arabidopsis thaliana (Mouse-ear cress)				Complete proteome; Nucleus; RNA-binding; Reference proteome; Repeat
SRR3420117_TR8315_c2_g6_i1_len=967	DCAM_CATRO	Q:1-429;H:208-350	78.32%ID	E:5e-75	S-adenosylmethionine decarboxylase proenzyme	PF01536.13*SAM_decarbox*Adenosylmethionine decarboxylase*1-125*E:3.7e-33 PF08315.9*cwf18*cwf18 pre-mRNA splicing factor*143-237*E:2.4e-26	0.235	-0.891	0.031	-1.638	0.001	6.58	0.017	5.851	0.443	-0.441	DCAM_CATRO	S-adenosylmethionine decarboxylase proenzyme (AdoMetDC) (SAMDC) (EC 4.1.1.50) [Cleaved into: S-adenosylmethionine decarboxylase alpha chain; S-adenosylmethionine decarboxylase beta chain]	SAMDC	Catharanthus roseus (Madagascar periwinkle) (Vinca rosea)	PATHWAY: Amine and polyamine biosynthesis; S-adenosylmethioninamine biosynthesis; S-adenosylmethionine from S-adenosyl-L-methionine: step 1/1.	Autocatalytic cleavage; Decarboxylase; Lyase; Polyamine biosynthesis; Pyruvate; S-adenosyl-L-methionine; Schiff base; Spermidine biosynthesis; Zymogen
SRR3420117_TR10528_c0_g1_i3_len=2256	KTNA1_ARATH	Q:321-1856;H:8-523	85.11%ID	E:0	Katanin p60 ATPase-containing subunit A1	PF05496.9*RuvB_N*Holliday junction DNA helicase ruvB N-terminus*268-337*E:8.2e-05 PF00004.26*AAA*ATPase family associated with various cellular activities (AAA)*269-406*E:1e-37 PF09336.7*vps4_C*Vps4 C terminal oligomerisation domain*470-515*E:4e-11	0.629	-1.177	0.068	-1.055	0.001	3.35	0.001	3.262	0.629	1.893	KTNA1_ARATH	Katanin p60 ATPase-containing subunit A1 (Katanin p60 subunit A1) (EC 3.6.4.3) (CAD ATPase) (Katanin-1) (Atp60) (Protein BOTERO 1) (Protein ECTOPIC ROOT HAIR 3) (Protein FAT ROOT) (Protein FRAGILE FIBER 2) (AtAAA1) (p60 katanin)	AAA1 BOT1 ERH3 FRA2 FTR KSS KTN1 LUE1 At1g80350 F5I6.10	Arabidopsis thaliana (Mouse-ear cress)		ATP-binding; Complete proteome; Cytoplasm; Cytoskeleton; Hydrolase; Microtubule; Nucleotide-binding; Reference proteome
SRR3420117_TR11113_c0_g7_i6_len=1759	TC120_ARATH	Q:1597-632;h:763-1085	71.52%ID	E:8e-152	Translocase of chloroplast 120, chloroplastic	PF11886.5*TOC159_MAD*Translocase of chloroplast 159/132, membrane anchor domain*43-305*E:8.5e-116	0.781	0.41	0.075	-0.751	0	7.187	0.009	5.934	0.719	-0.31	TC120_ARATH	Translocase of chloroplast 120, chloroplastic (AtToc120) (EC 3.6.5.-) (120 kDa chloroplast outer envelope protein)	TOC120 At3g16620 MGL6.15	Arabidopsis thaliana (Mouse-ear cress)				Acetylation; Chloroplast; Coiled coil; Complete proteome; Cytoplasm; GTP-binding; Hydrolase; Magnesium; Membrane; Metal-binding; Nucleotide-binding; Phosphoprotein; Plastid; Plastid outer membrane; Protein transport; Receptor; Reference proteome; Transmembrane; Transmembrane helix; Transport
SRR3420117_TR12681_c0_g1_i1_len=538	NA	NA	NA	NA	NA	.	0.548	-0.249	0.384	-0.307	0	1.752	0.006	1.27	0.441	-0.563	.	.	.	.				
SRR3420117_TR14705_c0_g2_i3_len=1792	Y5188_ARATH	Q:969-151;H:577-851	55.23%ID	E:5e-98	Probable LRR receptor-like serine/threonine-protein kinase At1g51880	PF00069.22*Pkinase*Protein kinase domain*1-200*E:6.6e-33 PF07714.14*Pkinase_Tyr*Protein tyrosine kinase*2-144*E:7.2e-28	1	-0.08	0.025	1.206	0.001	1.996	0.009	1.617	1	-0.284	Y5188_ARATH	Probable LRR receptor-like serine/threonine-protein kinase At1g51880 (EC 2.7.11.1)	At1g51880 T14L22.9	Arabidopsis thaliana (Mouse-ear cress)				Complete proteome; Membrane; Reference proteome; Transmembrane; Transmembrane helix
SRR3420117_TR16357_c1_g1_i1_len=663	PSAG_ARATH	Q:20-7629;H:27-220	72.34%ID	E:8e-67	Photosystem I reaction center subunit V, chloroplastic	PF01241.15*PSI_PSAK*Photosystem I psaG / psaK*53-144*E:2.5e-26	0.388	-0.239	0.4	0.05	0	1.468	0.019	0.942	0.433	0.21	PSAG_ARATH	Photosystem I reaction center subunit V, chloroplastic (PSI-G)	PSAG At1g55670 F20N2.21 F20N2.33 F20N2_3	Arabidopsis thaliana (Mouse-ear cress)				Chloroplast; Complete proteome; Membrane; Photosynthesis; Photosystem I; Plastid; Reference proteome; Thylakoid; Transfer; Transmembrane; Transmembrane helix
SRR3420117_TR17600_c3_g1_i1_len=728	PSC52_ARATH	Q:673-314;H:596-715	87.5%ID	E:4e-65	Delta-1-pyrroline-5-carboxylate synthase B	PF03051.14*Peptidase_C0*Peptidase family C0*2-377*E:1.1e-77	0.005	6.16	0.77	-0.162	0	8.246	0.502	4.373	1	0	PSC52_ARATH	Delta-1-pyrroline-5-carboxylate synthase B (PSC5 B) [Includes: Glutamate 5-kinase (GK) (EC 2.7.2.11) (Gamma-glutamyl kinase); Gamma-glutamyl phosphate reductase (GPR) (EC 1.2.1.41) (Glutamate-5-semialdehyde dehydrogenase) (Glutamyl-gamma-semialdehyde dehydrogenase)]	PSC5B PSC52 At3g55610 F11I6_20	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Amino-acid biosynthesis; L-proline biosynthesis; L-glutamate 5-semialdehyde from L-glutamate: step 1/2.; PATHWAY: Amino-acid biosynthesis; L-proline biosynthesis; L-glutamate 5-semialdehyde from L-glutamate: step 2/2.	ATP-binding; Alternative splicing; Amino-acid biosynthesis; Complete proteome; Kinase; Multifunctional enzyme; NADP; Nucleotide-binding; Oxidoreductase; Proline biosynthesis; Reference proteome; Transferase
SRR3420117_TR19058_c0_g5_i2_len=973	NA	NA	NA	NA	NA	.	0.059	0.618	0.306	0.339	0.001	1.932	0.001	1.826	0.355	-0.399	.	.	.	.				
SRR3420117_TR23868_c0_g1_i1_len=903	NA	NA	NA	NA	NA	.	0.051	1.09	0.848	0.201	1	2.531	0.147	1.107	1	0.289	.	.	.	.				
SRR3420117_TR27899_c3_g4_i1_len=505	ACO2M_ARATH	Q:46-258;H:920-990	36.96%ID	E:3e-36	Aconitate hydratase 2, mitochondrial	PF14279.3*HNH_5*HNH endonuclease*147-198*E:2.3e-17 PF01844.20*HNH*HNH endonuclease*147-189*E:7e-13 PF13395.3*HNH_4*HNH endonuclease*153-190*E:3.1e-07	0.271	-0.333	1	0.002	0	1.366	0.08	0.703	0.005	-0.857	ACO2M_ARATH	Aconitate hydratase 2, mitochondrial (Aconitase 2) (EC 4.2.1.3) (Citrate hydro-lyase 2)	ACO2 At2g05710 T3P4.5	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Carbohydrate metabolism; tricarboxylic acid cycle; isocitrate from oxaloacetate: step 2/2.	4Fe-4S; Complete proteome; Glyoxylate bypass; Iron; Iron-sulfur; Lyase; Metal-binding; Mitochondrion; Reference proteome; Transit peptide; Tricarboxylic acid cycle
SRR3420117_TR30393_c0_g3_i1_len=1333	FLS_PETCR	Q:1230-559;H:44-271	36.8%ID	E:9e-40	Flavonol synthase/flavanone 3-hydroxylase	PF14226.3*DIOX_N*non-haem dioxygenase in morphine synthesis N-terminal*35-139*E:9.7e-23 PF03171.17*2OG-Fe(II_Oxy*2OG-Fe(II) oxygenase superfamily*188-255*E:1.3e-13	0	1.961	0.009	4.594	0	3.049	0.001	2.57	0.02	1.353	FLS_PETCR	Flavonol synthase/flavanone 3-hydroxylase (EC 1.14.11.23) (EC 1.14.11.9)	FLS	Petroselinum crispum (Parsley) (Petroselinum hortense)	PATHWAY: Secondary metabolite biosynthesis; flavonoid biosynthesis.	Dioxygenase; Flavonoid biosynthesis; Iron; Metal-binding; Oxidoreductase; Vitamin C
SRR3420117_TR31911_c1_g3_i4_len=1511	FKB62_ARATH	Q:337-1071;H:307-550	82.45%ID	E:2e-123	Peptidyl-prolyl cis-trans isomerase FKBP62	PF02254.25*FKBP_C*FKBP-type peptidyl-prolyl cis-trans isomerase*30-86*E:2.2e-15 PF14559.3*TPR_19*Tetratricopeptide repeat*176-236*E:3.5e-06 PF00515.25*TPR_1*Tetratricopeptide repeat*193-232*E:1.6e-08 PF07719.14*TPR_2*Tetratricopeptide repeat*200-232*E:1.7e-06 PF13181.3*TPR_8*Tetratricopeptide repeat*200-232*E:1.1e-06 PF00582.23*Usp*Universal stress protein family*8-153*E:4.6e-33	0.84	-0.357	0.793	-0.211	0	2.35	0.04	1.509	0.728	-0.122	FKB62_ARATH	Peptidyl-prolyl cis-trans isomerase FKBP62 (PPIase FKBP62) (EC 5.2.1.8) (70 kDa peptidyl-prolyl isomerase) (PKS06-binding protein 62) (AtFKBP62) (Immunophilin FKBP62) (Peptidyl-prolyl isomerase ROF1) (Protein ROTAMASE FKBP 1) (Rotamase)	FKBP62 ROF1 At3g25230 MJL12.19	Arabidopsis thaliana (Mouse-ear cress)		Acetylation; Alternative splicing; Calmodulin-binding; Chaperone; Complete proteome; Cytoplasm; Isomerase; Nucleus; Reference proteome; Repeat; Rotamase; TPR repeat
SRR3420119_TR508_c0_g1_i2_len=1062	NA	NA	NA	NA	NA	.	0.811	0.293	0.006	0.08	0	4.237	0.003	3.899	0.629	-0.949	.	.	.	.				
SRR3420119_TR14652_c1_g1_i3_len=1999	WTR41_ARATH	Q:1747-578;H:13-356	41.77%ID	E:1e-80	WAT1-related protein At5g40230	PF00892.17*EamA*EamA-like transporter family*17-156*E:1.1e-13	0.003	1.385	0.012	1.03	0	2.694	0.014	1.72	1	0.971	WTR41_ARATH	WAT1-related protein At5g40230	At5g40230 MSN9.130	Arabidopsis thaliana (Mouse-ear cress)				Complete proteome; Membrane; Reference proteome; Repeat; Transmembrane; Transmembrane helix
SRR3420119_TR17901_c0_g1_i1_len=903	NA	NA	NA	NA	NA	.	0.836	-0.127	0.586	0.238	0	1.54	0.027	1.054	1	0	.	.	.	.				
SRR3420119_TR18099_c0_g1_i1_len=842	NA	NA	NA	NA	NA	.	0.063	0.694	0.001	1.525	0.001	1.416	0.38	-0.468	0.005	1.034	.	.	.	.				
SRR3420119_TR18305_c3_g2_i2_len=2465	BGH3B_BACOV	Q:305-2065;H:35-658	31.32%ID	E:5e-83	Beta-glucosidase BoGH3B	PF00933.18*Glyco_hydro_3*Glycosyl hydrolase family 3 N terminal domain*51-379*E:3.7e-71 PF01915.19*Glyco_hydro_3_C*Glycosyl hydrolase family 3 C-terminal domain*416-620*E:1.7e-33	0.652	-0.13	0.663	0.149	0	2.294	0.043	1.242	0.098	-0.487	BGH3B_BACOV	Beta-glucosidase BoGH3B (EC 3.2.1.21) (Glycosyl hydrolase family protein 3B) (BoGH3B)	BACOVA_02659	Bacteroides ovatus (strain ATCC 8483 / DSM 1896 / JCM 5824 / NCTC 11153)	PATHWAY: Glucan metabolism; xyloglucan degradation. (ECO:0000269	PubMed:24463512).	Carbohydrate metabolism; Complete proteome; Glycosidase; Hydrolase; Periplasm; Polysaccharide degradation; Signal
SRR3420119_TR18596_c0_g1_i2_len=787	14KD_DAUCA	Q:313-561;H:54-136	71.08%ID	E:5e-32	14 kDa proline-rich protein DC2.15	PF03926.13*DUF642*Protein of unknown function (DUF642)*37-133*E:1.2e-37	0.093	-0.393	0.015	-0.546	0.001	1.232	0.003	1.112	1	0.034	14KD_DAUCA	14 kDa proline-rich protein DC2.15	Daucus carota (Wild carrot)				Membrane; Signal; Transmembrane; Transmembrane helix
SRR3420119_TR18824_c6_g1_i4_len=727	NLTP2_TOBAC	Q:131-481;H:1-114	55.93%ID	E:4e-26	Non-specific lipid-transfer protein 2	PF14368.3*LTP_2*Probable lipid transfer*15-105*E:1.6e-06 PF02034.19*Trypsin_alpha_amyl*Protease inhibitor/seed storage/LTP family*30-113*E:9.6e-08	0.054	0.485	0.606	0.139	0	0.916	0.078	0.415	0.157	0.303	NLTP2_TOBAC	Non-specific lipid-transfer protein 2 (LTP 2)		Nicotiana tabacum (Common tobacco)		Disulfide bond; Lipid-binding; Signal; Transport	
SRR3420119_TR25523_c1_g1_i3_len=2015	TCP13_ARATH	Q:376-640;H:61-214	82.02%ID	E:2e-39	Transcription factor TCP13	PF03634.10*TCP*TCP family transcription factor*60-180*E:1.8e-30	0.107	0.574	0.008	0.894	0	1.408	0.026	0.889	0.496	-0.255	TCP13_ARATH	Transcription factor TCP13 (Plastid transcription factor 1) (TFPD)	TCP13 PTF1 At3g02150 F14P3.20 F1C9.6	Arabidopsis thaliana (Mouse-ear cress)		Alternative splicing; Chloroplast; Complete proteome; DNA-binding; Developmental protein; Nucleus; Plastid; Reference proteome; Transcription; Transcription regulation
SRR3420119_TR27500_c1_g2_i3_len=1179	EF1A_TOBAC	Q:1113-817;H:238-436	97.99%ID	E:3e-135	Elongation factor 1-alpha	PF00009.22*GTP_EFTu_D2*Elongation factor Tu domain 2*7-50*E:2.2e-07 PF03144.14*GTP_EFTU_

SRR648705_TR18488_c0_g3_i1_len=1982	NA	NA	NA	NA	NA	PF04640.11*PLATZ*PLATZ transcription factor*48-119*E:5.7e-30	0,692	1,272	0,008	2,839	0	2,646	0,002	2,474	1	3,044	-	-	-	-	-	-	-	-	-	-	-
SRR648705_TR19299_c0_g3_i2_len=590	IF5A2_NICPL	0:242-415,H:102-159	89.66%ID	E:1e-30	Eukaryotic translation initiation factor 5A-2	PF01112.20*Peptidase_C1*Papain family cysteine protease*62-277*E:2.2e-78 PF00396.15*Granulin*Granulin*319-365*E:1.7e-10	0,424	-0,209	0,707	0,093	0	1,232	0,054	0,629	0,088	-0,45	IF5A2_NICPL	Eukaryotic translation initiation factor 5A-2 (eIF-5A-2) (eIF-4D)	EIF-5A2	Os04g0650000 LOC_Os04g55650 H0212B02.7 OSJNBb0059K02.8	Nicotiana plumbaginifolia (Leadworttreated tobacco) (Tex-Mex tobacco)	Hypusine; Initiation factor; Protein biosynthesis	Complete protein; Direct protein sequencing; Disulfide bond; Glycoprotein; Hydrolase; Protease; Reference proteome; Signal; Thiol protease; Zymogen
SRR648705_TR24298_c0_g2_i1_len=1980	ORYA_ORYSJ	Q:1735-449,H:32-448	46.06%ID	E:1e-114	Oryzain alpha chain	PF00112.20*Peptidase_C1*Papain family cysteine protease*62-277*E:2.2e-78 PF00396.15*Granulin*Granulin*319-365*E:1.7e-10	0,027	0,803	0,631	-0,204	0	1,764	0,053	0,904	0,319	0,918	ORYA_ORYSJ	Oryzain alpha chain (EC 3.4.22.-)	-	Os04g0650000 LOC_Os04g55650 H0212B02.7 OSJNBb0059K02.8	Oryza sativa subsp. japonica (Rice)	-	Complete protein; Direct protein sequencing; Disulfide bond; Glycoprotein; Hydrolase; Protease; Reference proteome; Signal; Thiol protease; Zymogen
SRR648705_TR27003_c0_g1_i1_len=1817	NA	NA	NA	NA	NA	PF05678.11*VQ*VQ motif*157-184*E:5.2e-11	0,299	1,661	0,003	3,952	0	2,89	0,017	2,16	1	-0,013	-	-	-	-	-	-	-	-	-	-	-
SRR648705_TR34506_c0_g2_i1_len=1548	RBG3_ARATH	Q:1350-991,H:1-120	68.33%ID	E:6e-50	Glycine-rich RNA-binding protein 3, mitochondrial	PF00076.19*RRM_1*RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)*42-112*E:2.2e-23 PF13893.3*RRM_5*RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)*58-116*E:0.031	0,013	-0,629	0,205	0,206	0	1,478	0,056	0,851	0,351	-0,312	-0,327	RBG3_ARATH	Glycine-rich RNA-binding protein 3, mitochondrial (AtGR-RBP3) (AtRBG3) (Mitochondrial RNA-binding protein 2a) (At-mRBP2a)	RBG3 GR-RBP3 MRBP2A Atlg61030 MAF19_30	Arabidopsis thaliana (Mouse-ear cress)	-	Complete protein; Mitochondrion; RNA-binding; Reference proteome; Transit peptide
SRR648705_TR35323_c0_g2_i1_len=514	NA	NA	NA	NA	NA	-	1	-3,66	0	-1,375	0	6,869	0,001	6,413	0	-2,501	-	-	-	-	-	-	-	-	-	-	-
SRR648705_TR36889_c0_g1_i1_len=1558	P2C21_ARATH	Q:211-1200,H:1-332	79.8%ID	E:0	Probable protein phosphatase 2C 21	PF00481.18*PP2C*Protein phosphatase 2C*23-102*E:1.2e-12 PF00481.18*PP2C*Protein phosphatase 2C*139-312*E:2.7e-61	0,917	0,102	0,918	-0,078	0	1,758	0,008	1,263	0,908	-0,099	P2C21_ARATH	Probable protein phosphatase 2C 21 (AtPP2C21) (EC 3.1.3.16) (AtPPC4;2)	PPC4;2 At2g25070 F13D4.1 F27C12	Arabidopsis thaliana (Mouse-ear cress)	-	Complete proteome; Hydrolase; Magnesium; Manganese; Metal-binding; Protein phosphatase; Reference proteome
SRR648705_TR44621_c0_g1_i1_len=915	CCB12_ORYSJ	Q:747-406,H:1-114	45.22%ID	E:2e-22	Cyclin-B1-2	PF05348.8*UMP1*Proteasome maturation factor UMP1*72-185*E:1.2e-29	1	-0,056	0,608	0,27	0	2,047	0,002	1,786	1	0,383	CCB12_ORYSJ	Cyclin-B1-2 (G2/mitotic-specific cyclin-B1-2) (CycB1;2)	CYCB1-2 Os02g0801300 LOC_Os02g55720	Oryza sativa subsp. japonica (Rice)	-	Cell cycle; Cell division; Complete proteome; Cyclin; Reference proteome
SRR648705_TR45105_c0_g1_i3_len=1616	FB330_ARATH	Q:260-1270,H:19-353	69.14%ID	E:3e-157	F-box protein At3g58530	PF13516.3*LRR_6*Leucine Rich repeat*18-136*E:0.0078 PF13516.3*LRR_6*Leucine Rich repeat*170-188*E:1.6*PF13516.3*LRR_6*Leucine Rich repeat*270-294*E:0.0087	0,62	-0,459	0,189	1,595	0	0,001	6,611	0,005	0,152	0,811	0,365	FB330_ARATH	F-box protein At3g58530	At3g58530 F14P22.120	Arabidopsis thaliana (Mouse-ear cress)	-	Complete proteome; Reference proteome
SRR648707_TR1542_c0_g1_i1_len=804	PIR7A_ORYSJ	Q:38-667,H:52-262	35.98%ID	E:2e-41	Probable esterase PIR7A	-	0,897	0,152	0,242	-0,936	0	2,157	0,001	1,933	0,518	-0,337	PIR7A_ORYSJ	Probable esterase PIR7A (EC 3.1.-.-)	PIR7A Os01g0934800 LOC_Os01g70860 P0423A12.27 P0492G09.8	Oryza sativa subsp. japonica (Rice)	-	Complete proteome; Hydrolase; Reference proteome; Serine esterase
SRR648707_TR10326_c0_g2_i2_len=2205	ORYA_ORYSJ	Q:177-1463,H:32-448	46.06%ID	E:4e-114	Oryzain alpha chain	PF00246.9*Inhibitor_I29*Cathepsin propeptide inhibitor domain (I29)*49-108*E:6.5e-12 PF00112.20*Peptidase_C1*Papain family cysteine protease*142-357*E:3.4e-78 PF00396.15*Granulin*Granulin*399-440*E:2.1e-10	0,396	0,242	0,278	0,357	0	1,232	0,026	0,7	0,007	0,707	ORYA_ORYSJ	Oryzain alpha chain (EC 3.4.22.-)	Os04g0650000 LOC_Os04g55650 H0212B02.7 OSJNBb0059K02.8	Oryza sativa subsp. japonica (Rice)	-	Complete proteome; Direct protein sequencing; Disulfide bond; Glycoprotein; Hydrolase; Protease; Reference proteome; Signal; Thiol protease; Zymogen
SRR648707_TR11505_c0_g2_i1_len=1892	SCP19_ARATH	Q:177-1577,H:3-465	52.67%ID	E:2e-164	Serine carboxypeptidase-like 19	PF00450.19*Peptidase_S10*Serine carboxypeptidase*35-468*E:6.9e-121	1	-0,01	1	0	0	2,747	0,006	2,175	1	0	SCP19_ARATH	Serine carboxypeptidase-like 19 (Protein SINAPOYLGLUCOSE ACCUMULATOR 2) (Sinapoylglucose-choline O-sinapoyltransferase) (SCT) (EC 2.3.1.91) [Cleaved into: Serine carboxypeptidase-like 19 chain A; Serine carboxypeptidase-like 19 chain B]	SCPL19 SCT SNG2 At5g09640 F1H14.170	Arabidopsis thaliana (Mouse-ear cress)	-	3D-structure; Acyltransferase; Complete proteome; Disulfide bond; Glycoprotein; Reference proteome; Secreted; Signal; Transferase
SRR648707_TR14283_c1_g2_i5_len=779	CGS1_ARATH	Q:97-345,H:48-563	84.34%ID	E:2e-40	Cystathionine gamma-synthase 1, chloroplastic (EC:0000305)	PF01053.19*Cys_Met_Met_PLP*Cystathionine gamma-synthase, conserved domain*1-157*E:1.5e-06 PF01053.19*Cys_Met_Met_PLP*Cystathionine gamma-synthase, conserved domain*158-479*E:1.2e-100	0,691	0,208	0	-1,307	0	6,697	1	0	0	-3,012	CGS1_ARATH	Cystathionine gamma-synthase 1, chloroplastic (AtCGS1) (EC 2.5.1.48) (METHIONINE OVERACCUMULATION 1) (O-succinylhomoserine (thiol)-lyase)	CGS1 CYS1 MTO1 At3g01120 T4P13.19	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Amino-acid biosynthesis; L-methionine biosynthesis via de novo pathway; L-cystathionine from O-succinyl-L-homoserine: step 1/1. [ECO:0000305].	Amino-acid biosynthesis; Chloroplast; Complete proteome; Direct protein sequencing; Methionine biosynthesis; Plastid; Polymorphism; Pyridoxal phosphate; Reference proteome; Transferase; Transit peptide
SRR648707_TR16194_c0_g1_i1_len=984	ISAM1_ARATH	Q:804-412,H:1-328	73.88%ID	E:5e-65	Iron-sulfur assembly protein IscA-like 1, mitochondrial	PF01521.17*Fe-S_biosyn*Iron-sulphur cluster biosynthesis*80-179*E:2.3e-19	0,842	-0,146	0,042	0,906	0,001	1,313	0,002	1,244	0,882	-0,144	ISAM1_ARATH	Iron-sulfur assembly protein IscA-like 1, mitochondrial	At2g16710 T24D21.12	Arabidopsis thaliana (Mouse-ear cress)	-	Alternative splicing; Complete proteome; Iron; Iron-sulfur; Metal-binding; Mitochondrion; Reference proteome; Transit peptide
SRR648707_TR17590_c0_g2_i9_len=1614	GSTZ_EUPES	Q:301-927,H:11-219	65.55%ID	E:8e-95	Glutathione S-transferase zeta class	PF02798.17*GST_N*Glutathione S-transferase, N-terminal domain*13-86*E:2.9e-17 PF13417.3*GST_N_3*Glutathione S-transferase, N-terminal domain*16-92*E:2.1e-18 PF13409.3*GST_N_2*Glutathione S-transferase, N-terminal domain*22-87*E:2.9e-17 PF14497.3*GST_C_3*Glutathione S-transferase, C-terminal domain*139-208*E:0.0001	0,547	0,318	0,242	0,549	0	1,703	0,008	1,333	0,937	-0,052	GSTZ_EUPES	Glutathione S-transferase zeta class (EC 2.5.1.18)	-	Euphorbia esula (Leafy spurge)	-	Cytoplasm; Transferase
SRR648707_TR19558_c0_g2_i9_len=2095	C72A1_CATRO	Q:1156-317,H:245-524	97.86%ID	E:0	Secologanin synthase	PF00067.19*p450*Cytochrome P450*93-235*E:1.4e-16	0,039	0,999	0,013	1,59	0	1,972	0,005	1,37	0,075	0,857	C72A1_CATRO	Secologanin synthase (SLS) (EC 1.3.3.9) (CYPLXXII) (Cytochrome P450 72A1)	CYP72A1 CYP72 P450CR3	Catharanthus roseus (Madagascar periwinkle) (Vinca rosea)	PATHWAY: Alkaloid biosynthesis; secologanin biosynthesis.	Alkaloid metabolism; Heme; Iron; Membrane; Metal-binding; Monooxygenase; NADP; Oxidoreductase; Transferase; Transmembrane helix; Vacuole
SRR648707_TR22887_c0_g3_i1_len=1374	DHAR2_ARATH	Q:1012-383,H:1-213	72.99%ID	E:2e-107	Glutathione S-transferase DHAR2	PF13417.3*GST_N_3*Glutathione S-transferase, N-terminal domain*21-89*E:5.3e-19 PF02798.17*GST_N*Glutathione S-transferase, N-terminal domain*21-78*E:1.5e-06 PF13409.3*GST_N_2*Glutathione S-transferase, N-terminal domain*22-84*E:1e-14 PF13410.3*GST_C_2*Glutathione S-transferase, C-terminal domain*121-184*E:6.2e-08	0,11	0,483	0,031	0,668	0	1,152	0,003	0,884	0,708	0,125	DHAR2_ARATH	Glutathione S-transferase DHAR2 (EC 2.5.1.18) (Chloride intracellular channel homolog 2) (CLIC homolog 2) (Glutathione-dependent dehydroascorbate reductase 2) (AtDHAR2) (CyDHAR) (GSH-dependent dehydroascorbate reductase 2)	DHAR2 DHAR Atlg75270 F22H5.1	Arabidopsis thaliana (Mouse-ear cress)	-	Complete proteome; Cytoplasm; Detoxification; Glutathionylation; Reference proteome; Stress response; Transferase
SRR648707_TR28023_c0_g8_i1_len=844	NA	NA	NA	NA	NA	-	0,538	-0,189	0,053	0,524	0	1,085	0,003	0,919	0,87	-0,059	-	-	-	-	-	-	-	-	-	-	-
SRR648707_TR28049_c0_g2_i1_len=2065	DAT_CATRO	Q:96-761,H:11-237	46.72%ID	E:1e-69	Deacetylvindoline O-acetyltransferase	PF02458.12*Transferase*Transferase family*6-192*E:2.7e-32	0,057	0,63	0,027	0,817	0	1,491	0,026	0,983	0,011	0,828	DAT_CATRO	Deacetylvindoline O-acetyltransferase (EC 2.3.1.107) (Acetyl-coenzyme A deacetylvindoline 4-O-acetyltransferase)	DAT	Catharanthus roseus (Madagascar periwinkle) (Vinca rosea)	PATHWAY: Alkaloid biosynthesis; vindoline biosynthesis; vindoline from tabersonine: step 6/6.	Acyltransferase; Coiled coil; Direct protein sequencing; Transferase
SRR648707_TR32373_c0_g1_i1_len=831	H2B_GOSHI	Q:507-199,H:45-147	96.12%ID	E:3e-58	Histone H2B	PF00125.21*Histone*Core histone H2A/H2B/H3/H4*9-124*E:7.3e-23 PF00808.20*CBFD_NFYB_HMF*Histone-like transcription factor (CBF/NF-Y) and archaeal histone*66-122*E:4.4e-05	0	-1,06	0,032	-0,574	0	1,197	0,018	0,751	0,317	-0,514	H2B_GOSHI	Histone H2B	HIS2B	Gossypium hirsutum (Upland cotton) (Gossypium mexicanum)	-	Acetylation; Chromosome; DNA-binding; Isopeptide bond; Nucleosome core; Nucleus; Ubl conjugation
SRR648707_TR33512_c0_g2_i1_len=1573	RD19A_ARATH	Q:1420-392,H:27-364	75.51%ID	E:0	Cysteine proteinase RD19a	PF08246.9*Inhibitor_I29*Cathepsin propeptide inhibitor domain (I29)*51-107*E:1.8e-10 PF00112.20*Peptidase_C1*Papain family cysteine protease*138-361*E:5.6e-75	0,152	0,42	0,539	0,219	0	1,091	0,099	0,553	0,173	0,659	RD19A_ARATH	Cysteine proteinase RD19a (RD19) (EC 3.4.22.-)	RD19A At4g39090 F19H22.190	Arabidopsis thaliana (Mouse-ear cress)	-	Complete proteome; Disulfide bond; Glycoprotein; Hydrolase; Protease; Reference proteome; Signal; Thiol protease; Zymogen
SRR648707_TR35315_c0_g1_i1_len=2024	BADH2_ARATH	Q:175-1583,H:1-503	78.33%ID	E:0	Betaine aldehyde dehydrogenase 2, mitochondrial	PF00171.19*Aldedh*Aldehyde dehydrogenase family*16-485*E:1.9e-172	0,55	-0,295	0,003	1,59	0	2,227	0,094	1,26	0,049	1,355	BADH2_ARATH	Betaine aldehyde dehydrogenase 2, mitochondrial (BADH) (EC 1.2.1.8) (Aldehyde dehydrogenase family 10 member A9)	ALDH10A9 At3g48170 T24C20.50	Arabidopsis thaliana (Mouse-ear cress)	-	Complete proteome; Mitochondrion; NAD; Oxidoreductase; Reference proteome; Transit peptide
SRR648707_TR38345_c0_g1_i1_len=768	NA	NA	NA	NA	NA	-	0,212	0,979	0,031	1,326	0	1,877	0,002	1,719	1	0,095	-	-	-	-	-	-	-	-	-	-	-
SRR924147_TR13760_c0_g1_i1_len=953	MTND1_VITVI	Q:836-276,H:1-188	81.38%ID	E:1e-110	1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase 1 (ECO:0000255)HAMAP-Rule:MF_03154)	PF03079.11*ARD*ARD/ARD' family*44-197*E:1.6e-58 PF02311.16*AraC_binding*AraC-like ligand binding domain*124-196*E:3.5e-07 PF07883.8*Cupin_2*Cupin domain*127-185*E:1.9e-10	0,206	0,706	0,784	-0,148	0	1,017	0,026	0,628	1	-0,296	MTND1_VITVI	1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase 1 (EC 1.13.11.54) (Acireductone dioxygenase (Fe(2+)-requiring) 1) (ARD 1) (Fe-ARD 1)	VIT_05s0020g04070	Vitis vinifera (Grape)	PATHWAY: Amino-acid biosynthesis; L-methionine biosynthesis via salvage pathway; L-methionine from 5-methylthio-D-ribose 1-phosphate: step 5/6. [ECO:0000255]HAMAP-Rule:MF_03154].	Amino-acid biosynthesis; Complete proteome; Cytoplasm; Dioxygenase; Iron; Metal-binding; Methionine biosynthesis; Nucleus; Oxidoreductase; Reference proteome
SRR924147_TR17644_c1_g1_i3_len=824	SAP8_ORYSJ	Q:751-257,H:1-171	61.4%ID	E:1e-67	Zinc finger A20 and AN1 domain-containing stress-associated protein 8	PF01754.13*zfA20*A20-like zinc finger*16-38*E:5.4e-13 PF01428.13*zfAN1*AN1-like Zinc finger*106-142*E:1.4e-08	0,017	-5,84	0,022	1,149	0	7,245	0,005	6,264	1	2,295	SAP8_ORYSJ	Zinc finger A20 and AN1 domain-containing stress-associated protein 8 (OsSAP8) (Stress-associated protein 3)	SAP8 SAP3 Os06g0612800 LOC_Os06g14010 Osj_021110 P0417D12.11 P0429G06.28	Oryza sativa subsp. japonica (Rice)	-	Complete proteome; Metal-binding; Reference proteome; Stress response; Zinc; Zinc-finger
SRR924147_TR27043_c0_g1_i1_len=771	NA	NA	NA	NA	NA	-	1	0	0,013	-1,701	0	7,767	0,001	6,427	1	1,925	-	-	-	-	-	-	-	-	-	-	-
SRR924147_TR27246_c0_g1_i1_len=1043	RRA3_ARATH	Q:752-255,H:1-166	76.51%ID	E:2e-89	Putative 4-hydroxy-4-methyl-2-oxoglutarate aldolase 3	PF03737.12*Methyltransf_6*Demethylmenaquinone methyltransferase*6-159*E:2.1e-43	1	0,008	0,532	-0,191	0	1,195	0,004	0,938	0,429	-0,232	RRA3_ARATH	Putative 4-hydroxy-4-methyl-2-oxoglutarate aldolase 3 (HMG aldolase 3) (EC 4.1.3.17) (Oxaloacetate decarboxylase) (OAA decarboxylase) (EC 4.1.1.3) (Regulator of ribonuclease activity homolog 3) (RraA-like protein 3)	At5g56260 K24C1.7	Arabidopsis thaliana (Mouse-ear cress)	-	Acetylation; Complete proteome; Lyase; Metal-binding; Reference proteome
SRR924147_TR30185_c0_g1_i1_len=1522	TET3_ARATH	Q:1147-293,H:1-285	72.63%ID	E:7e-141	Tetraspanin-3	PF00335.17*Tetraspanin*Tetraspanin family*5-255*E:5.8e-92	0,073	0,702	0,002	1,302	0	1,574	0,019	0,933	0,438	0,343	TET3_ARATH	Tetraspanin-3	TET3 At3g45600 F9K21.18	Arabidopsis thaliana (Mouse-ear cress)	-	Complete proteome; Glycoprotein; Membrane; Reference proteome; Transmembrane; Transmembrane helix
SRR924147_TR36395_c0_g2_i1_len=1343	NUDT2_ARATH	Q:1050-285,H:19-272	57.42%ID	E:2e-104	Nudix hydrolase 2	PF00293.25*NUDIX*NUDIX domain*109-228*E:3.2e-23	0,783	0,242	0,319	0,825	0	1,782	0,001	6,481	0,77	-0,188	NUDT2_ARATH	Nudix hydrolase 2 (ANUDT2) (EC 3.6.1.-) (ADP-ribose pyrophosphatase) (EC 3.6.1.13) (NADH pyrophosphatase) (EC 3.6.1.22)	NUDT2 NUDX2 At5g47650 MNJ7.24	Arabidopsis thaliana (Mouse-ear cress)	-	Complete proteome; Hydrolase; Magnesium; Manganese; Metal-binding; NAD; Reference proteome
SRR924147_TR37526_c0_g2_i1_len=2103	CYSP_PEA	Q:1924-761,H:24-362	67.1%ID	E:0	Cysteine proteinase 15A	PF08246.9*Inhibitor_I29*Cathepsin propeptide inhibitor domain (I29)*84-140*E:2.5e-09 PF00112.20*Peptidase_C1*Papain family cysteine protease*171-312*E:6.7e-46	0,217	0,321	0,009	0,682	0	1,843	0,011	1,316	1	0,181	CYSP_PEA	Cysteine proteinase 15A (EC 3.4.22.-) (Turgor-responsive protein 15A)	-	Pisum sativum (Garden pea)	-	Disulfide bond; Glycoprotein; Hydrolase; Protease; Signal; Stress response; Thiol protease; Zymogen
SRR924147_TR490_c0_g2_i1_len=656	NA	NA	NA	NA	NA	-	0,011	0,596	0,835	0,051	0,001	0,801	0,001	0,756	0,57	0,345	-	-	-	-	-	-	-	-	-	-	-
SRR924147_TR972_c0_g1_i1_len=717	NA	NA	NA	NA	NA	-	0,312	-0,334	0,612	0,144	0	1,136	0,041	0,602	0,143	-0,375	-	-	-	-	-	-	-	-	-	-	-
SRR924148_TR9339_c0_g1_i5_len=1298	RAN3_ARATH	Q:1115-453,H:1-221	98.64%ID	E:3e-143	GTP-binding nuclear protein Ran-3	PF00025.18*Arf*ADP-ribosylation factor family*13-139*E:3.1e-11 PF00071.19*Ras*Ras family*15-171*E:4.5e-50 PF08477.10*Roc*Ras of Complex, Roc, domain of DAPkinase*15-128*E:1.7e-29 PF00910.19*RNA_helicase*RNA helicase*117-139*E:3.4e-05	0,251	-0,289	0,001	0,8	0	1,002	0,006	0,723	0,937	-0,034	RAN3_ARATH	GTP-binding nuclear protein Ran-3 (Ras-related nuclear protein 3)	RAN3 At5g55190 MCO15.14	Arabidopsis thaliana (Mouse-ear cress)	-	Complete proteome; GTP-binding; Nucleotide-binding; Nucleus; Protein transport; Reference proteome; Transport
SRR924148_TR14151_c0_g1_i2_len=957	HSP12_MEDSA	Q:736-263,H:1-158	86.71%ID	E:4e-75	18.2 kDa class I heat shock protein	PF04969.13*CS*CS domain*52-143*E:0.011 PF00011.18*HSP20*Hsp20/alpha crystallin family*54-157*E:9.3e-33	1	0,297	0,118	1,802	0	1,001	2,939	0,066	1,982	1	0,366	HSP12_MEDSA	18.2 kDa class I heat shock protein	HSP18.2	Medicago sativa (Alfalfa)	-	Cytoplasm; Stress response
SRR924148_TR14205_c0_g2_i3_len=1070	SMD2_DROME	Q:851-582,H:23-112	87.78%ID	E:3e-41	Probable small nuclear ribonucleoprotein Sm D2	PF01423.19*LSM*LSM domain*84-159*E:4.1e-19	0,025	-0,612	0,775	-0,089	0	1,726	0,006	1,318	0,022	-0,614	SMD2_DROME	Probable small nuclear ribonucleoprotein Sm D2 (Sm-D2) (snRNP core protein D2)	SmD2 snRNP2 CG1249	Drosophila melanogaster (Fruit fly)	-	Complete proteome; Nucleus; Reference proteome; Ribonucleoprotein; mRNA processing; mRNA splicing
SRR924148_TR15158_c0_g1_i2_len=530	NA	NA	NA	NA	NA	PF01323.17*DSBA*DSBA-like thioredoxin domain*16-69*E:4.5e-12	1	-0,003	0,034	3,252	0	6,915	0,017	5,731	1	-2,251	-	-	-	-	-	-	-	-	-	-	-
SRR924148_TR16062_c2_g1_i5_len=660	NA	NA	NA	NA	NA	-	0,502	-4,265	1	0	0	3,907	1	-3,208	0,034	5,633	-	-	-	-	-	-	-	-	-	-	-
SRR924148_TR28419_c0_g3_i2_len=1336	PIP1_SOLLC	Q:203-1048,H:1-282	86.52%ID	E:3e-179	Probable aquaporin PIP-type pTOM75	PF00230.17*MIP*Major intrinsic protein*45-274*E:3.2e-84	0,907	-0,045	0	-1,305	0	1,49	0,001	0,818	0,444	0,317	PIP1_SOLLC	Probable aquaporin PIP-type pTOM75 (Ripening-associated membrane protein) (RAMP)	-	Solanum lycopersicum (Tomato) (Lycopersicon esculentum)	-	Cell membrane; Complete proteome; Membrane; Reference proteome; Repeat; Stress response; Transmembrane; Transmembrane helix; Transport
SRR924148_TR28419_c0_g3_i3_len=1425	PIP1_SOLLC	Q:203-1051,H:1-283	86.93%ID	E:7e-180	Probable aquaporin PIP-type pTOM75	PF00230.17*MIP*Major intrinsic protein*45-274*E:3.7e-84	0,270	-0,484	0,274	0,479	0	1,373	0,054	0,706	0,792	-0,064	PIP1_SOLLC	Probable aquaporin PIP-type pTOM75 (Ripening-associated membrane protein) (RAMP)	-	Solanum lycopersicum (Tomato) (Lycopersicon esculentum)	-	Cell membrane; Complete proteome; Membrane; Reference proteome; Repeat; Stress response; Transmembrane; Transmembrane helix; Transport
SRR924148_TR29013_c0_g1_i1_len=855	MIRA_SYNDU	Q:221-754,H:34-217	54.84%ID	E:1e-56	Miraculin	PF00197.15*Kunitz_legume*Trypsin and trypsin inhibitor*31-205*E:4.7e-61	1	-0,04	0,226	0,78	0	4,265	0,073	1,735	0,377	-0,628	MIRA_SYNDU	Miraculin (MIR)	-	Synsepalum dulcificum (Miracle fruit) (Richadella dulcifica)	-	Direct protein sequencing; Disulfide bond; Glycoprotein; Signal; Taste-modifying protein
SRR924148_TR31476_c1_g4_i1_len=1224	RL211_ARATH	Q:270-761,H:1-164	84.76%ID	E:9e-98	60S ribosomal protein L21-1	PF01157.15*Ribosomal_L21e*Ribosomal protein L21e*5-98*E:4.7e-44	0,017	-0,643	0,609	-0,145	0,001	1,074	0,083	0,591	0,248	-0,268	RL211_ARATH	60S ribosomal protein L21-1	RPL21A At1g09590 F14J9.25; RPL21C At1g09690 F21M12.8	Arabidopsis thaliana (Mouse-ear cress)	-	Complete proteome; Reference proteome; Ribonucleoprotein; Ribosomal protein
SRR924148_TR34514_c0_g2_i1_len=1927	CTA29_PANGI	Q:157-39,H:10-515	60.55%ID	E:0	Cytochrome P450 CYP72A219	PF00067.19*p450*Cytochrome P450*100-515*E:3e-89	1	1,864	0,254	4,657	0	6,759	0,066	5,319	1	0,942	CTA29_PANGI	Cytochrome P450 CYP72A219 (EC 1.14.--.-) (Cytochrome P450 CYP72A129)	-	Panax ginseng (Korean ginseng)	-	Heme; Iron; Membrane; Metal-binding; Monooxygenase; Oxidoreductase; Transmembrane; Transmembrane helix
SRR924148_TR35468_c0_g2_i1_len=1310	CFI51_ARATH	Q:279-905,H:13-221	65.55%ID	E:2e-82	Pre-mRNA cleavage factor Im 25 kDa subunit 1 (ECO:0000303)PubMed:18479511)	PF13869.3*NUDIX_2*Nucleotide hydrolase*33-219*E:1.2e-75	1	0,858	0,073	1,995	0	1,314	0,069	0,73	0,258	0,994	CFI51_ARATH	Pre-mRNA cleavage factor Im 25 kDa subunit 1 (Cleavage and polyadenylation specificity factor 25 kDa subunit) (ACF-25) (CFIm-25) (CPSF 25 kDa subunit) (Cleavage and polyadenylation specificity factor subunit 25)	CFI51 CFIM25 At4g29820 F27B13.60	Arabidopsis thaliana (Mouse-ear cress)	-	Complete proteome; Metal-binding; Nucleus; RNA-binding; Reference proteome; mRNA processing
SRR924148_TR35599_c0_g1_i1_len=1604	FTSZ1_ARATH	Q:1353-295,H:36-397	87.29%ID	E:5e-171	Cell division protein FtsZ homolog 1, chloroplastic	PF00091.22*Tubulin*Tubulin/FtsZ family, GTPase domain*64-224*E:2.4e-42 PF12327.5*FtsZ_C*FtsZ family, C-terminal domain*273-365*E:8.8e-30	0	-7,253	0	-6,68	0	6,834	1	0	0,37	0,432	FTSZ1_ARATH	Cell division protein FtsZ homolog 1, chloroplastic (AtFtsZ1) (AtFtsZ-1) (Chloroplast FtsZ) (CpFtsZ) (Protein ACCUMULATION AND REPLICATION OF CHLOROPLASTS 10) (Protein PLASTID MOVEMENT IMPAIRED4)	FTSZ1 ARC10 FTSZ-1 PMI4 At5g55280 MCO15.23	Arabidopsis thaliana (Mouse-ear cress)	-	Acetylation; Cell cycle; Chloroplast; Complete proteome; GTP-binding; Membrane; Nucleotide-binding; Plastid; Reference proteome; Thylakoid; Transit peptide

MsDamaged24h_MsIntact24h

Transcript (CDF97)	Uniprot homolog	BLASTX Position	BLASTX %identity	BLASTX evalue	Uniprot descr	Pfam	PValue_Ms6h	logFC_Ms6h	PValue_Ms8h	logFC_Ms8h	PValue_MsDamaged24h	logFC_MsDamaged24h	PValue_MsIntact24h	logFC_MsIntact24h	PValue_Ms1wk	logFC_Ms1wk	Entry name	Protein names	Gene names	Organism	Pathway	Keywords
SRR1144633_TR4067_c0_g3_i1_len=2840	BGAL_SOLLC	Q:28-2487,H:16-835	84.27%ID	E:0	Beta-galactosidase	PF01301.16*Glyco_hydro_35*Glycosyl hydrolases family 35*24-329*E:6e-118 PF02449.12*Glyco_hydro_42*Beta-galactosidase*45-193*E:6e-10 PF00240.15*Gal_Lectin*Galactose binding lectin domain*752-828*E:1.3e-20	0,277	0,517	0,214	0,769	0	1,698	0,001	1,541	0,16	-1,171	BGAL_SOLLC	Beta-galactosidase (EC 3.2.1.23) (Acid beta-galactosidase) (Lactase) (Exo-(1->4)-beta-D-galactanase)	-	Solanum lycopersicum (Tomato) (Lycopersicon esculentum)	-	Complete proteome; Direct protein sequencing; Glycosidase; Hydrolase; Reference proteome; Signal
SRR1144633_TR7251_c0_g1_i1_len=1269	CBSX3_ARATH	Q:221-994,H:1-206	64.48%ID	E:4e-109	CBS domain-containing protein CBSX3, mitochondrial	PF00571.25*CBS*CBS domain*34-67*E:0.00063 PF00571.25*CBS*CBS domain*79-134*E:1.9e-14	0,91	0,041	0,001	-1,009	0	1,34	0	1,347	1	0,86	CBSX3_ARATH	CBS domain-containing protein CBSX3, mitochondrial	CBSX3 At5g10860 T30N20.130	Arabidopsis thaliana (Mouse-ear cress)	-	CBS domain; Complete proteome; Direct protein sequencing; Mitochondrion; Reference proteome; Repeat; Transit peptide
SRR1144633_TR9803_c1_g4_i3_len=1550	MED6_ARATH	Q:526-1203,H:32-298	59.7%ID	E:8e-88	Mediator of RNA polymerase II transcription subunit 6	PF04934.11*Med6*MED6 mediator sub complex component*36-161*E:5.2e-42	0,326	0,559	0,37	-0,316	0	2,735	0	2,836	0,854	0,147	MED6_ARATH	Mediator of RNA polymerase II transcription subunit 6	MED6 MED6_1 At3g21350 MHC9	Arabidopsis thaliana (Mouse-ear cress)	-	Alternative splicing; Complete proteome; Nucleus; Reference proteome; Transcription; Transcription regulation
SRR1144633_TR20268_c0_g1_i2_len=981	RF56_ARATH	Q:178-942,H:1-263	73%ID	E:1e-133	Probable galactinol--sucrose galactosyltransferase 6	PF05691.9*Raffinose_syn*Raffinose synthase or seed imbibition protein Sip1*7-264*E:2.6e-107	0,002	2,404	0,002	3,187	0	1,602	0	1,723	0,16	0,481	RF56_ARATH	Probable galactinol--sucrose galactosyltransferase 6 (EC 2.4.1.82) (Protein DARK INDUCIBLE 10) (Raffinose synthase 6)	RF56 D

SRR1271857_TR20249_c0_g1_i1_len=812	NA	NA	NA	NA	NA	NA	.	0,895	-0,101	0,008	-1,238	0	1,386	0	1,288	1	0,858	.	.	.	.	.	.	.	.	.	.
SRR1271857_TR26300_c2_g2_i2_len=688	NA	NA	NA	NA	NA	NA	P14878.3*DLD*Death-like domain of SPT6*3-6?E:7.2e-13?P14633.3*SH2_2*SH2 domain*161-208*E:1.4e-07	1	0,007	0,109	1,038	0	6,678	0	6,86	0,517	0,879	.	.	.	.	.	.	.	.	.	.	.
SRR1271857_TR31278_c0_g1_i3_len=1262	RAG3F_ARATH	Q:270-887;H:1-206	92.72%ID	E:4e-139	Ras-related protein RABG3f	PF00025.18*ARF*ADP-ribosylation factor family*9-175*E:3.5e-14?PF00071.19*Ras*Ras family*10-178*E:4.8e-56?PF06477.10*Roc*Ras of Complex, Roc, domain of DAPkinase*110-128*E:4.7e-33?PF01926.20*MMR_HSR1*50S ribosome-binding GTPase*10-109*E:2.1e-07?PF04670.9*Gtr1_RagA*Gtr1/RagA G protein conserved region*10-130*E:4.9e-06	0,325	0,266	0,284	0,314	0	1,251	0	1,22	0,874	0,056	RAG3F_ARATH	Ras-related protein RABG3f (AtRABG3f) (Ras-related protein Rab7t) (AtRab71) (Ras-related protein Rab7B) (AtRab7B)	RABG3F RAB71 RAB7B At3g18820 MVE11.21	Arabidopsis thaliana (Mouse-ear cress)	.	.	.	.	.	.	Cell membrane; Complete proteome; GTP-binding; Lipoprotein; Membrane; Methylation; Nucleotide-binding; Prenylation; Protein transport; Reference proteome; Transport
SRR1271857_TR33931_c0_g1_i11_len=2240	NA	NA	NA	NA	NA	NA	PF00892.17*EamA*EamA-like transporter family*55-109*E:3.8e-09	0,059	1,618	0,187	0,996	0	2,82	0	2,55	0,593	0,731	.	.	.	.	.	.	.	.	.	.
SRR1271857_TR33931_c0_g1_i13_len=1989	NA	NA	NA	NA	NA	NA	PF00892.17*EamA*EamA-like transporter family*4-120*E:3.5e-08?PF00892.17*EamA*EamA-like transporter family*130-279*E:1.1e-13	0,065	1,281	0,027	1,354	0	3,086	0	3,219	0,882	-0,188	.	.	.	.	.	.	.	.	.	.	.
SRR1271857_TR33994_c0_g1_i1_len=1179	OP24B_ARATH	Q:1002-367;H:3-213	67.92%ID	E:1e-100	Outer envelope pore protein 24B, chloroplastic	.	.	0,18	0,792	0,001	1,417	0	3,067	0	3,394	1	0,318	OP24B_ARATH	Outer envelope pore protein 24B, chloroplastic (Chloroplastic outer envelope pore protein of 24 kDa B)	OEP24B At5g42960 MBD2.16	Arabidopsis thaliana (Mouse-ear cress)	.	.	.	.	.	Chloroplast; Complete proteome; Ion transport; Membrane; Plastid; Plastid outer membrane; Porin; Reference proteome; Transmembrane; Transmembrane beta strand; Transport
SRR1271857_TR41363_c0_g1_i1_len=750	NA	NA	NA	NA	NA	NA	.	0,629	1,304	0,739	0,306	0	2,875	0	3,101	0,004	2,371	.	.	.	.	.	.	.	.	.	.
SRR1271857_TR41398_c0_g1_i1_len=942	NA	NA	NA	NA	NA	NA	PF06521.8*PAR1*PAR1 protein*35-185*E:1.7e-73	0,044	2,472	0,226	2,577	0	8,523	0	6,949	1	-0,303	.	.	.	.	.	.	.	.	.	.
SRR1271858_TR3359_c0_g1_i1_len=775	ELOF1_ORYSJ	Q:648-385;H:1-89	92.13%ID	E:1e-41	Transcription elongation factor 1 homolog	.	.	0,009	0,928	0,035	0,598	0	2,462	0	2,979	0,808	-0,074	ELOF1_ORYSJ	Transcription elongation factor 1 homolog	Os07g0631100 LOC_Os07g43730 Os J_25233 P0519E12.3	Oryza sativa subsp. japonica (Rice)	.	.	.	.	.	Complete proteome; Metal-binding; Nucleus; Reference proteome; Transcription; Transcription regulation; Zinc; Zinc-finger
SRR1271858_TR6554_c0_g1_i2_len=1263	NA	NA	NA	NA	NA	NA	PF00561.17*Abhydrolase_1*alpha/beta hydrolase fold*53-156*E:1.6e-15?PF12697.4*Abhydrolase_6*Alpha/beta hydrolase family*54-170*E:2.2e-09	1	2,944	0,017	5,141	0	8,022	0	8,427	1	0	.	.	.	.	.	.	.	.	.	.	.
SRR1271858_TR11582_c0_g2_i1_len=1292	NA	NA	NA	NA	NA	NA	PF14009.3*DUF4228*Domain of unknown function (DUF4228)?1-240*E:3e-26	1	2,231	0,034	4,872	0	4,794	0	5,568	0,822	-0,273	.	.	.	.	.	.	.	.	.	.
SRR1271858_TR19955_c1_g2_i2_len=1765	ENL2_ARATH	Q:422-730;H:30-132	59.22%ID	E:2e-35	Early nodulin-like protein 2	PF02298.14*Cu_bind_like*Plastocyanin-like domain*44-127*E:1.8e-21	0,288	0,501	0,021	0,983	0	1,961	0	1,984	0,908	-0,083	ENL2_ARATH	Early nodulin-like protein 2 (Phytocyanin-like protein)	AtEp2T520 T29A15.10	Arabidopsis thaliana (Mouse-ear cress)	.	.	.	.	.	Cell membrane; Complete proteome; GPI-anchor; Glycoprotein; Lipoprotein; Membrane; Reference proteome; Signal
SRR1271858_TR26202_c0_g1_i1_len=377	NA	NA	NA	NA	NA	NA	PF12146.5*Hydrolase_4*Serine aminopeptidase, S33*34-148*E:7.2e-34?PF00561.17*Abhydrolase_1*alpha/beta hydrolase fold*35-144*E:5.5e-09?PF12697.4*Abhydrolase_6*Alpha/beta hydrolase family*38-144*E:1.9e-07	0,35	0,582	0,611	-0,457	0	3,216	0	2,622	0,011	-1,253	.	.	.	.	.	.	.	.	.	.	.
SRR1271858_TR28353_c0_g3_i2_len=1308	NA	NA	NA	NA	NA	NA	PF00364.17*Biotin_lipoyl*Biotin/lipoyl attachment*139-188*E:1.3e-14	0,502	2,827	0,034	4,777	0,001	5,957	0	6,218	1	1,135	.	.	.	.	.	.	.	.	.	.	.
SRR1271858_TR28609_c0_g4_i1_len=3258	IDN2_ARATH	Q:459-1886;H:21-501	51.56%ID	E:9e-148	Protein INVOLVED IN DE NOVO 2 (ECO:0000303)PubMed:19915591	PF03470.11*zfXS*XS zinc finger domain*48-91*E:6.4e-19?PF03468.11*XS*XS domain*120-231*E:3e-39	1	0,079	0,103	1,771	0	3,598	0	3,708	1	0,046	IDN2_ARATH	Protein INVOLVED IN DE NOVO 2 (Protein RNA-DIRECTED DNA METHYLATION 12)	IDN2 RDM12 At3g48670 T8P19.180	Arabidopsis thaliana (Mouse-ear cress)	.	.	.	.	.	3D-structure; Coiled coil; Complete proteome; RNA-binding; RNA-mediated gene silencing; Reference proteome
SRR1271858_TR28987_c0_g1_i4_len=1753	NA	NA	NA	NA	NA	NA	PF04117.9*Mpv17_PMP22*Mpv17/PMP22 family*250-311*E:1.7e-17	1	0,444	0,043	3,445	0	5,539	0	6,165	1	0,246	.	.	.	.	.	.	.	.	.	.
SRR1271858_TR31243_c0_g1_i6_len=2333	DOX1_ARATH	Q:88-1275;H:1-368	68.51%ID	E:0	Alpha-dioxygenase 1	PF03098.12*An_peroxidase*Animal haem peroxidase*2-221*E:1.8e-41	1	-0,086	0,001	5,21	0	9,913	0,008	3,99	DOX1_ARATH	Alpha-dioxygenase 1 (Alpha DOX1) (EC 1.14.99.-) (Fatty acid dioxygenase AlphaDOX1) (Pathogen-induced oxygenase) (Plant alpha dioxygenase 1)	DOX1 DIOX1 PADOX-1 PIOX At3g01420 T13O15.6	Arabidopsis thaliana (Mouse-ear cress)	.	.	.	.	.	3D-structure; Complete proteome; Dioxygenase; Fatty acid biosynthesis; Fatty acid metabolism; Glycoprotein; Hypersensitive response; Iron; Lipid biosynthesis; Lipid metabolism; Metal-binding; Oxidoreductase; Oxylipin biosynthesis; Peroxidase; Plant defense; Reference proteome; Signal
SRR1271858_TR37116_c0_g1_i3_len=2160	NA	NA	NA	NA	NA	NA	PF00106.22*adh_short*short chain dehydrogenase*17-197*E:1.4e-37?PF08659.7*KR*KR domain*18-195*E:5.7e-07?PF13561.3*adh_short_C2*Enoyl-(Acyl carrier protein) reductase*23-197*E:7.3e-24	1	0,558	0,034	3,772	0	6,997	0	7,202	1	-0,977	.	.	.	.	.	.	.	.	.	.	.
SRR1271858_TR37746_c0_g3_i1_len=783	KIRO_ACTDE	Q:174-608;H:1-145	48.97%ID	E:2e-35	Kirola (ECO:0000303)PubMed:21309790)	PF00407.16*Bet_v_1*Pathogenesis-related protein Bet v I family*4-147*E:1.5e-32	0,015	0,647	0,816	-0,069	0	1,393	0	1,202	0,162	0,457	KIRO_ACTDE	Kirola (allergen Act d 11)	.	Actinidia deliciosa (Kiwi)	.	.	.	.	.	.	.
SRR1271858_TR42752_c1_g1_i1_len=1899	CYSP_PEA	Q:127-1179;H:15-362	74.15%ID	E:0	Cysteine proteinase 15A	PF08246.9*Inhibitor_I29*Cathepsin propeptide inhibitor domain (I29)?6-132*E:3.3e-09?PF00112.20*Peptidase_C1*Papain family cysteine protease?163-386*E:3.7e-74	0,002	0,709	0,045	0,442	0	1,915	0	1,335	0,115	0,346	CYSP_PEA	Cysteine proteinase 15A (EC 3.4.22.-) (Turgor-responsive protein 15A)	.	Pisum sativum (Garden pea)	.	.	.	.	.	.	.
SRR1271858_TR43413_c0_g1_i1_len=1182	NA	NA	NA	NA	NA	NA	PF00847.17*AP2*AP2 domain*139-188*E:1.3e-14	1	0,454	0,254	4,481	0	3,981	0	4,145	0,129	-2,887	.	.	.	.	.	.	.	.	.	.
SRR1271858_TR46311_c2_g2_i1_len=2190	CB18E8_MEDTR	Q:245-1659;H:6-493	57.14%ID	E:0	Cytochrome P450 81E8 (ECO:0000303)PubMed:14617078)	PF00067.19*p450*Cytochrome P450*34-477*E:2.3e-90	0,534	0,403	0,001	1,88	0	2,407	0	2,845	0,629	1,184	CB18E8_MEDTR	Cytochrome P450 81E8 (EC 1.14.13.-)	CYP81E8	Medicago truncatula (Barrel medic) (Medicago tribuloides)	.	.	.	.	.	Heme; Iron; Membrane; Metal-binding; Monooxygenase; NADP; Oxidoreductase; Transmembrane; Transmembrane helix	
SRR1271858_TR46468_c0_g1_i1_len=344	NA	NA	NA	NA	NA	NA	.	0,431	-0,443	0	1,012	0	1,804	0,001	1,43	1	0,118	.	.	.	.	.	.	.	.	.	.
SRR1271858_TR53596_c0_g1_i2_len=1448	PEX13_ARATH	Q:664-2028;H:179-304	67.46%ID	E:2e-49	Peroxisomal membrane protein 13	.	1	0,031	0,005	1,08	0	1,562	0	1,714	0,511	-0,222	PEX13_ARATH	Peroxisomal membrane protein 13 (Peroxin-13) (AtPEX13) (Peroxisome biogenesis protein 13) (Pex13p) (Protein ABERRANT PEROXISOME MORPHOLOGY 2)	PEX13 APM2 At3g07560 F21O3.27	Arabidopsis thaliana (Mouse-ear cress)	.	.	.	.	.	Alternative splicing; Complete proteome; Membrane; Peroxisome; Peroxisome biogenesis; Protein transport; Reference proteome; Translocation; Transport	
SRR1271858_TR54104_c0_g4_i1_len=1244	EXLB1_ARATH	Q:156-890;H:1-247	54.66%ID	E:9e-92	Expansin-like B1	PF03330.15*DPBB_1*Lytic transglycolase*114-188*E:4.8e-12?PF01357.18*Pollen_allerg_1*Pollen allergen*202-283*E:2.3e-14	0,008	0,897	0,038	1,89	0	3,186	0	3,255	0,005	1,138	EXLB1_ARATH	Expansin-like B1 (AtEXPR1) (AtEXLB1) (AtEXPR1) (Ath-ExpBeta-3.1)	EXLB1 EXPR1 At4g17030 d14S45c	Arabidopsis thaliana (Mouse-ear cress)	.	.	.	.	.	Complete proteome; Glycoprotein; Reference proteome; Secreted; Signal	
SRR1271858_TR54435_c0_g1_i1_len=2840	SERC_ARATH	Q:263-2192;H:1-155	61.29%ID	E:1e-51	Phosphoserine phosphatase, chloroplastic	.	0,059	1,189	0,003	1,917	0	2,133	0	2,249	0,381	-2,009	SERC_ARATH	Phosphoserine phosphatase, chloroplastic (PSP) (PSPase) (EC 3.1.3.3) (O-phosphoserine phosphohydrolase)	PSP PSP1 At1g18640 F26I16.2	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Amino-acid biosynthesis; L-serine biosynthesis; L-serine from 3-phospho-D-glycerate: step 3/3.					Amino-acid biosynthesis; Chloroplast; Complete proteome; Hydrolase; Magnesium; Metal-binding; Phosphoprotein; Plastid; Reference proteome; Serine biosynthesis; Transit peptide	
SRR1271858_TR56671_c1_g1_i1_len=1490	GATLA_ARATH	Q:212-1168;H:37-352	67.08%ID	E:4e-146	Probable galacturonosyltransferase-like 10	PF01501.17*Glyco_transf_8*Glycosyl transferase family 8*70-330*E:6.3e-52	1	0,447	0,005	5,056	0	4,519	0	5,363	0,044	2,373	GATLA_ARATH	Probable galacturonosyltransferase-like 10 (EC 2.4.1.-) (Galactinol synthase 8) (AtGolS8) (GolS-8)	GATL10 GOLS8 At3g28340 MZF16.17	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Glycan metabolism; pectin biosynthesis.					Cell wall biogenesis/degradation; Complete proteome; Glycoprotein; Glycosyltransferase; Golgi apparatus; Membrane; Reference proteome; Signal-anchor; Transferase; Transmembrane helix	
SRR1271858_TR68167_c0_g1_i1_len=806	NA	NA	NA	NA	NA	NA	.	0,004	1,956	0,01	2,567	0	3,876	0	3,628	1	0,515	.	.	.	.	.	.	.	.	.	.
SRR1271858_TR68715_c1_g1_i2_len=2103	CKX5_ARATH	Q:178-219;H:10-521	71.81%ID	E:0	Cytokinin dehydrogenase 5	PF01565.20*FAD_binding_4*FAD binding domain*60-208*E:1.5e-15?PF09265.7*Cytokin-bind*Cytokinin dehydrogenase 1, FAD and cytokinin binding?240-522*E:3e-121	1	-0,111	0,066	3,842	0	2,668	0	3,445	1	0,205	CKX5_ARATH	Cytokinin dehydrogenase 5 (EC 1.5.99.12) (Cytokinin oxidase 5) (AtCKX5) (AtCKX6) (CKO5)	CKX5 CKX6 At1g75450 F18I16.2	Arabidopsis thaliana (Mouse-ear cress)	.	.	.	.	.	Alternative splicing; Complete proteome; FAD; Flavoprotein; Glycoprotein; Oxidoreductase; Reference proteome; Secreted; Signal	
SRR1271858_TR69362_c0_g4_i1_len=717	BGL14_ORYSJ	Q:13-538;H:376-513	52.14%ID	E:3e-40	Probable inactive beta-glucosidase 14	PF00232.15*Glyco_hydro_1*Glycosyl hydrolase family 1*6-125*E:1.4e-40	0	0,489	-0,53	0	2,483	0,001	2,639	0	2,893	0,461	-1,458	BGL14_ORYSJ	Probable inactive beta-glucosidase 14 (Os46gluI14)	BGLU14 Os04g0513100 LOC_Os04g43360 OSJNBa0034N05.21	Oryza sativa subsp. japonica (Rice)	.	.	.	.	.	Complete proteome; Disulfide bond; Glycoprotein; Hydrolase; Reference proteome; Signal	
SRR1271859_TR446_c3_g11_i15_len=2775	RBOHC_SOLTU	Q:419-2194;H:249-937	78.64%ID	E:0	Respiratory burst oxidase homolog protein C	PF01794.16*Ferric_reduct*Ferric reductase like transmembrane component*111-267*E:2.3e-23?PF08022.9*FAD_binding_8*FAD-binding domain*310-426*E:1.2e-35?PF08030.9*NAD_binding_6*Ferric reductase NAD binding domain*433-625*E:1.3e-50	0,517	1,262	0,003	1,968	0	5,676	0	7,234	0,458	-0,402	RBOHC_SOLTU	Respiratory burst oxidase homolog protein C (EC 1.11.1.-) (EC 1.6.3.-) (NADPH oxidase RBOHC) (SlRBOHC)	RBOHC	Solanum tuberosum (Potato)	.	.	.	.	.	Alternative splicing; Complete proteome; Cytoplasm; Cytoplasmic vesicle; ER-Golgi transport; Golgi apparatus; Membrane; Protein transport; Reference proteome; Transport; Transport; WD repeat	
SRR1271859_TR2483_c1_g1_i9_len=1301	RAE1C_ARATH	Q:193-798;H:15-216	93.07%ID	E:7e-117	Ras-related protein RABE1c	PF00025.18*ARF*ADP-ribosylation factor family*16-167*E:1.1e-19?PF00071.19*Ras*Ras family*17-178*E:1.6e-66?PF06477.10*Roc*Ras of Complex, Roc, domain of DAPkinase*17-132*E:4.6e-35?PF04670.9*Gtr1_RagA*Gtr1/RagA G protein conserved region*17-132*E:4.5e-05?PF01926.20*MMR_HSR1*50S ribosome-binding GTPase*18-128*E:4.7e-05	0,811	0,335	0,16	-0,589	0	8,307	0	7,859	0	-3,996	RAE1C_ARATH	Ras-related protein RABE1c (AtRABE1c) (Ras-related protein Ara-3) (Ras-related protein RabE4) (AtRabE4)	RABE1C ARA-3 RABE4 At3g46060 F12M12.30	Arabidopsis thaliana (Mouse-ear cress)	.	.	.	.	.	.	.
SRR1271859_TR4799_c0_g2_i1_len=947	RAC5_ORYSJ	Q:347-483;H:50-174	77.42%ID	E:2e-76	Rac-like GTP-binding protein 5	.	0,661	-0,247	0,044	-0,774	0	8,351	0	7,771	1	0	RAC5_ORYSJ	Rac-like GTP-binding protein 5 (GTPase protein RacD) (OsRac5)	RAC5 RACD Os02g0834000 LOC_Os02g35730 O12B2_E10_23 J12B2_E10_23-2 P0264G11.2-1 P0264G11.2-2	Oryza sativa subsp. japonica (Rice)	.	.	.	.	.	Alternative splicing; Complete proteome; Cytoplasm; GTP-binding; Lipoprotein; Membrane; Methylation; Nucleotide-binding; Prenylation; Reference proteome	
SRR1271859_TR15473_c0_g2_i7_len=3276	BAM3_ARATH	Q:3107-1404;H:1-548	65.67%ID	E:0	Beta-amylase 3, chloroplastic	PF01373.14*Glyco_hydro_14*Glycosyl hydrolase family 14*109-526*E:9e-167	0,196	0,855	0,277	0,59	0	1,529	0,739	-0,254	BAM3_ARATH	Beta-amylase 3, chloroplastic (EC 3.2.1.2) (1,4-alpha-D-glucan maltohydrolase) (Beta-amylase 8) (Chloroplast beta-amylase) (CT-BMY)	BAM3 BMY8 CTBMY At4g17090 d14S75c FCAAIL.5	Arabidopsis thaliana (Mouse-ear cress)	.	.	.	.	.	Carbohydrate metabolism; Chloroplast; Complete proteome; Glycosidase; Hydrolase; Plastid; Polysaccharide degradation; Reference proteome; Transit peptide	
SRR1271859_TR15652_c1_g2_i2_len=2722	TM1L2_MOUSE	Q:650-1429;H:17-303	29.17%ID	E:1e-26	TOM1-like protein 2	PF00790.16*VHS*VHS domain*22-132*E:4e-34?PF03127.11*GAT*GAT domain*216-288*E:4.4e-16	0,388	0,362	0,023	0,907	0	1,466	0,001	1,43	0,803	-0,2	TM1L2_MOUSE	TOM1-like protein 2 (Target of Myb-like protein 2)	Tom112	Mus musculus (Mouse)	.	.	.	.	.	Alternative splicing; Complete proteome; Membrane; Phosphoprotein; Protein transport; Reference proteome; Transport	
SRR1271859_TR24395_c0_g1_i7_len=1072	UBC4_SOLLC	Q:123-566;H:1-148	97.97%ID	E:1e-101	Ubiquitin-conjugating enzyme E2-17 kDa	PF00179.23*UQ_con*Ubiquitin-conjugating enzyme*5-141*E:3.2e-54	0,362	0,302	0,715	0,124	0	1,016	0	1,018	0,416	0,201	UBC4_SOLLC	Ubiquitin-conjugating enzyme E2-17 kDa (EC 2.3.2.23) (E2 ubiquitin-conjugating enzyme) (Ubiquitin carrier protein) (Ubiquitin-protein ligase)	Solanum lycopersicum (Tomato) (Lycopersicon esculentum)	PATHWAY: Protein modification; protein ubiquitination. [ECO:0000255]PROSITE-ProRule:PRU00388]					ATP-binding; Complete proteome; Cytoplasm; Cytoplasmic vesicle; Cytoskeleton; Lipoprotein; Membrane; Microtubule; Protein transport; Reference proteome; Transport; Ubl conjugation pathway; Vacuole	
SRR1271859_TR24419_c0_g2_i1_len=1845	TF2B_DICDI	Q:470-1042;H:122-342	32.98%ID	E:7e-28	Transcription initiation factor IIB	PF00382.16*TFIIB*Transcription factor TFIIB repeat*149-217*E:1.8e-06?PF00382.16*TFIIB*Transcription factor TFIIB repeat*243-313*E:3.6e-12	1	-0,092	0,257	0,817	0	2,384	0	2,795	0,643	0,44	TF2B_DICDI	Transcription initiation factor IIB (General transcription factor TFIIB)	gtf2b tfib DDB_G0290929	Dictyostelium discoideum (Slime mold)	.	.	.	.	.	Complete proteome; Metal-binding; Nucleus; Reference proteome; Repeat; Transcription; Transcription regulation; Zinc; Zinc-finger	
SRR1271859_TR27683_c0_g2_i1_len=1352	TET8_ARATH	Q:316-1050;H:20-267	68.55%ID	E:4e-92	Tetraspanin-8	PF00335.17*Tetraspanin*Tetraspanin family*6-253*E:2.7e-38	0,014	0,742	0,016	0,63	0,001	1,667	0	1,73	0,384	0,263	TET8_ARATH	Tetraspanin-8	TET8 At2g23810 F27L4.1	Arabidopsis thaliana (Mouse-ear cress)	.	.	.	.	.	Complete proteome; Glycoprotein; Membrane; Reference proteome; Transmembrane; Transmembrane helix	
SRR1271859_TR28455_c0_g3_i1_len=775	EF1A_TOBAC	Q:774-616;H:383-435	96.23%ID	E:9e-26	Elongation factor 1-alpha	.	0,15	-0,414	0,633	-0,114	0	2,607	0	2,1	1	-0,253	EF1A_TOBAC	Elongation factor 1-alpha (EF-1-alpha) (Vitronectin-like adhesion protein 1) (PVN1)	.	Nicotiana tabacum (Common tobacco)	.	.	.	.	.	Cytoplasm; Elongation factor; GTP-binding; Nucleotide-binding; Phosphoprotein; Protein biosynthesis	
SRR1271859_TR30604_c0_g1_i3_len=722	NA	NA	NA	NA	NA	NA	.	1	0,76	0,254	3,565	0	5,278	0	4,784	1	-0,295	.	.	.	.	.	.	.	.	.	.
SRR1271859_TR30921_c0_g1_i1_len=1568	RIC1_ARATH	Q:447-620;H:1-58	81.03%ID	E:4e-26	CRIB domain-containing protein RIC1	PF00786.25*PBD*P21-Rho-binding domain*28-69*E:1.9e-08	0	0,01	2,343	0,239	1,373	0	3,646	0	3,945	1	-0,062	RIC1_ARATH	CRIB domain-containing protein RIC1 (ROP-interactive CRIB motif-containing protein 1) (Target of ROP protein RIC1)	RIC1 At2g33460 F4P9.23	Arabidopsis thaliana (Mouse-ear cress)	.	.	.	.	.	Complete proteome; Cytoplasm; Cytoskeleton; Developmental protein; Growth regulation; Reference proteome	
SRR1271859_TR33858_c0_g1_i6_len=537	SODC2_MAIZE	Q:57-437;H:25-151	90.55%ID	E:3e-77	Superoxide dismutase [Cu-Zn] 2	PF00080.17*Sod_Cu*Copper/zinc superoxide dismutase (SODC)*19-141*E:3.6e-44	0,673	0,225	0,528	0,259	0	1,2	0	1,346	0,037	-1,32	SODC2_MAIZE	Superoxide dismutase [Cu-Zn] 2 (EC 1.15.1.1)	SODCC.1 SOD2	Zea mays (Maize)	.	.	.	.	.	Antioxidant; Complete proteome; Copper; Cytoplasm; Disulfide bond; Metal-binding; Oxidoreductase; Reference proteome; Zinc	
SRR1271859_TR39755_c0_g1_i1_len=4292	Y2182_ARATH	Q:832-2970;H:57-784	35.68%ID	E:6e-112	.	PF00263.9*LRRNT_2*Leucine rich repeat N-terminal domain*47-71*E:0.0002?PF13855.3*LRR_8*Leucine rich repeat*101-162*E:1.9e-07?PF00560.30*LRR_1*Leucine Rich Repeat*102-119*E:1.7?PF13516.3*LRR_6*Leucine Rich repeat*175-188*E:1.1?PF13855.3*LRR_8*Leucine rich repeat*413-471*E:4.7e-10?PF00560.30*LRR_1*Leucine Rich Repeat*460-482*E:0.018?PF13516.3*LRR_6*Leucine Rich repeat*529-544*E:1.2?PF00560.30*LRR_1*Leucine Rich Repeat*530-550*E:0.29?PF00069.22*Pkinase*Protein kinase domain*687-951*E:1.4e-11?PF07714.14*Pkinase_Tyr*Protein tyrosine kinase*701-851*E:1.7e-09	1	0,325	0,008	3,033	0	3,392	0	4,284	1	-0,591	PXC3_ARATH	Leucine-rich repeat receptor-like tyrosine-protein kinase PXC3 (EC 2.7.10.1) (Protein PXY/TDR-CORRELATED 3)	PXC3 At2g41820 T11A7.8	Arabidopsis thaliana (Mouse-ear cress)	.	.	.	.	.	ATP-binding; Cell membrane; Complete proteome; Glycoprotein; Kinase; Leucine-rich repeat; Membrane; Nucleotide-binding; Receptor; Reference proteome; Repeat; Signal; Transferase; Transmembrane; Transmembrane helix; Tyrosine-protein kinase	
SRR1271859_TR43882_c2_g5_i3_len=2275	PTR53_ARATH	Q:158-256;H:13-615	54.1%ID	E:0	Protein NRT1/ PTR FAMILY 2.11	PF00854.18*PTR2*POT family*5-247*E:8.2e-47	0,692	1,264	0,026	1,912	0	4,971	0	4,649	1	0,816	PTR53_ARATH	Protein NRT1/ PTR FAMILY 2.11 (AtNPF2.11) (Nitrate transporter 1.10) (Protein GLUCOSINOLATE TRANSPORTER 2)	NPF2.11 GTR2 NRT1.10 At5g62680 MRQ21.10	Arabidopsis thaliana (Mouse-ear cress)	.	.	.	.	.	Complete proteome; Membrane; Reference proteome; Transmembrane; Transmembrane helix; Transport	
SRR1271859_TR44909_c1_g1_i2_len=994	ARC5A_ARATH	Q:119-511;H:2-132	86.26%ID	E:3e-75	Actin-related protein 2/3 complex subunit 5A	PF04699.11*Pfk-Arc*ARP2/3 complex 16 kDa subunit (p16-Arc)*13-129*E:2.4e-21	0,559	0,363	0,316	0,64	0	2,186	0	2,44	0,52	0,462	ARC5A_ARATH	Actin-related protein 2/3 complex subunit 5A (Actin-related protein C5A) (Arp2/3 complex 16 kDa subunit) (p16-ARC) (Protein CROOKED)	ARPC5A CRK At4g01710 T15B16.22	Arabidopsis thaliana (Mouse-ear cress)	.	.	.	.	.	Acetylation; Actin-binding; Cell projection; Complete proteome; Cytoplasm; Cytoskeleton; Reference proteome	
SRR1271859_TR44971_c0_g2_i6_len=809	NOP10_ARATH	Q:525-334;H:1-64	84.38%ID	E:2e-30	H/ACA ribonucleoprotein complex subunit 3-like protein	.	0,402	0,814	0,283	0,645	0	7,444	0	7,357	1	-0,818	NOP10_ARATH	H/ACA ribonucleoprotein complex subunit 3-like protein (Nucleolar protein 10)	At2g20490 T13C7.8	Arabidopsis thaliana (Mouse-ear cress)	.	.	.	.	.	Alternative splicing; Complete proteome; Nucleus; Reference proteome; Ribonucleoprotein; Ribosome biogenesis; rRNA processing	
SRR1271859_TR46177_c0_g2_i2_len=2978	ACL5_ARATH	Q:118-256;H:29-338	76.13%ID	E:2e-171	Thermospermine synthase ACAULIS5	PF01564.14*Spermine_synth*Spermine/spermidine synthase*41-274*E:7.9e-55	1	0,032	0,381	-0,678	0	2,559	0,001	2,438	0,34	0,551	ACL5_ARATH	Thermospermine synthase ACAULIS5 (EC 2.5.1.79)	ACL5 TKV At5g19530 T20D1.50	Arabidopsis thaliana (Mouse-ear cress)	.	.	.	.	.	Alternative splicing; Complete proteome; Polyamine biosynthesis; References proteome; Transferase	
SRR3242017_TR620_c1_g7_i7_len=2956	NA	NA	NA	NA	NA	NA	PF07887.8*Calmodulin_bind*Calmodulin binding protein-like*91-380*E:7.9e-117	1	0,105	0,068	0,985	0	1,398	0	1,494	0,692	1,46	.	.	.	.	.	.	.	.	.	.
SRR3242017_TR2079_c0_g4_i3_len=1967	PP273_ARATH	Q:107-434;H:394-610	53%ID	E:5e-49	Pentatricopeptide repeat-containing protein At3g49240	PF04117.9*Mpv17_PMP22*Mpv17/PMP22 family*355-413*E:8.8e-15	0,298	-0,788	0,048	0,98	0	2,879	0	3,526	0,524	-0,594	PP273_ARATH	Pentatricopeptide repeat-containing protein At3g49240 (Protein EMBRYO DEFECTIVE 1796)	EMB1796 At3g49240 F2K15.100	Arabidopsis thaliana (Mouse-ear cress)	.	.	.	.	.	Complete proteome; Reference proteome; Repeat	
SRR3242017_TR5846_c0_g1_i2_len=690	NRPBC_ARATH	Q:602-450;H:1-51	90.2%ID	E:3e-26	DNA-directed RNA polymerases II, IV and V subunit 12	.	1	-0,173	0,074	0,925	0	7,409	0	6,759	0,461	-1,046	NRPBC_ARATH	DNA-directed RNA polymerases II, IV and V subunit 12 (DNA-directed RNA Polymerase II subunit K)	NRPB12 NRPD12 NRPE12 At5g41010 MEE8.8	Arabidopsis thaliana (Mouse-ear cress)	.	.	.	.	.	Complete proteome; DNA-directed RNA polymerase; Metal-binding; Nucleus; Reference proteome; Transcription; Zinc	
SRR3242017_TR7809_c1_g1_i3_len=1867	CXE1_ACTER	Q:184-970;H:44-333	47.12%ID	E:9e-92	Carboxylesterase 1	PF10340.6*DUF2424*Protein of unknown function (DUF2424)*45-155*E:5.1e-05?PF07859.10*Abhydrolase_3*alpha/beta hydrolase fold*52-271*E:1.2e-45	0,06	0,827	0,252	0,538	0	2,066	0	1,89	1	0,056	CXE1_ACTER	Carboxylesterase 1 (AeCXE1) (EC 3.1.1.1)	CXE1	Actinidia eriantha (Velvet vine) (Actinidia fulvicoma var. lanata)	.	.	.	.	.	3D-structure; Hydrolase; Serine esterase	
SRR3242017_TR9822_c1_g1_i1_len=845	UEV1C_ARATH	Q:624-187;H:1-145	89.73%ID	E:2e-88	Ubiquitin-conjugating enzyme E2 variant 1C	PF00179.23*UQ_con*Ubiquitin-conjugating enzyme*43-136*E:8.3e-15	0,407	0,375	0,881	0,053	0	2,757	0	3,479	0	-4,15	UEV1C_ARATH	Ubiquitin-conjugating enzyme E2 variant 1C (Ubc enzyme variant 1C) (Protein MMS ZWEI HOMOLOG 3)	UEV1C MMZ3 At2g36060 F11F19.3	Arabidopsis thaliana (Mouse-ear cress)	.	.	.

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SRR342023_TR3970_c2_g2_i1len=2037	C81F1_ARATH	G:316-1324:H:38-495	44.16%ID	E:9e-132	Cytochrome P450 81F1 (ECO:0000305)	PF00067.19*p450*Cytochrome P450*37-481*E:2.5e-92	0,93	-0,089	0,019	0,83	0	2,093	0	3,433	0,008	1,156 C81F1_ARATH	Cytochrome P450 81F1 (EC 1.14.--.-)	CYP81F1 CYP91A2 At4g37430 F6G17.80	Arabidopsis thaliana (Mouse-ear cress)			finger
SRR342023_TR4400_c0_g3_i2len=2180	LACS7_ARATH	G:2180-3993:H:10-697	79.06%ID	E:0	Long chain acyl-CoA synthetase 7, peroxisomal	PF00501:25*AMP-binding*AMP-binding enzyme*14-455*E:8.4e-109	0,684	0,212	0,05	0,711	0	2,003	0,001	1,917	0,594	-0,258 LACS7_ARATH	Long chain acyl-CoA synthetase 7, peroxisomal (EC 6.2.1.3)	LACS7 At5g27600 F15A18.60	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Lipid metabolism; fatty acid metabolism.		Complete proteome; Peroxisome
SRR342023_TR6699_c0_g1_i2len=1346	RP45C_ARATH	G:3-1179:H:301-359	77.97%ID	E:1e-23	Polyadenylate-binding protein RBP45C	PF00076.19*RRM_1*RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)*1-44*E:1.1e-08*PF13893.3*RRM_5*RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)*1-47*E:0.0057	0,257	0,849	0,748	0,193	0	1,524	0,001	1,471	0,214	-0,79 RP45C_ARATH	Polyadenylate-binding protein RBP45C (PolyA)-binding protein RBP45C) (RNA-binding protein 45C) (AtRBP45C)	RBP45C At4g27000 F10M23.340	Arabidopsis thaliana (Mouse-ear cress)			Complete proteome; Nucleus; RNA-binding; Reference proteome; Repeat; mRNA processing
SRR342023_TR6857_c1_g4_i4len=919	HSP13_SOYBN	G:74-1274:H:1-333	80.77%ID	E:1e-85	17.5 kDa class I heat shock protein	PF04969.13*CS*CS domain*50-141*E:0.022*PF00011.18*HSP20*Hsp20/alpha crystallin family*52-155*E:1.4e-32	0,545	0,462	0,121	0,78	0	2,661	0	2,176	0,44	0,648 HSP13_SOYBN	17.5 kDa class I heat shock protein (HSP 17.5-M)	HSP17.5-M	Glycine max (Soybean) (Glycine hispida)			Complete proteome; Cytoplasm; Reference proteome; Stress response
SRR342023_TR7599_c1_g2_i3len=1661	Y5133_ARATH	G:1-1158,H:69-456	62.47%ID	E:7e-170	BTB/POZ domain-containing protein At5g41330	-	0,611	0,347	0,124	0,936	0	2,353	0	2,19	0,635	0,325 Y5133_ARATH	BTB/POZ domain-containing protein At5g41330	At5g41330 MYC6.4	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Protein modification; protein ubiquitination.		Complete proteome; Reference proteome; Repeat; Ubl conjugation pathway; WD repeat
SRR342023_TR8361_c1_g2_i1len=2988	NA	NA	NA	NA	NA	PF09405.7*Ba*CASC3/Barentsz eIF4AIII binding*142-249*E:2e-20	1	0,102	0,177	-0,73	0	5,995	0	5,936	1	-0,55.	.	.	.			
SRR342023_TR8667_c0_g1_i1len=1115	EDR2L_ARATH	G:880-1786,H:489-711	44.68%ID	E:1e-50	Protein ENHANCED DISEASE RESISTANCE 2-like	PF07059.9*DUF1336*Protein of unknown function (DUF1336)*93-308*E:1.2e-68	0,581	0,364	0,002	1,704	0	2,077	0	2,18	1	0,009 EDR2L_ARATH	Protein ENHANCED DISEASE RESISTANCE 2-like	EDR2L At5g45560 MFC19.23	Arabidopsis thaliana (Mouse-ear cress)			Cell membrane; Complete proteome; Endoplasmic reticulum; Endosome; Membrane; Plant defense; Reference proteome; Transmembrane; Transmembrane helix
SRR342023_TR10547_c3_g1_i1len=1517	PTR27_ARATH	G:1517-429,H:195-555	78.79%ID	E:7e-168	Protein NRT1/ PTR FAMILY 6.2	PF00854.18*PTR2*POT family*2-328*E:3.2e-75	0,732	0,795	0,017	1,256	0	1,587	0	1,142	0,748	-0,299 PTR27_ARATH	Protein NRT1/ PTR FAMILY 6.2 (ANPF6.2) (Nitrate transporter 1.4)	NPF6.2 NRT1.4 NTP2 At2g26690 F18A8.6	Arabidopsis thaliana (Mouse-ear cress)			Complete proteome; Membrane; Nitrate assimilation; Reference proteome; Symport; Transmembrane; Transmembrane helix; Transport
SRR342023_TR10607_c1_g1_i1len=619	RS273_ARATH	G:50:2251,H:1-84	95.24%ID	E:2e-52	40S ribosomal protein S27-3	-	1	0,048	0,007	-2,2	0	2,471	0	3,552	0,502	-3,798 RS273_ARATH	40S ribosomal protein S27-3	RPS27D AR527B At5g47930 K16F13.1	Arabidopsis thaliana (Mouse-ear cress)			Complete proteome; Metal-binding; Reference proteome; Ribonucleoprotein; Ribosomal protein; Zinc; Zinc-finger
SRR342023_TR10280_c0_g2_i1len=1012	ABT1_ARATH	G:62-883,H:201-475	61.09%ID	E:3e-121	Protein ABC17, chloroplastic	PF01458.14*UPF0051*Uncharacterized protein family (UPF0051)*4-229*E:3.4e-60	0,78	0,545	0,601	0,16	0	1,272	0,001	1,005	0,978	0,015 ABT1_ARATH	Protein ABC17, chloroplastic (ABC transporter I family member 7) (ABC transporter ABC1.7) (AtABC17) (Non-intrinsic ABC protein 6) (Plastid SuB-like protein)	ABC17 NAP6 At1g32500 F5D14.28	Arabidopsis thaliana (Mouse-ear cress)			Chloroplast; Complete proteome; Plastid; Reference proteome; Transit peptide
SRR342023_TR19508_c3_g10_i1len=931	NA	NA	NA	NA	NA	-	0,034	5,518	1	-0,065	0	7,363	0,001	6,582	0,381	2,011.	.	.	.			
SRR342023_TR20611_c2_g3_i1len=552	CHID_SOLLC	G:157-552,H:4-135	73.48%ID	E:3e-59	Basic endochitinase	PF00182.16*Glycos_hydro_19*Chitinase class I*25-152*E:1.3e-66	0	0,03	0,03	0,93	0	7,973	0	6,953	0,103	1,588 CHID_SOLLC	Basic endochitinase (EC 3.2.1.14) (Fragment)	CHI14	Solanum lycopersicum (Tomato) (Lycopersicon esculentum)			Carbohydrate metabolism; Chitin degradation; Complete proteome; Disulfide bond; Glycosidase; Hydrolase; Plant defense; Polysaccharide degradation; Reference proteome; Secreted
SRR342023_TR24545_c0_g1_i2len=906	ISAM1_ARATH	G:203-589,H:1-192	75%ID	E:4e-65	Iron-sulfur assembly protein IscA-like 1, mitochondrial	PF01521.17*Fe-S_biosyn*Iron-sulphur cluster biosynthesis*20-119*E:8.5e-20	0,513	0,207	0,359	0,323	0	1,232	0	1,179	0,424	0,316 ISAM1_ARATH	Iron-sulfur assembly protein IscA-like 1, mitochondrial	At2g16710 T24I21.12	Arabidopsis thaliana (Mouse-ear cress)			Alternative splicing; Complete proteome; Iron; Iron-sulfur; Metal-binding; Mitochondrion; Reference proteome; Transit peptide
SRR342023_TR26043_c3_g3_i3len=1890	SKIP5_ARATH	G:332-565,H:53-130	78.21%ID	E:4e-34	F-box protein SKIP5	-	1	-1,58	0,175	-0,96	0	8,619	0	9,318	1	0,26 SKIP5_ARATH	F-box protein SKIP5 (SKP1-interacting partner 5)	SKIP5 At3g54480 T14E10.50	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Protein modification; protein ubiquitination.		Alternative splicing; Complete proteome; Reference proteome; Ubl conjugation pathway
SRR342023_TR26203_c0_g2_i2len=2408	PTR18_ARATH	G:518-2236,H:12-590	74.18%ID	E:0	Protein NRT1/ PTR FAMILY 3.1	PF00854.18*PTR2*POT family*88-512*E:1.1e-101	0,064	0,984	0,034	0,998	0	1,967	0	1,624	0,281	-0,564 PTR18_ARATH	Protein NRT1/ PTR FAMILY 3.1 (ANPP3.1)	NPF3.1 NITR At1g68570 F24J5.19	Arabidopsis thaliana (Mouse-ear cress)			Complete proteome; Membrane; Nitrate assimilation; Reference proteome; Transmembrane; Transmembrane helix; Transport
SRR342023_TR27607_c1_g1_i1len=2563	ACOX3_ARATH	G:431-2338,H:41-675	75.47%ID	E:0	Acyl-coenzyme A oxidase 3, peroxisomal	PF02770.16*Acyl-CoA_dh_M*Acyl-CoA dehydrogenase, middle domain*192-300*E:8.7e-14*PF00441.21*Acyl-CoA_dh_1*Acyl-CoA dehydrogenase, C-terminal domain*334-469*E:1.3e-28*PF01756.16*ACOX*Acyl-CoA oxidase*539-665*E:1.3e-17	0,415	0,38	0,321	1,053	0	1,884	0	1,959	0,626	0,297 ACOX3_ARATH	Acyl-coenzyme A oxidase 3, peroxisomal (AOX 3) (Acyl-CoA oxidase 3) (EC 1.3.3.6) (Medium-chain acyl-CoA oxidase) (AICX3)	ACX3 At1g06290 At1g06300 F9P14.15 F9P14_11 T2D23.1	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Lipid metabolism; peroxisomal fatty acid beta-oxidation.		Complete proteome; FAD; Fatty acid metabolism; Flavoprotein; Lipid metabolism; Oxidoreductase; Peroxisome; Reference proteome; Transit peptide
SRR346572_TR2358_c0_g1_i5len=1447	NA	NA	NA	NA	NA	PF06200.11*tify domain*68-119*E:1.2e-16 PF09425.7*CCT_2*Divergent CCT motif*226-239*E:1.2e-05	0,052	1,488	0,034	5,697	0	3,166	0	3,68	0,335	0,661.	.	.	.			
SRR346572_TR6469_c0_g2_i13len=1024	SAC8_ARATH	G:158-454,H:76-174	49.49%ID	E:4e-21	Phosphoinositide phosphatase SAC8	-	0,221	0,418	0,005	0,921	0	1,06	0	1,058	1	-0,025 SAC8_ARATH	Phosphoinositide phosphatase SAC8 (AtSAC8) (EC 3.1.3.-) (Protein SUPPRESSOR OF ACTIN 1A) (AtSAC1a) (Protein SUPPRESSOR OF ACTIN 8) (Putative transmembrane protein G5p) (AtG5) (SAC domain protein 8) (SAC1-like protein AtSAC1a)	SAC8 G5 SAC1A At3g51830 ATEM1.8	Arabidopsis thaliana (Mouse-ear cress)			Alternative splicing; Complete proteome; Endoplasmic reticulum; Hydrolase; Membrane; Reference proteome; Transmembrane; Transmembrane helix
SRR346572_TR11019_c0_g2_i1len=792	NA	NA	NA	NA	NA	-	0,679	0,178	0,008	0,975	0	2,307	0	2,539	0,487	0,262.	.	.	.			
SRR346572_TR13497_c0_g1_i1len=1218	IN21B_ORYSJ	G:785-1513,H:29-241	68.08%ID	E:9e-99	Protein IN2-1 homolog B	PF13417.3*GST_N_3*Glutathione S-transferase, N-terminal domain*111-188*E:1.6e-20*PF13409.3*GST_N_2*Glutathione S-transferase, N-terminal domain*116-182*E:3.6e-13*PF16865.2*GST_C_5*Glutathione S-transferase, C-terminal domain*199-285*E:3.7e-06 PF00043.22*GST_C*Glutathione S-transferase, C-terminal domain*224-292*E:8.4e-05*PF13410.3*GST_C_2*Glutathione S-transferase, C-terminal domain*226-288*E:2e-10	0,494	0,287	0,021	0,837	0	1,7	0	1,421	0,608	-0,216 IN21B_ORYSJ	Protein IN2-1 homolog B (Glutathione S-transferase GSTZ5)	GSTZ5 Os03g0283100 LOC_Os03g17470	Oryza sativa subsp. japonica (Rice)			Complete proteome; Reference proteome
SRR346572_TR20127_c0_g1_i2len=532	TCP10_ARATH	G:165-386,H:1-67	91.89%ID	E:1e-41	Transcription factor TCP10	PF03634.10*TCP*TCP family transcription factor*68-172*E:3.7e-34	0,017	5,757	0,01	2,281	0	7,623	0	7,824	0,402	-1,106 TCP10_ARATH	Transcription factor TCP10	TCP10 At2g31070 T16B12.12	Arabidopsis thaliana (Mouse-ear cress)			Complete proteome; DNA-binding; Developmental protein; Nucleus; Reference proteome; Transcription; Transcription regulation
SRR346572_TR24001_c1_g1_i2len=3205	SLK2_ARATH	G:2012-1077,H:28-593	74.04%ID	E:4e-164	Probable transcriptional regulator SLK2	PF01803.13*LIM_bind*LIM-domain binding protein*291-551*E:9.6e-59	0,196	0,814	0,027	2,129	0	1,912	0	0,699	0,582	0,478 SLK2_ARATH	Probable transcriptional regulator SLK2 (AtSLK2) (Protein SEUSS-like 2)	SLK2 At5g62090 MTG10.12	Arabidopsis thaliana (Mouse-ear cress)			Complete proteome; Developmental protein; Differentiation; Flowering; Nucleus; Reference proteome; Transcription; Transcription regulation
SRR346572_TR30597_c0_g1_i1len=1332	NA	NA	NA	NA	NA	PF00168.27*C2*C2 domain*1-64*E:1e-13*PF08372.7*PRT_C*Plant phosphoribosyltransferase C-terminal*209-364*E:6e-81	0,156	1,134	0,028	1,525	0	2,451	0	3,087	0,282	1,129.	.	.	.			
SRR346596_TR1244_c0_g1_i6len=3997	SYK_ARATH	G:292-1899,H:80-615	81.34%ID	E:0	-	PF01336.22*tRNA_anti-codon*OB-fold nucleic acid binding domain*88-166*E:2.9e-13*PF00152.17*tRNA-synt_2*RNA synthetases class (I, II, K and N)*206-555*E:2.8e-82	0,781	0,508	0,212	0,98	0	3,153	0	2,942	1	0,04 SYKC_ARATH	Lysine--tRNA ligase, cytoplasmic (EC 6.1.1.6) (Lysyl-tRNA synthetase) (LysRS) (Lysyl-tRNA synthetase 1) (AtKRS-1)	At3g11710 T19F11.11	Arabidopsis thaliana (Mouse-ear cress)			Complete proteome; Cytoplasm; Ligase; Nucleotide-binding; Protein biosynthesis; Reference proteome
SRR346596_TR1359_c0_g1_i8_len=3891	GLR36_ARATH	G:273-265,H:1-790	60.69%ID	E:0	Glutamate receptor 3.6	PF13458.3*Peripla_BP_6*Periplasmic binding protein*43-409*E:2.3e-18*PF01094.25*ANF_receptor*Receptor family ligand binding region*56-414*E:1.7e-82*PF10613.5*Lig_chan-Glu_bd*Ligated ion channel L-glutamate- and glycine-binding site*490-576*E:4.7e-09 PF00497.17*SBP_bac_3*Bacterial extracellular solute-binding proteins, family 3*531-814*E:6.6e-20 PF00060.23*Lig_chan*Ligand-gated ion channel*595-647*E:9.7e-35	0,271	0,945	0,004	1,716	0	2,468	0	2,832	1	0,279 GLR36_ARATH	Glutamate receptor 3.6 (Ligand-gated ion channel 3.6) (AtGLR3.6)	GLR3.6 At3g51480 F26O13.120	Arabidopsis thaliana (Mouse-ear cress)			Complete proteome; Glycoprotein; Ion channel; Ion transport; Ligand-gated ion channel; Membrane; Receptor; Reference proteome; Signal; Transmembrane; Transmembrane helix; Transport
SRR346596_TR2684_c0_g1_i15len=2068	NA	NA	NA	NA	NA	-	0,008	3,385	0,008	2,82	0,001	2,445	0	2,741	1	-0,461.	.	.	.			
SRR346596_TR11097_c0_g1_i1len=1054	IFS3_SOLTU	G:809-339,H:1-157	92.99%ID	E:7e-102	Eukaryotic translation initiation factor 5A-3	PF01287.17*eIF-5a*Eukaryotic elongation factor 5A hypusine, DNA-binding OB fold*85-154*E:1.3e-27	0,895	0,173	0,077	0,781	0	2,511	0	0,9	0,52	0,489 IFS3_SOLTU	Eukaryotic translation initiation factor 5A-3 (eIF-5A-3) (eIF-4D)	EIF5A3	Solanum tuberosum (Potato)			Complete proteome; Hypusine; Initiation factor; Protein biosynthesis; Reference proteome
SRR346596_TR11837_c0_g1_i1len=1040	NA	NA	NA	NA	NA	-	0,059	1,641	0,008	4,157	0	7,082	0	7,591	1	1,116.	.	.	.			
SRR346596_TR18518_c0_g1_i1len=1873	DR100_ARATH	G:1717-782,H:26-345	36.22%ID	E:5e-52	DNA-damage-repair/toleration protein DRT100	PF08263.9*LRRNT_2*Leucine rich repeat N-terminal domain*56-95*E:2e-10*PF13855.3*LRR_8*Leucine rich repeat*203-262*E:8.2e-11 PF00560.30*LRR_1*Leucine Rich Repeat*227-246*E:0.32 PF13855.3*LRR_8*Leucine rich repeat*277-335*E:4.8e-09 PF13516.3*LRR_6*Leucine Rich repeat*299-313*E:1.8 PF08263.9*LRRNT_2*Leucine rich repeat N-terminal domain*355-369*E:960	0,727	0,114	0,054	0,64	0	1,779	0	1,482	0,214	-0,386 DR100_ARATH	DNA-damage-repair/toleration protein DRT100	DRT100 At3g12610 MMF12.5 T2E22.8 T2E22_107	Arabidopsis thaliana (Mouse-ear cress)			Complete proteome; DNA damage; DNA repair; Leucine-rich repeat; Reference proteome; Repeat; Signal
SRR346596_TR19915_c1_g1_i1len=913	HS22C_PETHY	G:85-744,H:1-227	62.77%ID	E:1e-87	Small heat shock protein, chloroplastic	PF00011.18*HSP20*Hsp20/alpha crystallin family*153-251*E:1.2e-28	0,629	1,094	1	0,34	0	4,984	0,001	2,915	1	-0,333 HS22C_PETHY	Small heat shock protein, chloroplastic	HSP22	Petunia hybrida (Petunia)			Chloroplast; Plastid; Stress response; Transit peptide
SRR346596_TR20016_c1_g1_i1len=7314	SDP1_ARATH	G:1030-347,H:1-784	72.31%ID	E:0	Triacylglycerol lipase SDP1	PF11815.5*DUF3336*Domain of unknown function (DUF3336)*99-229*E:6.9e-29*PF01734.19*Patatin*Patatin-like phospholipase*236-430*E:3.4e-18	1	0,706	0,629	1,74	0	4,919	0	5,137	1	0,331 SDP1_ARATH	Triacylglycerol lipase SDP1 (EC 3.1.1.3) (Protein SUGAR-DEPENDENT 1)	SDP1 At5g04040 F8F6.10 F8F6.250	Arabidopsis thaliana (Mouse-ear cress)			Complete proteome; Glycerol metabolism; Glycoprotein; Hydrolase; Lipid degradation; Lipid droplet; Lipid metabolism; Membrane; Reference proteome; Transmembrane; Transmembrane helix
SRR346596_TR21231_c0_g1_i1len=545	NA	NA	NA	NA	NA	-	0,949	0,242	0,057	0,571	0	2,2	0	1,754	0,061	-0,729.	.	.	.			
SRR346596_TR22122_c0_g1_i3len=1945	DCAM_CATRO	G:1437-367,H:1-527	100%ID	E:0	S-adenosylmethionine decarboxylase proenzyme	PF01536.13*SAM_decarbox*Adenosylmethionine decarboxylase*9-332*E:9.8e-110	0,352	0,468	0,114	0,25	0	1,371	0	1,462	1	-0,264 DCAM_CATRO	S-adenosylmethionine decarboxylase proenzyme (AdoMetDC) (SAMDC) (EC 4.1.1.50) [Cleaved into: S-adenosylmethionine decarboxylase alpha chain; S-adenosylmethionine decarboxylase beta chain]	SAMDC	Catharanthus roseus (Madagascar periwinkle) (Vinca rosea)	PATHWAY: Amine and polyamine biosynthesis; S-adenosylmethioninamine biosynthesis; S-adenosyl-L-methionine; Self-Incompatibility (SI) response; Spermidine biosynthesis; Zymogen			Autocatalytic cleavage; Decarboxylase; Lyase; Polyamine biosynthesis; Pyruvate; S-adenosyl-L-methionine; Self-Incompatibility (SI) response; Spermidine biosynthesis; Zymogen
SRR346596_TR24381_c0_g1_i1len=1227	MSRB3_ORYSJ	G:644-1033,H:98-227	86.92%ID	E:3e-77	Peptide methionine sulfoxide reductase B3, chloroplastic	PF01641.15*SelR*SelR domain*74-192*E:1.7e-47	1	0,03	0,04	5,532	0	7,497	0	8,71	1	-3,497 MSRB3_ORYSJ	Peptide methionine sulfoxide reductase B3, chloroplastic (OsMSRB3) (EC 1.8.4.12) (Peptide-methionine (R)-S-oxide reductase)	MSRB3 Os05g0404200 LOC_Os05g33510 OSJNBb0006J12.16	Oryza sativa subsp. japonica (Rice)			Chloroplast; Complete proteome; Disulfide bond; Electron transport; Metal-binding; Oxidoreductase; Plastid; Redox-active center; Reference proteome; Transit peptide; Transport; Zinc
SRR346596_TR25673_c0_g1_i1len=665	NA	NA	NA	NA	NA	-	0,006	1,747	0,282	1,057	0	4,239	0	4,333	0,319	1,107.	.	.	.			
SRR346596_TR25676_c0_g1_i1len=689	PR51_SOLTU	G:124-567,H:1-155	35.9%ID	E:9e-22	Pathogenesis-related protein STH-21	PF04007.16*Bet_v_1*Pathogenesis-related protein Bet v I family*4-142*E:1.1e-12	0,629	2,416	0,068	1,061	0	3,508	0	2,579	0,083	-0,744 PR51_SOLTU	Pathogenesis-related protein STH-21	STH-21	Solanum tuberosum (Potato)			Complete proteome; Pathogenesis-related protein; Plant defense; Reference proteome
SRR346604_TR1107_c0_g1_i1len=4751	PR5_ARATH	G:1058-366,H:7-239	55.27%ID	E:2e-63	Pathogenesis-related protein 5	PF01764.22*Lipase_3*Lipase (class 3)*412-548*E:4.6e-26	1	-1,67	0,034	4,734	0	6,245	0	6,978	1	1,614 PR5_ARATH	Pathogenesis-related protein 5 (PR-5)	At1g75040 F9E10.11	Arabidopsis thaliana (Mouse-ear cress)			Apoptosis; Complete proteome; Direct protein sequencing; Disulfide bond; Pathogenesis-related protein; Plant defense; Reference proteome; Secreted; Signal
SRR346604_TR1303_c1_g1_i2len=1834	TT12_ARATH	G:1699-197,H:5-501	48.21%ID	E:3e-136	-	PF01554.15*MatE*MatE*44-224*E:2e-33*PF01554.15*MatE*MatE*286-447*E:8.6e-30	1	3,261	0,009	4,322	0	4,299	0	3,586	1	0,451 DTX41_ARATH	Protein DETOXIFICATION 41 (AtDTX41) (Multidrug and toxic compound extrusion protein 41) (MATE protein 41) (Protein TANNIN-DEFICIENT SEED 3) (Protein TRANSPARENT TESTA 12)	DTX41 TDS3 TT12 At3g59030 F17J16_80	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Secondary metabolite biosynthesis; flavonoid biosynthesis.		Antiport; Complete proteome; Flavonoid biosynthesis; Membrane; Reference proteome; Transmembrane; Transmembrane helix; Transport; Vacuole
SRR346604_TR1685_c0_g1_i1len=2325	NA	NA	NA	NA	NA	-	1	-0,295	0,034	4,098	0	5,734	0	6,989	1	3,377.	.	.	.			
SRR346604_TR1973_c0_g2_i2len=2046	VPE_CITSI	G:1910-444,H:1-494	73.95%ID	E:0	Vacuolar-processing enzyme	PF01650.15*Peptidase_C13*Peptidase C13 family*54-324*E:7.1e-116	0,037	0,567	0,366	-0,282	0	1,072	1	2,896	VPE_CITSI	Vacuolar-processing enzyme (VPE) (EC 3.4.22.-)	Citrus sinensis (Sweet orange) (Citrus aurantium var. sinensis)					Glycoprotein; Hydrolase; Protease; Signal; Thiol protease
SRR346604_TR3235_c0_g1_i1len=1234	RFS6_ARATH	G:1178-300,H:26-1549	83.28%ID	E:3e-177	Probable galactinol--sucrose galactosyltransferase 6	PF05691.9*Raffinose_syn*Raffinose synthase or seed imbibition protein Sip1*8-311*E:8.4e-148	1	0,139	0,044	2,055	0	1,987	0	2,024	0,811	0,273 RFS6_ARATH	Probable galactinol--sucrose galactosyltransferase 6 (EC 2.4.1.82) (Protein DARK INDUCIBLE 10) (Raffinose synthase 6)	RFS6 DIN10 RS6 At5g20250 F5O24.140	Arabidopsis thaliana (Mouse-ear cress)			Alternative splicing; Carbohydrate metabolism; Complete proteome; Glycosyltransferase; Reference proteome; Transferase
SRR346604_TR7114_c0_g1_i1len=900	NA	NA	NA	NA	NA	PF13639.3*zf-RING_2*Ring finger domain*109-162*E:6.7e-12 PF17123.2*zf-RING_11*RING-like zinc finger*119-148*E:1.3e-07	0	-1,196	0,943	-0,023	0	9,099	0	10,06	1	0.	.	.	.			
SRR346604_TR7319_c0_g1_i6len=3664	NA	NA	NA	NA	NA	PF00106.22*adh_short*short chain dehydrogenase*6-100*E:4.2e-07*PF13561.3*adh_short_C2*Enoyl-(Acyl carrier protein) reductase*17-269*E:3.5e-07	1	0,915	0,002	5,571	0	6,979	0	7,11	1	-0,302.	.	.	.			
SRR346604_TR8057_c0_g1_i34len=5115	LOXC1_ORYSJ	G:469-1821,H:119-583	53.76%ID	E:0	Lipoxygenase 7, chloroplastic	PF01477.20*PLAT/LH2 domain*144-212*E:3.3e-07*PF00305.16*Lipoxygenase*Lipoxygenase*225-569*E:1.3e-138	0,732	0,798	0,001	1,36	0	7,084	0	6,886	1	-0,489 LOXC1_ORYSJ	Lipoxygenase 7, chloroplastic (EC 1.13.11.12)	CM-LOX1 LOX2.1 Os03g0508800 LOC_Os03g39840 B1163A08.24	Oryza sativa subsp. japonica (Rice)	PATHWAY: Lipid metabolism; oxylipin biosynthesis. [ECO:0000255]PROSITE-ProRule:PRU00726].		Chloroplast; Complete proteome; Dioxygenase; Fatty acid biosynthesis; Fatty acid metabolism; Iron; Lipid biosynthesis; Lipid metabolism; Metal-binding; Oxidoreductase; Oxylipin biosynthesis; Plastid; Reference proteome; Transit peptide
SRR346604_TR11161_c0_g1_i1len=2489	PLT5_ARATH	G:219-1709,H:26-525	69.86%ID	E:0	Polyol transporter 5	PF00083.21*Sugar_tr*Sugar (and other) transporter*36-493*E:3.3e-109*PF07690.13*MFS_1*Major Facilitator Superfamily*41-431*E:1.8e-28	0,118	1,706	0,001	4,77	0	2,077	0	2,014	1	-0,69 PLT5_ARATH	Polyol transporter 5 (Protein POLYOL TRANSPORTER 5) (AtPLT5) (Sugar-proton symporter PLT5)	PLT5 At3g18830 MVE11.10 MVE11.22	Arabidopsis thaliana (Mouse-ear cress)			Cell membrane; Complete proteome; Membrane; Reference proteome; Sugar transport; Symport; Transmembrane; Transmembrane helix; Transport
SRR346604_TR12279_c0_g2_i1len=655	NA	NA	NA	NA	NA	-	0,232	-0,316	0,001	-0,926	0	1,237	0,001	1,067	0,86	-0,191.	.	.	.			
SRR346604_TR12815_c1_g1_i3len=4404	POLX_TOBAC	G:1648-1208,H:884-1033	42.38%ID	E:6e-42	Retrovirus-related Pol polyprotein from transposon TNT 1-94	-	0,006	2,539	0,041	4,099	1	3,668	0	4,099	1	0,837 POLX_TOBAC	Retrovirus-related Pol polyprotein from transposon TNT 1-94 [Includes: Protease (EC 3.4.23.-); Reverse transcriptase (EC 2.7.7.49); Endonuclease]		Nicotiana tabacum (Common tobacco)			Aspartyl protease; Endonuclease; Hydrolase; Metal-binding; Nuclease; Nucleotidyltransferase; Protease; RNA-directed DNA polymerase; Transferase; Transposable element; Zinc; Zinc-finger
SRR346604_TR13798_c0_g2_i1len=811	SUI1_ORYSJ	G:560-222,H:1-115	92.17%ID	E:4e-70	Protein translation factor SUI1 homolog	PF01253.19*SUI1*Translation initiation factor SUI1*28-102*E:5.4e-26	0,04	0,467	0,02	0,537	0	1,442	0	1,329	0	-1,392 SUI1_ORYSJ	Protein translation factor SUI1 homolog (Protein GOS2) (Protein eIF1) (Translation initiation factor 1)	GOS2 Os07g0529800 LOC_Os07g34589	Oryza sativa subsp. japonica (Rice)			Complete proteome; Initiation factor; Protein biosynthesis; Reference proteome; Translation regulation
SRR346604_TR17589_c0_g1_i1len=1951	WRKY7_ARATH	G:1553-468,H:1-345	48.57%ID	E:1e-90	Probable WRKY transcription factor 7	PF10533.6*Plant_zn_clust*Plant zinc cluster domain*237-286*E:1.2e-21 PF08031.9*BBE*Berberine and berberine like*371-428*E:2.4e-22	1	0,035	0,707	0,36	0	1,897	0	0,74	0,249	2,35 WRKY7_ARATH	Probable WRKY transcription factor 7 (WRKY DNA-binding protein 7)	WRKY7 At4g24240 T22A6.70	Arabidopsis thaliana (Mouse-ear cress)			Complete proteome; DNA-binding; Nucleus; Reference proteome; Transcription; Transcription regulation
SRR346604_TR17596_c1_g1_i2len=1658	PRSP1_SPIOL	G:590-1312,H:56-292	70.97%ID	E:9e-110	Ribosome-binding factor PSRP1, chloroplastic	PF02482.16*Ribosomal_S30AE*Sigma 54 modulation protein / S30EA ribosomal protein*85-181*E:2.2e-21*PF16321.2*Ribosom_S30AE_C*Sigma 54 modulation/S30EA ribosomal protein C terminus*223-277*E:4.4e-25	0,306	-0,506	0,6	-0,338	0	1,284	0	1,208	0,041	-0,902 PRSP1_SPIOL	Ribosome-binding factor PSRP1, chloroplastic (30S ribosomal protein 1) (CS-S5) (CS5) (Plastid-specific 30S ribosomal protein 1) (PSRP-1) (Ribosomal protein 1) (S22)	PSRP1 RPS22 RPS30	Spinacia oleracea (Spinach)			Chloroplast; Direct protein sequencing; Plastid; RNA-binding; Transit peptide; rRNA-binding
SRR346604_TR20006_c1_g1_i4len=1523	ACCH1_ARATH	G:1235-183,H:20-365	47.44%ID	E:2e-111	1-aminocyclopropane-1-carboxylate oxidase homolog 1	PF14226.3*DIOX_N*non-haem dioxygenase in morphine synthesis N-terminal*113-214*E:1.7e-18 PF03171.17*2OG-Fe(II)_Oxy*2OG-Fe(II) oxygenase superfamily*273-365*E:1.8e-22	0,221	0,606	0,009	1,066	0	2,878	0	2,777	1	0,691 ACCH1_ARATH	1-aminocyclopropane-1-carboxylate oxidase homolog 1	At1g06620 F12K11.24 F12K11.6	Arabidopsis thaliana (Mouse-ear cress)			Complete proteome; Iron; Metal-binding; Oxidoreductase; Reference proteome
SRR346604_TR21469_c0_g2_i1len=2115	SFR2_ORYSJ	G:93-934,H:342-633	71.58%ID	E:5e-149	Beta-glucosidase-like SFR2, chloroplastic	PF00232.15*Glyco_hydro_1*Glycosyl hydrolase family 1*18-226*E:1.1e-23	0,507	0,36	0,87	0,174	0	2,164	0	1,7	0,762	-1,614 SFR2_ORYSJ	Beta-glucosidase-like SFR2, chloroplastic (Beta-glucosidase 36) (Os11bglu36) (Protein SENSITIVE TO FREEZING 2) (OsSFR2)	CHLG1 Os11bglu36 Os11g0561500 LOC_Os11g45710 Os2_34793	Oryza sativa subsp. japonica (Rice)			Chloroplast; Complete proteome; Glycoprot

SRR924148_TR5782_c0_g1_i1_len=1026	NA	NA	NA	NA	NA	PF02466.16*Tim17*Tim17/Tim22/Tim23/Pmp24 family*35-127*E:1e-09	.	0	-6,81	0,277	-0,503	0	2,002	0	1,85	1	-0,055	.	.	.	.	.	.	.	.	.	.
SRR924148_TR6159_c1_g1_i1_len=2250	CBP22_HORVU	Q:1605-466,H:54-436	69.97%ID	E:0	Serine carboxypeptidase II-2	PF00450.19*Peptidase_S10*Serine carboxypeptidase*1-242*E:1.6e-57	0,783	0,202	0,016	1,299	0	2,879	0	2,944	1	0,681	CBP22_HORVU	Serine carboxypeptidase II-2 (EC 3.4.16.6) (CP-MII.2) [Cleaved into: Serine carboxypeptidase II-2 chain A; Serine carboxypeptidase II-2 chain B] (Fragment)	CXP:2-2	.	.	Hordeum vulgare (Barley)	.	.	.	Carbopeptidase; Direct protein sequencing; Disulfide bond; Glycoprotein; Hydrolase; Protease; Zymogen
SRR924148_TR6556_c0_g3_i1_len=1355	NA	NA	NA	NA	NA	PF04640.11*PLATZ*PLATZ transcription factor*113-188*E:9.1e-27	1	1,544	0,034	4,074	0	4,865	0	5,728	1	-0,144	.	.	.	.	.	.	.	.	.	.
SRR924148_TR12937_c0_g1_i1_len=1992	MASY_RICCO	Q:1910-249,H:13-667	88.65%ID	E:0	Malate synthase, glyoxysomal	PF10274.19*Malate_synthase*Malate synthase*41-571*E:1.1e-220	0,76	-0,437	0,402	1,113	0	2,784	0	3,572	0,732	-0,739	MASY_RICCO	Malate synthase, glyoxysomal (EC 2.3.3.9)	.	Ricinus communis (Castor bean)	PATHWAY: Carbohydrate metabolism; glyoxylate cycle; (S)-malate from isocitrate: step 2/2.	.	.	.	.	Glyoxylate bypass; Glyoxysome; Peroxisome; Transferase; Tricarboxylic acid cycle
SRR924148_TR17236_c0_g2_i3_len=1407	APX1_ARATH	Q:294-1043,H:1-250	85.6%ID	E:4e-145	L-ascorbate peroxidase 1, cytosolic	PF00141.20*peroxidase*Peroxidase*22-22*E:4.7e-49	0,986	0,007	0,005	0,638	.	1,123	0	1,015	0	-1,554	APX1_ARATH	L-ascorbate peroxidase 1, cytosolic (AP) (AtAPx01) (EC 1.11.1.11)	APX1 At1g07890 F24B9.2	Arabidopsis thaliana (Mouse-ear cress)	.	.	.	.	.	Alternative splicing; Calcium; Complete proteome; Cytoplasm; Direct protein sequencing; Heme; Hydrogen peroxide; Iron; Metal-binding; Oxidoreductase; Peroxidase; Phosphoprotein; Potassium; Reference proteome
SRR924148_TR20364_c1_g4_i6_len=4616	GATLA_ARATH	Q:866-1717,H:37-317	65.14%ID	E:1e-111	Probable galacturonosyltransferase-like 10	PF01501.17*Glyco_transf_8*Glycosyl transferase family 8*70-301*E:5.8e-46	1	0,434	0,004	2,671	0	2,967	0	3,488	1	-0,191	GATLA_ARATH	Probable galacturonosyltransferase-like 10 (EC 2.4.1.-) (Galactinol synthase 8) (AtGolS8) (GolS-8)	GATL10 GOLS8 At3g28340 MZF16.17	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Glycan metabolism; pectin biosynthesis.	.	.	.	.	Cell wall biogenesis/degradation; Complete proteome; Glycoprotein; Glycosyltransferase; Golgi apparatus; Membrane; Reference proteome; Signal-anchor; Transferase; Transmembrane; Transmembrane helix
SRR924148_TR20791_c0_g2_i1_len=878	NA	NA	NA	NA	NA	.	0,941	-0,03	0,302	0,358	0	1,664	0	1,562	1	0,082	.	.	.	.	.	.	.	.	.	.	.
SRR924148_TR28513_c0_g1_i1_len=780	NA	NA	NA	NA	NA	.	1	0,006	0,537	0,157	0	1,066	0,001	0,901	0,383	-0,252	.	.	.	.	.	.	.	.	.	.	.
SRR924148_TR30094_c0_g4_i1_len=1108	NA	NA	NA	NA	NA	.	0,228	1,015	0,043	3,051	0	3,439	0	3,452	1	0,322	.	.	.	.	.	.	.	.	.	.	.
SRR924148_TR32919_c1_g1_i1_len=1921	WRK11_ARATH	Q:1051-1308,H:224-309	83.72%ID	E:2e-43	Probable WRKY transcription factor 11	.	0,729	0,276	0,822	0,396	0	2,048	0	2,696	0,895	0,042	WRK11_ARATH	Probable WRKY transcription factor 11 (WRKY DNA-binding protein 11)	WRKY11 At4g31550 F3L17.120	Arabidopsis thaliana (Mouse-ear cress)	.	.	.	.	.	Alternative splicing; Complete proteome; DNA-binding; Nucleus; Reference proteome; Transcription; Transcription regulation
SRR924148_TR35978_c0_g1_i2_len=968	NA	NA	NA	NA	NA	.	1	3,267	0,629	1,626	0	3,425	0,001	3,327	1	-0,022	.	.	.	.	.	.	.	.	.	.	.

MsIntact24h

Transcript (CDF97)	Uniprot homolog	BLASTX Position	BLASTX %Identity	BLASTX evalue	Uniprot descr	Pfam	PValue_Ms6h	logFC_Ms6h	PValue_Ms8h	logFC_Ms8h	PValue_MsDamaged24h	logFC_MsDamaged24h	PValue_MsIntact24h	logFC_MsIntact24h	PValue_Ms1wk	logFC_Ms1wk	Entry.name	Protein names	Gene names	Organism	Pathway	Keywords
SRR114633_TR1121_c0_g1_i1_len=1878	PP1_ORYSJ	Q:361-1263,H:15-316	89.74%ID	E:0	Serine/threonine-protein phosphatase PP1	PF16891.2*STPPase_N*Serine/threonine protein phosphatase N-terminal domain*6-52*E:1.4e-22 PF00149.25*Metallopho*Calcineurin-like phosphoesterase*54-245*E:2e-40	0,87	0,08	0,041	0,692	0	2,044	0	1,287	0	1,577	0,931	-0,07	PP1_ORYSJ	Serine/threonine-protein phosphatase PP1 (EC 3.1.3.16)	Os03g0268000 LOC_Os03g16110 OJ1364E02.17 OJA1364E02.7	Oryza sativa subsp. japonica (Rice)	.	.	.	Complete proteome; Hydrolase; Manganese; Metal-binding; Protein phosphatase; Reference proteome
SRR114633_TR3195_c0_g1_i1_len=3680	XPO2_ARATH	Q:232-3087,H:1-950	70.29%ID	E:0	Exportin-2	PF03810.16*IBN_N*Importin-beta N-terminal domain*29-108*E:2.3e-13 PF08506.7*Cse1*Cse1*167-536*E:3.8e-139 PF03378.12*CAS_CSE1*CAS/CSE protein, C-terminus*537-964*E:1.2e-152	0,312	-0,572	0,017	1,373	0	0,08	1,232	0,001	1,99	1	0,421	XPO2_ARATH	Exportin-2 (Exp2) (Cellular apoptosis susceptibility protein homolog) (Importin-alpha re-exporter)	CAS At2g46520 F11C10 F13A10.5	Arabidopsis thaliana (Mouse-ear cress)	.	.	.	.	Complete proteome; Cytoplasm; Nucleus; Protein transport; Reference proteome
SRR114633_TR11716_c0_g2_i1_len=1771	PAP3_BRACM	Q:137-506,H:8-359	63.79%ID	E:2e-115	Plastid lipid-associated protein 3, chloroplastic	PF04755.9*PAP_fibrillin*PAP_fibrillin*153-368*E:1.5e-67	0,897	0,041	0,177	0,405	0	0,904	0	0,988	0	1,234	0,317	0,374	PAP3_BRACM	Plastid lipid-associated protein 3, chloroplastic	PAP3	Brassica campestris (Field mustard)	.	.	.	Chloroplast; Plastid; Transit peptide
SRR114633_TR14448_c0_g1_i2_len=860	GSTFB_ARATH	Q:103-750,H:1-211	53.24%ID	E:1e-77	Glutathione S-transferase F11	PF02798.17*GST_N*Glutathione S-transferase, N-terminal domain*2-75*E:1.6e-17 PF13409.3*GST_N_2*Glutathione S-transferase, N-terminal domain*13-75*E:1.3e-07 PF13417.3*GST_N_3*Glutathione S-transferase, N-terminal domain*15-80*E:8.1e-11 PF00043.22*GST_C*Glutathione S-transferase, C-terminal domain*115-208*E:7.5e-12 PF13410.3*GST_C_2*Glutathione S-transferase, C-terminal domain*133-189*E:1.1e-06	1	0	0,254	4,716	0,066	5,392	0	6,783	1	-1,579	GSTFB_ARATH	Glutathione S-transferase F11 (AtGSTF11) (EC 2.5.1.18) (AtGSTF6) (GST class-phi) (GST class-phi member 11)	GSTF11 GSTF6 At3g03190 T17B22.12	Arabidopsis thaliana (Mouse-ear cress)	.	.	.	Complete proteome; Cytoplasm; Detoxification; Reference proteome; Transferase
SRR114633_TR15197_c0_g2_i1_len=2404	ASPG1_ARATH	Q:1342-188,H:106-500	37.93%ID	E:5e-70	Protein ASPARTIC PROTEASE IN GUARD CELL 1	PF00026.20*Asp*Eukaryotic aspartyl protease*17-513*E:4.2e-23 PF14543.3*TAXI_N*Xylanase inhibitor N-terminal*18-347*E:1.1e-53 PF14541.3*TAXI_C*Xylanase inhibitor C-terminal*367-513*E:2.5e-34	1	-0,005	0,043	-0,64	0,002	1,142	0	1,363	0,5	-0,642	ASPG1_ARATH	Protein ASPARTIC PROTEASE IN GUARD CELL 1 (AtASPG1) (EC 3.4.23.-)	ASPG1 At3g18490 MYF24.22	Arabidopsis thaliana (Mouse-ear cress)	.	.	.	Aspartyl protease; Complete proteome; DNA-binding; Disulfide bond; Endoplasmic reticulum; Hydrolase; Protease; Reference proteome; Signal
SRR114633_TR19956_c0_g2_i1_len=2208	TAL_SHEAM	Q:1923-949,H:5-312	35.47%ID	E:1e-46	Transaldolase (ECO:0000255|HAMAP-Rule:MF_00492)	PF00923.16*Transaldolase*Transaldolase*79-386*E:4.2e-49	0,741	0,119	0,381	0,3	0,012	1,103	0	1,457	0,502	2,638	TAL_SHEAM	Transaldolase (EC 2.2.1.2)	tal Sama_0913	Shewanella amazonensis (strain ATCC BAA-1098 / SB2B)	PATHWAY: Carbohydrate degradation; pentose phosphate pathway; D-glyceraldehyde 3-phosphate and beta-D-fructose 6-phosphate from D-ribose 5-phosphate and D-xylulose 5-phosphate (non-oxidative stage): step 2/3. (ECO:0000255|HAMAP-Rule:MF_00492)	Complete proteome; Cytoplasm; Pentose shunt; Reference proteome; Schiff base; Transferase
SRR114633_TR22423_c0_g1_i1_len=2171	GSHB_SOLLC	Q:302-1825,H:42-546	74.21%ID	E:0	Glutathione synthetase, chloroplastic	PF03917.14*GSH_synth_ATP*Eukaryotic glutathione synthase, ATP binding domain*103-568*E:4.1e-139 PF03199.12*GSH_synthase*Eukaryotic glutathione synthase*298-397*E:9.5e-35	0,683	0,292	0,233	0,739	0	0,858	0	1,337	0,849	0,077	GSHB_SOLLC	Glutathione synthetase, chloroplastic (GSH synthetase) (GSH-S) (Glutathione synthase) (EC 6.3.2.3)	GSH2	Solanum lycopersicum (Tomato) (Lycopersicon esculentum)	PATHWAY: Sulfur metabolism; glutathione biosynthesis; glutathione from L-cysteine and L-glutamate: step 2/2.	ATP-binding; Chloroplast; Complete proteome; Glutathione biosynthesis; Ligase; Magnesium; Metal-binding; Nucleotide-binding; Plastid; Reference proteome; Transit peptide
SRR114633_TR25443_c0_g1_i1_len=2147	SCL15_ARATH	Q:1680-235,H:25-486	46.75%ID	E:4e-124	Scarecrow-like protein 15	PF03514.11*GRAS*GRAS family domain family*210-571*E:1.5e-89	1	0,443	0,088	1,537	0	1,497	0	2,025	1	0,251	SCL15_ARATH	Scarecrow-like protein 15 (AtSCL15) (GRAS family protein 25) (AtGRAS-25)	SCL15 At4g36710 C7A10.650	Arabidopsis thaliana (Mouse-ear cress)	.	.	.	.	Complete proteome; Nucleus; Reference proteome; Transcription; Transcription regulation
SRR114634_TR2142_c0_g1_i1_len=1943	BCS1B_DICDI	Q:597-1460,H:181-457	33.45%ID	E:9e-31	Probable mitochondrial chaperone BCS1-B	PF00004.26*AAA*ATPase family associated with various cellular activities (AAA)*35-190*E:1.8e-14 PF05496.9*RuvB_N*Holliday junction DNA helicase ruvB N-terminus*35-91*E:0.00014	0,049	1,413	0,014	1,823	0,004	1,401	0	1,793	1	0,411	BCS1B_DICDI	Probable mitochondrial chaperone BCS1-B (BCS1-like protein 2)	bcs1b DDB_G0291910	Dictyostelium discoideum (Slime mold)	.	.	.	.	ATP-binding; Chaperone; Complete proteome; Membrane; Mitochondrion; Mitochondrion inner membrane; Nucleotide-binding; Reference proteome; Transmembrane; Transmembrane helix
SRR114634_TR17530_c0_g1_i4_len=1302	GSHB_SOLLC	Q:1187-123,H:192-546	77.46%ID	E:0	Glutathione synthetase, chloroplastic	PF03917.14*GSH_synth_ATP*Eukaryotic glutathione synthase, ATP binding domain*3-357*E:8.2e-105 PF03199.12*GSH_synthase*Eukaryotic glutathione synthase*91-190*E:4.3e-35	0,848	0,182	0,854	-0,282	0,001	1,395	0	1,499	1	-0,55	GSHB_SOLLC	Glutathione synthetase, chloroplastic (GSH synthetase) (GSH-S) (Glutathione synthase) (EC 6.3.2.3)	GSH2	Solanum lycopersicum (Tomato) (Lycopersicon esculentum)	PATHWAY: Sulfur metabolism; glutathione biosynthesis; glutathione from L-cysteine and L-glutamate: step 2/2.	ATP-binding; Chloroplast; Complete proteome; Glutathione biosynthesis; Ligase; Magnesium; Metal-binding; Nucleotide-binding; Plastid; Reference proteome; Transit peptide
SRR114634_TR18582_c0_g1_i1_len=930	NA	NA	NA	NA	NA	.	0,132	1,349	0,003	2,409	0,014	3,479	0	4,404	1	-0,604	.	.	.	.	.	.	.	.	.	.	.
SRR114634_TR21850_c0_g2_i1_len=1765	DGK5_ARATH	Q:1682-726,H:1-320	74.92%ID	E:0	Diacylglycerol kinase 5	PF00781.21*DAGK_cat*Diacylglycerol kinase catalytic domain*65-192*E:7.6e-26 PF00609.16*DAGK_acc*Diacylglycerol kinase accessory domain*258-308*E:7.1e-14	0,807	0,188	0,115	0,754	0,017	1,196	0	1,922	0,004	DGK5_ARATH	Diacylglycerol kinase 5 (AtDGK5) (DAG kinase 5) (EC 2.7.1.107) (Diglyceride kinase 5) (DGK 5)	DGK5 At2g20900 F5H14.13	Arabidopsis thaliana (Mouse-ear cress)	.	.	.	.	ATP-binding; Alternative splicing; Complete proteome; Kinase; Nucleotide-binding; Plant defense; Reference proteome; Stress response; Transferase
SRR114634_TR37303_c0_g2_i4_len=4925	LOX31_SOLTU	Q:2459-4924,H:1-826	79.21%ID	E:0	Linoleate 13S-lipoxygenase 3-1, chloroplastic	PF12166.5*Pfam2case_Serine aminopeptidase, S33*68-184*E:1e-08 PF01477.20*PLAT*PLAT/LH2 domain*592-676*E:1.4e-12 PF00330.15*Lipoxygenase*Lipoxygenase*689-1285*E:9.5e-273 PF08240.9*ADH_N*Alcohol dehydrogenase GroES-like domain*39-152*E:1.2e-27 PF00107.23*ADH_zinc_N*Zinc-binding dehydrogenase*195-317*E:2e-18	0,112	1,27	0,001	2,401	0,001	6,457	0	7,338	1	0	LOX31_SOLTU	Linoleate 13S-lipoxygenase 3-1, chloroplastic (EC 1.13.11.12)	LOX3.1 LOX-H3	Solanum tuberosum (Potato)	PATHWAY: Lipid metabolism; oxylipin biosynthesis. (ECO:0000255|PROSITE-ProRule:PRU00726).	Chloroplast; Complete proteome; Dioxygenase; Fatty acid biosynthesis; Fatty acid metabolism; Iron; Lipid biosynthesis; Lipid metabolism; Metal-binding; Oxidoreductase; Oxylipin biosynthesis; Plastid; Reference proteome; Thylakoid; Transit peptide
SRR122236_TR4154_c0_g1_i1_len=1464	MTDH_FRAAN	Q:187-1182,H:4-397	70.34%ID	E:2e-159	Probable mannitol dehydrogenase	PF05678.8*AvrRp1-cleavage*Cleavage site for pathogenic type III effector avirulence factor AvrRp1*199-235*E:2.6e-22	0,009	6,062	0,349	0,395	0,066	5,245	0	7,238	0	-9,752	MTDH_FRAAN	Probable mannitol dehydrogenase (EC 1.1.1.255) (NAD-dependent mannitol dehydrogenase)	CAD	Fragaria ananassa (Strawberry)	.	.	.	.	.	Metal-binding; NAD; Oxidoreductase; Zinc
SRR122236_TR5111_c0_g1_i1_len=699	GRXC9_ARATH	Q:607-221,H:1-137	54.2%ID	E:8e-40	Glutaredoxin-C9	PF00462.21*Glutaredoxin*Glutaredoxin*47-115*E:2.5e-09	0,381	2,207	0,003	3,114	0,004	2,199	0	3,715	1	-3,216	GRXC9_ARATH	Glutaredoxin-C9 (AtGrxC9) (Protein ROXY 19)	GRXC9 GRX480 ROXY19 At1g28480 F3M18.8	Arabidopsis thaliana (Mouse-ear cress)	.	.	.	.	Complete proteome; Cytoplasm; Disulfide bond; Electron transport; Nucleus; Redox-active center; Reference proteome; Transport
SRR122237_TR10367_c0_g1_i1_len=958	NA	NA	NA	NA	NA	PF02519.11*Auxin_inducible*Auxin responsive protein*17-115*E:1.1e-15	0,502	-1,643	0,254	3,942	0,017	5,014	0	6,797	0,059	-1,799	.	.	.	.	.	.	.	.	.	.	.
SRR122238_TR1035_c0_g1_i6_len=2350	SLK2_ARATH	Q:391-1254,H:309-693	73.61%ID	E:7e-150	Probable transcriptional regulator SLK2	PF01803.13*LIM_bind*LIM-domain binding protein*9-204*E:7.6e-46	0,163	0,719	0,407	0,435	0,003	1,371	0	1,585	1	0,073	SLK2_ARATH	Probable transcriptional regulator SLK2 (AtSLK2) (Protein SEUSS-like 2)	SLK2 At5g62090 MTG10.12	Arabidopsis thaliana (Mouse-ear cress)	.	.	.	.	Complete proteome; Developmental protein; Differentiation; Flowering; Nucleus; Reference proteome; Transcription; Transcription regulation
SRR122238_TR2305_c0_g1_i1_len=1328	NA	NA	NA	NA	NA	PF14009.3*DUF4228*Domain of unknown function (DUF4228)*1-171*E:5e-35	0,461	0,932	0,003	3,56	0,023	1,634	0	2,487	1	0,111	.	.	.	.	.	.	.	.	.	.	.
SRR122238_TR8025_c0_g1_i1_len=977	NA	NA	NA	NA	NA	PF04520.10*Senescence_reg*Senescence regulator*81-204*E:9.9e-37	0,62	0,53	0,01	1,882	0,006	2,547	0	3,33	0,811	0,233	.	.	.	.	.	.	.	.	.	.	.
SRR122238_TR11364_c1_g2_i2_len=1783	BGLU45_ARATH	Q:778-1527,H:259-510	53.36%ID	E:2e-153	Beta-glucosidase 45	PF00232.15*Glyco_hydro_1*Glycosyl hydrolase family 1*48-228*E:2e-78	0,917	0,052	0,008	1,938	0,006	2,385	0,001	2,785	0,262	0,464	BGLU45_ARATH	Beta-glucosidase 45 (AtBGLU45) (EC 3.2.1.21)	BGLU45 At1g61810 F8K4.2 T13M11.19	Arabidopsis thaliana (Mouse-ear cress)	.	.	.	.	Alternative splicing; Complete proteome; Disulfide bond; Glycoprotein; Glycosidase; Hydrolase; Reference proteome; Signal
SRR122238_TR11402_c0_g1_i1_len=912	MES10_ARATH	Q:850-129,H:22-275	50.79%ID	E:1e-91	Methylesterase 10	PF12146.9*Pfam2case_Serine aminopeptidase, S33*5-137*E:1.5e-09 PF00561.17*Abhydrolase_1*alpha/beta hydrolase fold*2-116*E:6.7e-14 PF12697.4*Abhydrolase_6*Alpha/beta hydrolase family*9-248*E:8.4e-13	1	2,089	0,129	2,915	0,034	4,277	0	5,425	1	-2,167	MES10_ARATH	Methylesterase 10 (AtMES10) (EC 3.1.1.-)	MES10 At3g50440 T20E23_40	Arabidopsis thaliana (Mouse-ear cress)	.	.	.	.	Complete proteome; Hydrolase; Reference proteome
SRR122238_TR11783_c0_g1_i1_len=1725	MIOX_ORYSJ	Q:531-1361,H:32-308	71.84%ID	E:4e-144	Probable inositol oxygenase	PF05153.12*MIOX*Myo-inositol oxygenase*101-350*E:2.1e-124	0,017	1,205	0,132	1,394	0	2,086	0	3,36	0,692	0,956	MIOX_ORYSJ	Probable inositol oxygenase (EC 1.13.99.1) (Myo-inositol oxygenase) (MI oxygenase)	Os06g0561000 LOC_Os06g36560 P0456F09.5 P0528E12.30	Oryza sativa subsp. japonica (Rice)	PATHWAY: Polyol metabolism; myo-inositol degradation into D-glucuronate; D-glucuronate from myo-inositol: step 1/1.	Ascorbate biosynthesis; Complete proteome; Cytoplasm; Iron; Metal-binding; Oxidoreductase; Reference proteome
SRR122238_TR15254_c0_g3_i4_len=908	APX3_ARATH	Q:875-351,H:111-287	78.53%ID	E:5e-74	L-ascorbate peroxidase 3, peroxisomal	PF00141.20*peroxidase*Peroxidase*28-125*E:3.8e-20	0,506	-0,199	0,046	-0,549	0,007	0,723	0,001	0,884	0,009	-5,96	APX3_ARATH	L-ascorbate peroxidase 3, peroxisomal (AtAPx03) (EC 1.11.1.11)	APX3 APX APXIII At4g35000 M4E13.60	Arabidopsis thaliana (Mouse-ear cress)	.	.	.	.	Acetylation; Calcium; Complete proteome; Glycosylation; Heme; Hydrogen peroxide; Iron; Membrane; Metal-binding; Oxidoreductase; Peroxidase; Peroxisome; Potassium; Reference proteome; Transit peptide; Transmembrane; Transmembrane helix
SRR122238_TR16864_c0_g1_i2_len=2560	KSG1_ARATH	Q:272-1492,H:2-405	81.42%ID	E:0	Shaggy-related protein kinase alpha	PF00069.22*Pkinase*Protein kinase domain*73-357*E:3e-64 PF07714.14*Pkinase_Tyr*Protein tyrosine kinase*76-279*E:1.7e-24	0,865	0,211	0,021	1,59	0,003	2,041	0	2,344	0,739	-0,207	KSG1_ARATH	Shaggy-related protein kinase alpha (EC 2.7.11.1) (ASK-alpha)	ASK1 At5g26751 F2P16.21	Arabidopsis thaliana (Mouse-ear cress)	.	.	.	.	ATP-binding; Acetylation; Complete proteome; Kinase; Nucleotide-binding; Phosphoprotein; Reference proteome; Serine/threonine-protein kinase; Transferase
SRR122238_TR20547_c0_g2_i1_len=1209	NA	NA	NA	NA	NA	.	1	-0,379	0,129	4,962	0,034	3,883	0	5,488	1	-0,91	.	.	.	.	.	.	.	.	.	.	.
SRR122238_TR22324_c0_g1_i1_len=1347	FB237_ARATH	Q:1300-245,H:6-380	36.9%ID	E:8e-64	F-box protein At4g18380	PF00646.30*F-box*F-box domain*11-49*E:0.0099 PF12937.4*F-box-like*F-box-like*12-46*E:5.4e-08	0,502	2,312	0,132	3,233	0,034	4,753	0	5,798	1	-1,114	FB237_ARATH	F-box protein At4g18380	At4g18380 F28J12.40	Arabidopsis thaliana (Mouse-ear cress)	.	.	.	.	Complete proteome; Reference proteome
SRR122238_TR22745_c0_g1_i4_len=2323	MLO6_ARATH	Q:2152-344,H:1-583	60.59%ID	E:0	MLO-like protein 6	PF03094.12*Mlo*Mlo family*8-500*E:5.7e-250	0,44	0,748	0,663	0,397	0,035	1,295	0	2,206	0,299	-1,75	MLO6_ARATH	MLO-like protein 6 (AtMlo6)	MLO6 At1g61560 T25B24.9	Arabidopsis thaliana (Mouse-ear cress)	.	.	.	.	Alternative splicing; Calmodulin-binding; Complete proteome; Membrane; Pathogenesis-related protein; Plant defense; Reference proteome; Transmembrane; Transmembrane helix
SRR122238_TR23432_c0_g2_i1_len=878	NA	NA	NA	NA	NA	.	0,506	-0,179	0,218	-0,34	0,009	0,794	0	1,16	0,764	-0,103	.	.	.	.	.	.	.	.	.	.	.
SRR122238_TR3821_c0_g1_i1_len=1232	DNJ72_ARATH	Q:184-396,H:2-126	63.38%ID	E:2e-23	Chaperone protein dnaJ 72	PF00226.28*DnaJ*DnaJ domain*63-130*E:2e-24	0,409	0,431	0,378	0,473	0,002	1,297	0	1,51	1	0,023	DNJ72_ARATH	Chaperone protein dnaJ 72 (AtDjC72) (AtJ72)	ATJ72 C72 LCR51 At2g41000 T3K9.22	Arabidopsis thaliana (Mouse-ear cress)	.	.	.	.	Alternative splicing; Chaperone; Complete proteome; Membrane; Reference proteome; Transmembrane; Transmembrane helix
SRR122238_TR4501_c0_g3_i2_len=2188	PME3_PHAVU	Q:2089-335,H:1-578	57.55%ID	E:0	Pectinesterase 3	PF04043.12*PMEI*Plant invertase/pectin methylesterase inhibitor*74-229*E:1.6e-25 PF01095.16*Pectinesterase*Pectinesterase*281-574*E:1.9e-134	0,444	0,319	0,086	0,86	0,032	0,752	0	1,343	0,779	-0,121	PME3_PHAVU	Pectinesterase 3 (PE 3) (EC 3.1.1.11) (Pectin methylesterase 3)	MPE3	Phaseolus vulgaris (Kidney bean) (French bean)	PATHWAY: Glycan metabolism; pectin degradation; 2-dehydro-3-deoxy-D-gluconate from pectin: step 1/5.	Asparty l esterase; Cell wall; Cell wall biogenesis/degradation; Disulfide bond; Glycoprotein; Hydrolase; Secreted; Signal
SRR122238_TR4575_c1_g1_i4_len=3521	LOX31_SOLTU	Q:619-3204,H:114-914	77.64%ID	E:0	Linoleate 13S-lipoxygenase 3-1, chloroplastic	PF00305.16*Lipoxygenase*Lipoxygenase*1-2621*E:9.2e-100	1	2,176	0,254	4,593	0,009	3,945	0	4,699	1	0,608	LOX31_SOLTU	Linoleate 13S-lipoxygenase 3-1, chloroplastic (EC 1.13.11.12)	LOX3.1 LOX-H3	Solanum tuberosum (Potato)	PATHWAY: Lipid metabolism; oxylipin biosynthesis. (ECO:0000255|PROSITE-ProRule:PRU00726).	Chloroplast; Complete proteome; Dioxygenase; Fatty acid biosynthesis; Fatty acid metabolism; Iron; Lipid biosynthesis; Lipid metabolism; Metal-binding; Oxidoreductase; Oxylipin biosynthesis; Plastid; Reference proteome; Thylakoid; Transit peptide
SRR122238_TR4985_c0_g1_i1_len=1508	FPPS1_LUPAL	Q:1310-285,H:1-342	79.53%ID	E:0	Farnesyl pyrophosphate synthase 1	PF00348.14*polyprenyl_synt*Polyprenyl synthetase*33-296*E:2e-94	1	0,007	0,034	0,87	0,003	1,053	0	1,548	0,555	-0,271	FPPS1_LUPAL	Farnesyl pyrophosphate synthase 1 (FPP synthase 1) (FPS 1) (EC 2.5.1.10) ((2E,6E)-farnesyl diphosphate synthase 1) (Dimethylallyltranstransferase 1) (EC 2.5.1.1) (Farnesyl diphosphate synthase 1) (Geranyltranstransferase 1)	FPS1	Lupinus albus (White lupin) (Lupinus termis)	PATHWAY: Isoprenoid biosynthesis; farnesyl diphosphate biosynthesis; farnesyl diphosphate from geranyl diphosphate and isopentenyl diphosphate: step 1/1. PATHWAY: Isoprenoid biosynthesis; geranyl diphosphate biosynthesis; geranyl diphosphate from dimethylallyl diphosphate and isopentenyl diphosphate: step 1/1.	Cholesterol biosynthesis; Cholesterol metabolism; Cytoplasm; Isoprene biosynthesis; Lipid biosynthesis; Lipid metabolism; Magnesium; Metal-binding; Steroid biosynthesis; Steroid metabolism; Sterol biosynthesis; Sterol metabolism; Transferase
SRR122238_TR52070_c1_g5_i2_len=1384	EXPA1_ARATH	Q:155-898,H:1-283	84.4%ID	E:1e-114	Expansin-A1	PF03330.15*DPBB_1*Lytic transglycolase*60-145*E:3.7e-22 PF03211.13*Pollen_allerg_1*Pollen allergen*156-233*E:1.2e-30	0,3	0,329	0,024	0,601	0,175	0,548	0	1,761	0,545	-0,45	EXPA1_ARATH	Expansin-A1 (AtEXPA1) (Alpha-expansin-1) (AtEXP1) (AtEx1) (Ath-Exp Alpha-1.2)	EXPA1 EXP1 At1g69530 F10D13_18	Arabidopsis thaliana (Mouse-ear cress)	.	.	.	.	Alternative splicing; Cell wall; Cell wall biogenesis/degradation; Complete proteome; Disulfide bond; Membrane; Reference proteome; Secreted; Signal
SRR122238_TR60656_c1_g1_i1_len=1153	ERD2_PETHY	Q:74-130,H:1-215	92.09%ID	E:5e-133	ER lumen protein-retaining receptor	PF00810.15*ER_lumen_recept*ER lumen protein retaining receptor*28-171*E:2.2e-51	0,816	-0,11	0,001	1,367	0,045	0,861	0	1,404	1	-0,563	ERD2_PETHY	ER lumen protein-retaining receptor (HDEL receptor) (PGP169-12)	ERD2	Petunia hybrida (Petunia)	.	.	.	.	ER-Golgi transport; Endoplasmic reticulum; Membrane; Protein transport; Receptor; Transmembrane; Transmembrane helix; Transport
SRR122238_TR62934_c0_g1_i2_len=652	RPD6A_ARATH	Q:495-259,H:61-139	94.94%ID	E:1e-46	DNA-directed RNA polymerases II, IV and V subunit 6A	PF01192.19*RNA_pol_Rpb6*RNA polymerase Rpb6*53-104*E:6.3e-17	0	-2,234	0,014	-1,012	1	0	0	6,919	1	-1,817	RPD6A_ARATH	DNA-directed RNA polymerases II, IV and V subunit 6A (RNA polymerase Rpb6)	NRPB6A NRPD6A NRPE6A At5g15940 MSG15.2	Arabidopsis thaliana (Mouse-ear cress)	.	.	.	.	Complete proteome; DNA-directed RNA polymerase; Nucleus; Reference proteome; Transcription
SRR122238_TR69049_c2_g1_i3_len=1046	SUI11_ARATH	Q:270-608,H:1-113	90.27%ID	E:2e-68	Protein translation factor SUI1 homolog 1	PF01253.19*SUI1*Translation initiation factor SUI1*28-102*E:4.3e-26	0,672	-0,132	0,914	-0,056	0,005	0,985	0,001	1,148	1	0,009	SUI11_ARATH	Protein translation factor SUI1 homolog 1	At4g27130 F20D21.11 T24A18.80	Arabidopsis thaliana (Mouse-ear cress)	.	.	.	.	Acetylation; Complete proteome; Protein biosynthesis; Reference proteome; Translation; Translation regulation
SRR122238_TR77058_c1_g1_i6_len=612	F16P1_SPIOL	Q:368-844,H:51-342	65.98%ID	E:9e-32	Fructose-1,6-bisphosphatase, chloroplastic	PF00316.17*FBPase*Fructose-1-6-bisphosphatase, N-terminal domain*117-176*E:2.7e-12	0,001	-6,56	1	0	0,034	5,65	0	6,729	1	1,197	F16P1_SPIOL	Fructose-1,6-bisphosphatase, chloroplastic (FBPase) (EC 3.1.3.11) (D-fructose-1,6-bisphosphate 1-phosphotrylase)	.	Spinacia oleracea (Spinach)	PATHWAY: Carbohydrate biosynthesis; Calvin cycle.	Chloroplast; Complete proteome; Cytoplasm; Hydrolase; Magnesium; Manganese; Met

		293/F:1/20			Chloroplast																							
SRR342017_TR31846_c0_g2_i1_len=776	NA	NA	NA	NA	NA	(Acyl carrier protein) reductase*88-322*E:4.3e-67																						
SRR342019_TR4570_c1_g1_i1_len=1375	CAP13_ARATH	Q:121-1230;H:1-332	42.47%ID	E:3e-94	Putative clathrin assembly protein At1g25240	PF07651.13*ANTH*ANTH domain*33-293*E:2.4e-49	1	0.574	0.239	1.352	0.017	2.376	0	3.117	1	-0.021 CAP13_ARATH	Putative clathrin assembly protein At1g25240	At1g25240 F4F7.37	Arabidopsis thaliana (Mouse-ear cress)			
SRR342019_TR4692_c0_g1_i2_len=2781	MFPA_CUCSA	Q:166-2298;H:4-714	80.59%ID	E:0	Glycosyosomal fatty acid beta-oxidation multifunctional protein MFP-a	PF00378.17*ECH_1*Enoyl-CoA hydratase/isomerase*68-263*E:8.3e-06 PF16113.2*ECH_2*Enoyl-CoA hydratase/isomerase family*60-246*E:4e-24 PF02737.15*3HCDH_N*3-hydroxyacyl-CoA dehydrogenase, NAD binding domain*366-544*E:1.3e-60 PF00725.19*3HCDH*3-hydroxyacyl-CoA dehydrogenase, C-terminal domain*547-640*E:1.1e-20	1	-0.423	0.118	2.113	0.009	3.854	0	4.531	1	0.451 MFPA_CUCSA	Glycosyosomal fatty acid beta-oxidation multifunctional protein MFP-a [Includes: Enoyl-CoA hydratase/3-2/trans-enoyl-CoA isomerase/3-hydroxybutyryl-CoA epimerase (EC 4.2.1.17) (EC 5.1.2.3) (EC 5.3.3.8); 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35)]	Cucumis sativus (Cucumber)	PATHWAY: Lipid metabolism; fatty acid beta-oxidation.			
SRR342019_TR10250_c0_g1_i4_len=2875	NA	NA	NA	NA	NA	NA	0.5	0.691	0.299	1.413	0.004	3.328	0	3.982	0.461	-1.111	.	.	.			
SRR342019_TR10559_c0_g4_i2_len=2559	TT12_ARATH	Q:958-2340;H:45-605	39.83%ID	E:6e-93	.	PF01554.15*MatE*MatE*51-211*E:6.5e-29 PF01554.15*MatE*MatE*274-433*E:6.7e-28	0.798	0.287	1	0.063	0.002	1.561	0	2.129	1	-0.078 DTX41_ARATH	Protein DETOXIFICATION 41 (AtDTX41) (Multidrug and toxic compound extrusion protein 41) (MATE protein 41) (Protein TANNIN-DEFICIENT SEED 3) (Protein TRANSPARENT TESTA 12)	DTX41 TDS3 TT12 At3g59030 F17J16_60	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Secondary metabolite biosynthesis; flavonoid biosynthesis.			
SRR342019_TR10890_c5_g1_i2_len=1480	PDCB3_ARATH	Q:1027-827;H:20-86	71.64%ID	E:4e-30	PLASMODESMATA CALLOSE-BINDING PROTEIN 3	PF07983.10*X8*X8 domain*21-92*E:1.8e-19	0.122	-0.411	0.541	0.2	0.001	1.113	0.001	1.17	0.732	-0.549 PDCB3_ARATH	PLASMODESMATA CALLOSE-BINDING PROTEIN 3 (AtPDCB3)	PDCB3 At1g18650 F25I16.1	Arabidopsis thaliana (Mouse-ear cress)			
SRR342019_TR18451_c0_g1_i2_len=1723	FAM10_ARATH	Q:1470-736;H:1-243	65.85%ID	E:6e-87	FAM10 family protein At4g22670	PF13181.3*TPR_8*Tetratricopeptide repeat*134-157*E:0.064 PF00515.25*TPR_1*Tetratricopeptide repeat*161-191*E:1.2e-04 PF13181.3*TPR_8*Tetratricopeptide repeat*161-191*E:0.0012 PF13432.3*TPR_16*Tetratricopeptide repeat*164-215*E:0.0048	0.223	-0.401	0.558	-0.233	0.002	1.022	0.001	1.125	1.5	-0.705 F10L_ARATH	FAM10 family protein At4g22670	At4g22670 T12H17.60	Arabidopsis thaliana (Mouse-ear cress)			
SRR342019_TR18877_c0_g1_i4_len=2587	AZG1_ARATH	Q:2519-837;H:10-567	77.9%ID	E:0	Adenine/guanine permease AZG1	PF00860.17*Xan_ur_permease*Permease family*141-545*E:2.9e-24	1	0.067	0.643	0.61	0.021	1.785	0.001	2.119	1	-0.174 AZG1_ARATH	Adenine/guanine permease AZG1 (AzgA-homolog protein) (Protein AZAGUANINE RESISTANT 1) (AtAzg1)	AZG1 At3g10960 F9F8.22	Arabidopsis thaliana (Mouse-ear cress)			
SRR342019_TR31828_c0_g1_i2_len=1317	SDR1_PICAB	Q:926-162;H:17-271	60.55%ID	E:6e-102	Short-chain type dehydrogenase/reductase	PF00106.22*adh_short*short chain dehydrogenase*19-213*E:7.6e-42 PF08659.7*KR*KR domain*21-191*E:7.3e-11 PF13561.3*adh_short_C2*Enoyl-(Acyl carrier protein) reductase*24-261*E:1.1e-08	0.528	0.327	0.005	1.116	0.002	1.563	0	1.874	1	0.381 SDR1_PICAB	Short-chain type dehydrogenase/reductase (EC 1.-.-.-)	Picea abies (Norway spruce) (Picea excelsa)	Arabidopsis thaliana (Mouse-ear cress)			
SRR342019_TR35444_c0_g2_i1_len=1748	NA	NA	NA	NA	NA	.	0.505	-0.491	0.679	-0.461	0.049	1.34	0.001	1.967	0.319	0.9 .	.	.	.			
SRR342019_TR38237_c0_g1_i1_len=515	NA	NA	NA	NA	NA	.	1	0.671	0.017	4.02	0.017	4.423	0	5.787	0.629	1.99 .	.	.	.			
SRR342019_TR39237_c0_g2_i1_len=2418	NA	NA	NA	NA	NA	PF00168.27*C2*C2 domain*16-68*E:5.7e-06 PF00168.27*C2*C2 domain*140-246*E:2.7e-17 PF00168.27*C2*C2 domain*302-373*E:5.1e-16	1	0.345	0.008	2.962	0.002	2.017	0	2.961	1	1.988 .	.	.	.			
SRR342022_TR667_c1_g1_i1_len=2615	NA	NA	NA	NA	NA	.	0.317	-0.498	1	0.037	0.029	1.21	0	1.822	0.77	0.26 .	.	.	.			
SRR342022_TR985_c10_g1_i1_len=1176	MYC2_ARATH	Q:256-849;H:64-253	37.37%ID	E:3e-40	Transcription factor MYC2	PF14215.3*bHLH-MYC_N*bHLH-MYC and R2R3-MYB transcription factors N-terminal*16-208*E:2.9e-52	0.037	0.927	0.01	1.124	0.002	1.014	0	1.668	MYC2_ARATH	Transcription factor MYC2 (AtMYC2) (Basic helix-loop-helix protein 6) (AtbHLH6) (bHLH 6) (Protein JASMONATE INSENSITIVE 1) (Ft-homologous Arabidopsis protein 1) (RAP-1) (Transcription factor EN 38) (Z-box binding factor 1 protein) (bHLH transcription factor bHLH006) (rs22BP1)	MYC2 BHLH6 EN38 JAI1 JIN1 RAP1 RD22BP1 ZBF1 At3g20440 F6N18.4	Arabidopsis thaliana (Mouse-ear cress)			
SRR342022_TR3295_c2_g3_i1_len=3147	BGAL_SOLLC	Q:2717-219;H:3-835	83.43%ID	E:0	Beta-galactosidase	PF01301.16*Glyco_hydro_35*Glycosyl hydrolases family 35*36-341*E:6.2e-118 PF02449.12*Glyco_hydro_42*Beta-galactosidase*57-205*E:6.2e-10 PF00229.15*Gal_Lectin*Galactose binding lectin domain*764-840*E:1.4e-20	0.52	0.428	0.239	1.554	0.005	1.527	0.001	1.797	0.629	0.981 BGAL_SOLLC	Beta-galactosidase (EC 3.2.1.23) (Acid beta-galactosidase) (Lactase) (Exo-(1->4)-beta-D-galactanase)	Solanum lycopersicum (Tomato) (Lycopersicon esculentum)	Arabidopsis thaliana (Mouse-ear cress)			
SRR342022_TR10678_c0_g1_i1_len=1206	NA	NA	NA	NA	NA	.	0.502	4.179	1	0	0.009	6.028	0	6.795	1	-0.142 .	.	.	.			
SRR342022_TR11701_c0_g1_i1_len=1560	NA	NA	NA	NA	NA	.	0.461	1.501	1	-0.394	0.005	5.352	0	5.94	1	0.044 .	.	.	.			
SRR342022_TR12749_c1_g9_i1_len=2782	SPEA_BACSU	Q:221-1231;H:148-474	34.41%ID	E:2e-43	Arginine decarboxylase	PF05889.10*SepSecS*O-phosphoseryl-tRNA(Sec) selenium transferase, SepSecS*6.77*E:0.00021 PF01276.17*OKR_DC_1*Ornithine decarboxylase, major domain*11-218*E:2.3e-27 PF03711.12*OKR_DC_1_C*Ornithine decarboxylase, C-terminal domain*259-321*E:6.7e-09	1	1.051	0.129	5.144	0.017	5.755	0	7.079	1	2.41 SPEA_BACSU	Arginine decarboxylase (EC 4.1.1.19)	speA cad BSU14630	Bacillus subtilis (strain 168)	PATHWAY: Amine and polyamine biosynthesis; agmatine biosynthesis; agmatine from L-arginine: step 1/1.		
SRR342022_TR13042_c0_g2_i1_len=1816	PP1145_ARATH	Q:77-178;3,H:31-603	59.93%ID	E:0	Pentatricopeptide repeat-containing protein At2g02980, chloroplastic (ECO:0000305)	PF13812.3*PPR_3*Pentatricopeptide repeat domain*188-228*E:0.011 PF13041.3*PPR_2*PPR repeat family*189-236*E:1.2e-10 PF01535.17*PPR*PPR repeat*192-220*E:6.7e-07 PF01535.17*PPR*PPR repeat*265-328*E:0.00052 PF01535.17*PPR*PPR repeat*294-321*E:3.1e-05 PF01535.17*PPR*PPR repeat*437-460*E:0.014 PF14432.3*DYW_deaminase*DYW family of nucleic acid deaminases*464-584*E:4.8e-28	1	-0.04	1	0.449	0.005	3.941	0	6.025	1	0.285 PP145_ARATH	Pentatricopeptide repeat-containing protein At2g02980, chloroplastic (Protein ORGANELLE TRANSCRIPT PROCESSING 85)	PCMP-H26 OTP85 At2g02980 T1/M13.15	Arabidopsis thaliana (Mouse-ear cress)			
SRR342022_TR15143_c0_g1_i2_len=1152	VPS25_ARATH	Q:344-856;H:7-179	75.14%ID	E:6e-92	Vacuolar protein sorting-associated protein 25	.	0.864	0.096	0.088	0.597	0.014	1.184	0.001	1.511	0.866	0.065 VPS25_ARATH	Vacuolar protein sorting-associated protein 25 (AtVPS25) (ESCRT-II complex subunit VPS25)	VPS25 At4g19003 F13C5	Arabidopsis thaliana (Mouse-ear cress)			
SRR342022_TR18873_c0_g3_i2_len=1092	NA	NA	NA	NA	NA	.	0.075	0.828	0.069	0.491	0.016	0.716	0	1.356	0.842	0.137 .	.	.	.			
SRR342022_TR21147_c3_g1_i6_len=1877	IPC52_ARATH	Q:996-1525;H:1-305	77.74%ID	E:3e-176	Phosphatidylinositol ceramide inositolphosphotransferase 2	PF14360.3*PAP2_C*PAP2 superfamily C-terminal*172-240*E:1.3e-22	1	0.016	0.133	1.155	0.152	0.816	0.001	1.705	0.707	0.443 IPC52_ARATH	Phosphatidylinositol ceramide inositolphosphotransferase 2 (EC 2.7.8.-) (Inositol-phosphorylceramide synthase 2) (AtIPC32) (IPC synthase 2) (Protein ENHANCING RPW8-MEDIATED HR-LIKE CELL DEATH 1) (Sphingolipid synthase 2)	IPC52 ERH1 At2g37940 T8P21.15	Arabidopsis thaliana (Mouse-ear cress)			
SRR342022_TR23948_c0_g1_i1_len=1758	ITPK1_MAIZE	Q:1404-481;H:18-324	58.58%ID	E:3e-130	Inositol-tetrakisphosphate 1-kinase 1	PF05770.8*Ins134_P3_kin*Inositol 1, 3, 4-trisphosphate 5/6-kinase*4-311*E:2.8e-125	0.005	1.47	0.043	1.283	0.003	2.241	0	2.589	0.822	-0.219 ITPK1_MAIZE	Inositol-tetrakisphosphate 1-kinase 1 (EC 2.7.1.134) (Inositol 1,3,4-trisphosphate 5/6-kinase 1) (Inositol-trisphosphate 5/6-kinase 1) (Ins(1,3,4)P(3) 5/6-kinase 1) (EC 2.7.1.159) (Low phytic acid protein 2) (Zmlpk)	ITPK1 LPA2	Zea mays (Maize)			
SRR342022_TR26348_c3_g6_i3_len=1381	MECR_ARATH	Q:26-1189;H:11-375	70.1%ID	E:0	Probable trans-2-enoyl-CoA reductase, mitochondrial	PF08240.9*ADH_N*Alcohol dehydrogenase GroES-like domain*74-135*E:1.8e-07 PF00107.23*ADH_zinc_N*Zinc-binding dehydrogenase*199-334*E:6.9e-17	0.77	0.129	0.044	1.19	0.001	1.451	0.001	1.505	0.666	-0.304 MECR_ARATH	Probable trans-2-enoyl-CoA reductase, mitochondrial (EC 1.3.1.38)	At3g45770 T6D9.100	Arabidopsis thaliana (Mouse-ear cress)			
SRR342022_TR26609_c1_g19_i2_len=4014	NA	NA	NA	NA	NA	PF07724.11*AAA_2*AAA domain (Cdc48 subfamily)*744-880*E:9.1e-07	0.87	0.159	0.025	1.435	0.009	1.64	0	2.085	0.147	0.999 .	.	.	.			
SRR342022_TR27537_c0_g3_i1_len=1748	NA	NA	NA	NA	NA	.	0.731	0.115	0.085	0.464	0.004	0.881	0	1.095	0.41	0.264 .	.	.	.			
SRR342022_TR28115_c4_g2_i2_len=3376	ACCA_ARATH	Q:424-2499;H:14-791	62.75%ID	E:0	Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha, chloroplastic	PF03255.11*ACCA*Acetyl co-enzyme A carboxylase carboxyltransferase alpha subunit*99-2415*E:4.6e-70 PF10539.15*Carboxyl_trans*Carboxyl transferase domain*178-339*E:6.8e-09	0.24	-0.334	0.19	0.41	0.281	0.337	0	1.101	0.619	0.16 ACCA_ARATH	Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha, chloroplastic (ACCase subunit alpha) (Acetyl-CoA carboxylase carboxyltransferase subunit alpha) (EC 6.4.1.2)	CAC3 At2g38040 T8P21.5	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Lipid metabolism; malonyl-CoA biosynthesis; malonyl-CoA from acetyl-CoA: step 1/1.		
SRR342022_TR30015_c0_g1_i2_len=725	NA	NA	NA	NA	NA	.	0.945	-0.043	0.07	-0.642	0.057	0.771	0	1.31	0.471	-0.561 .	.	.	.			
SRR342022_TR30111_c0_g1_i1_len=591	NA	NA	NA	NA	NA	.	1	0.32	0.254	3.427	0.158	1.767	0	2.995	0.502	3.19 .	.	.	.			
SRR342023_TR5185_c1_g1_i1_len=1438	CLPP4_ARATH	Q:1167-487;H:67-292	81.94%ID	E:1e-125	ATP-dependent Clp protease proteolytic subunit 4, chloroplastic (ECO:0000303|PubMed:11299370)	PF00574.20*CLP_protease*Clp protease*102-276*E:3.8e-70	0.2	-0.403	0.406	-0.316	0.004	1.193	0	1.417	1	-0.318 CLPP4_ARATH	ATP-dependent Clp protease proteolytic subunit 4, chloroplastic (EC 3.4.21.92) (Endopeptidase Clp*4) (nClp*4) (nClp*3)	CLPP4 NCLPP3 NCLPP4 At5g45390 MFC19.5	Arabidopsis thaliana (Mouse-ear cress)			
SRR342023_TR11224_c0_g2_i1_len=1170	PNAE_RAUSE	Q:223-774;H:5-256	45.41%ID	E:4e-52	Polyneuridine-aldehyde esterase	PF00561.17*Abhydrolase_1*alpha/beta hydrolase fold*45-167*E:2.9e-14 PF12146.5*Hydrolase_4*Serine aminopeptidase, S33*45-158*E:4.7e-12 PF12697.4*Abhydrolase_6*Alpha/beta hydrolase family*48-150*E:1.4e-11 PF08246.9*Inhibitor_I29*Cathepsin propeptide inhibitor domain (I29)*57-113*E:1.1e-09 PF00112.20*Peptidase_C1*Papain family cysteine protease*144-202*E:5.2e-24	0.788	0.221	1	0.048	0.003	1.768	0.001	1.907	0.195	0.856 PNAE_RAUSE	Polyneuridine-aldehyde esterase (EC 3.1.1.78) (Polyneuridine aldehyde esterase)	PNAE	Rauvolfia serpentina (Serpentine wood) (Ophioxylon serpentinum)	PATHWAY: Alkaloid biosynthesis; ajmaline biosynthesis.		
SRR342023_TR11881_c0_g2_i1_len=719	RD19A_ARATH	Q:186-716;H:25-198	73.45%ID	E:1e-88	Cysteine proteinase RD19a	PF00112.20*Peptidase_C1*Papain family cysteine protease*144-202*E:5.2e-24	0.11	-0.469	1	2.449	0.502	3.844	0	7.075	0.502	2.48 RD19A_ARATH	Cysteine proteinase RD19a (RD19) (EC 3.4.22.-)	RD19A At4g39090 F19H22.190	Arabidopsis thaliana (Mouse-ear cress)			
SRR342023_TR15682_c2_g8_i8_len=3256	NA	NA	NA	NA	NA	.	0.502	3.949	0.502	4.237	0.066	4.027	0.001	5.221	1	1.928 .	.	.	.			
SRR342023_TR20558_c0_g1_i3_len=2993	ADO3_ARATH	Q:747-2486;H:46-618	83.48%ID	E:0	Adagio protein 3	PF00989.22*PAS*PAS fold*61-166*E:6.3e-06 PF13426.4*PAS_9*PAS domain*66-187*E:1.3e-14 PF08448.3S/*S-box/*F-box domain*216-257*E:5.4e-05 PF13418.3*Kelch_4*Galactose oxidase, central domain*310-360*E:3.8e-11 PF13415.3*Kelch_3*Galactose oxidase, central domain*319-368*E:4.7e-07 PF13418.3*Kelch_4*Galactose oxidase, central domain*361-411*E:8.2e-09 PF13415.3*Kelch_3*Galactose oxidase, central domain*375-421*E:1e-11 PF13418.3*Kelch_4*Galactose oxidase, central domain*413-461*E:1.8e-07 PF13415.3*Kelch_3*Galactose oxidase, central domain*424-475*E:1e-09 PF13418.3*Kelch_4*Galactose oxidase, central domain*464-514*E:1.6e-09	0.699	-0.157	0.336	-0.329	0.002	3.119	0	5.937	0.411	0.301 ADO3_ARATH	Adagio protein 3 (F-box only protein 2a) (FBX2a) (Flavin-binding kelch repeat F-box protein 1)	ADO3 FKF1 At1g68050 T23K23.10	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Protein modification; protein ubiquitination.		
SRR342023_TR23730_c2_g6_i1_len=1528	ASIL2_ARATH	Q:1528-926;H:1-206	56.76%ID	E:2e-52	Trihelix transcription factor ASIL2 (ECO:0000305)	PF13837.3*Myb_DNA-bind_4*Myb/SANT-like DNA-binding domain*67-158*E:7.2e-26	0.729	0.272	0.278	0.75	0.01	1.302	0.001	1.616	0.066	3.821 ASIL2_ARATH	Trihelix transcription factor ASIL2 (6B-interacting protein 1-like 2) (Trihelix DNA-binding protein ASIL2)	ASIL2 At3g14180 MAG2.16	Arabidopsis thaliana (Mouse-ear cress)			
SRR342023_TR31226_c2_g9_i9_len=7814	AB10C_ARATH	Q:5608-1187;H:2-1451	65.72%ID	E:0	ABC transporter C family member 10	PF00664.20*ABC_membrane*ABC transporter transmembrane region*310-569*E:7.2e-23 PF00005.24*ABC_tran*ABC transporter*644-779*E:1.6e-24 PF00664.20*ABC_membrane*ABC transporter transmembrane region*918-1178*E:1.3e-25 PF00005.24*ABC_tran*ABC transporter*1252-1399*E:9.6e-30	0.763	0.245	0.068	1.019	0.01	0.867	0	1.29	1	0.037 AB10C_ARATH	ABC transporter C family member 10 (ABC transporter ABCC.10) (AtABCC10) (EC 3.6.3.44) (ATP-dependent Glutathione S-conjugate pump 14) (Glutathione S-conjugate-transporting ATPase 14) (Multidrug resistance-associated protein 14)	ABCC10 MRP10 MRP14 At3g59140 F17J16.190	Arabidopsis thaliana (Mouse-ear cress)			
SRR346572_TR13187_c0_g1_i1_len=1315	M3K2_ARATH	Q:1172-333;H:68-347	39.06%ID	E:2e-54	Mitogen-activated protein kinase kinase kinase 2	PF00069.22*Pkinase*Protein kinase domain*6-268*E:1.4e-55 PF07714.14*Pkinase_Tyr*Protein tyrosine kinase*6-261*E:1.7e-35	0.629	1.916	0.025	3.685	0.01	2.102	0	3.226	1	0.28 M3K2_ARATH	Mitogen-activated protein kinase kinase kinase 2 (EC 2.7.11.25) (Arabidopsis NPK1-related protein kinase 2)	ANP2 At1g54960 F14C21.49 T24C10.1	Arabidopsis thaliana (Mouse-ear cress)			
SRR346572_TR20908_c0_g2_i1_len=1888	GME1_ORYSI	Q:1632-605;H:1-378	92.59%ID	E:0	GDP-mannose 3,5-epimerase 1	PF01370.18*Epimerase*NAD dependent epimerase/dehydratase family*30-261*E:6.2e-46 PF16363.2*GDP_Man_Dehyd*GDP-mannose 4,6 dehydratase*32-329*E:9.7e-28 PF07993.16*3Beta_HSD*3-beta hydroxysteroid dehydrogenase/isomerase family*32-185*E:1.6e-09	0.212	-0.396	0.942	-0.042	0.001	1.427	0	1.595	0.807	-0.149 GME1_ORYSI	GDP-mannose 3,5-epimerase 1 (GDP-Man 3,5-epimerase) 1) (EC 5.1.3.18) (OsGME1)	Os1_032456	Oryza sativa subsp. indica (Rice)	PATHWAY: Cofactor biosynthesis; L-ascorbate biosynthesis via GDP-alpha-D-mannose pathway; L-ascorbate from GDP-alpha-D-mannose: step 1/5. (ECO:0000269|PubMed:9620799).		
SRR346572_TR21312_c0_g1_i1_len=829	NA	NA	NA	NA	NA	.	0.648	0.196	0.182	0.535	0.002	1.209	0.001	1.317	0.388	-0.351 .	.	.	.			
SRR346574_TR32716_c0_g1_i2_len=2150	ACCC1_POPTR	Q:134-1708;H:9-528	89.9%ID	E:0	Biotin carboxylase 1, chloroplastic	PF00289.19*Biotin_carb_N*Biotin carboxylase, N-terminal domain*71-178*E:1.3e-40 PF02786.14*CPSase_L_D2*Carbamoyl-phosphate synthase L chain, ATP binding domain*183-390*E:6e-63 PF02222.19*ATP-grasp*ATP-grasp domain*205-360*E:6e-10 PF07478.10*Dala_Dala_lig_C*D-ala D-ala ligase C-terminus*209-359*E:9.5e-08 PF02785.16*Biotin_carb_C*Biotin carboxylase C-terminal domain*404-503*E:4.2e-39	0.134	-0.406	0.031	-0.628	0.157	0.445	0	1.398	0.935	-0.029 ACCC1_POPTR	Biotin carboxylase 1, chloroplastic (EC 6.3.4.14) (Acetyl-CoA carboxylase subunit A 1) (ACC) (EC 6.4.1.2)	POPTRDRAFT_831870	Populus trichocarpa (Western balsam poplar) (Populus balsamifera subsp. trichocarpa)	PATHWAY: Lipid metabolism; malonyl-CoA biosynthesis; malonyl-CoA from acetyl-CoA: step 1/1.		
SRR346596_TR1350_c2_g1_i1_len=2436	HTSF1_HUMAN	Q:550-152;H:48-355	34.43%ID	E:3e-39	HIV Tat-specific factor 1	PF14237.3*DUF4339*Domain of unknown function (DUF4339)*29-73*E:1.8e-13 PF00076.19*RRM_1*RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)*249-321*E:4.2e-09 PF13893.3*RRM_5*RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)*294-336*E:0.56 PF00076.19*RRM_1*RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)*402-457*E:7.6e-10 PF13893.3*RRM_5*RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)*413-457*E:0.55	0.484	1	0.204	1.688	0.017	1.205	0.034	4.855	0	5.966	0.692	-1.257 HTSF1_HUMAN	HIV Tat-specific factor 1 (Tat-SF1)	HTATSF1	Homo sapiens (Human)			
SRR346596_TR5568_c0_g1_i1_len=913	PTI5_SOLLC	Q:176-622;H:1-143	63.46%ID	E:2e-42	Pathogenesis-related genes transcriptional activator PTI5	PF00847.17*AP2 domain*66-116*E:1.2e-14	1	1.573	0.502	3.511	0.009	6.032	0	6.75	1	0.595 PTI5_SOLLC	Pathogenesis-related genes transcriptional activator PTI5 (PTO-interacting protein 5)	PTI5	Solanum lycopersicum (Tomato) (Lycopersicon esculentum)			
SRR346596_TR7456_c0_g1_i2_len=1909	NAC2_ARATH	Q:543-1283;H:54-289	59.22%ID	E:2e-76	NAC domain-containing protein 2	PF02365.12*NAM*No apical meristem (NAM) protein*9-27*E:2e-14	0.629	0.937	0.025	3.066	0.025	3.647	0	4.685	0.692	-0.682 NAC2_ARATH	NAC domain-containing protein 2 (ANAC002)	NAC002 ATAF1 At1g01720 T1N6.12	Arabidopsis thaliana (Mouse-ear cress)			
SRR346596_TR15471_c0_g1_i1_len=5321	MNS3_ARATH	Q:293-2089;H:1-624	68.84%ID	E:0	Mannosyl-oligosaccharide 1,2-alpha-mannosidase MNS3	PF03776.8*Glycosyl_transf_2*Ion channel*208-300*E:2.1e-11 PF00227.26*cullin*Cullin family*Cullin nucleotide-binding domain*398-482*E:9.3e-15 PF11834.5*KHA*KHA, dimerisation domain of potassium ion channel*698-767*E:4.2e-22	0.16	1.202	0.212	0.924	0.003	1.796	0	2.173	0.014	-2.735 MNS3_ARATH	Mannosyl-oligosaccharide 1,2-alpha-mannosidase MNS3 (EC 3.2.1.113)	MNS3 At1g30000 T1P2.10	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Protein modification; protein glycosylation.		
SRR346596_TR16289_c0_g1_i1_len=3534	PP377_ARATH	Q:1133-710;H:25-822	55.87%ID	E:0	Putative pentatricopeptide repeat-containing protein At5g13230, mitochondrial	PF13041.3*PPR_2*PPR repeat family*432-475*E:1.3e-11 PF01535.17*PPR*PPR repeat*430-459*E:1.3e-05 PF01535.17*PPR*PPR repeat*503-529*E:0.00098 PF13041.3*PPR_2*PPR repeat family*528-576*E:1.9e-10 PF13812.3*PPR_3*Pentatricopeptide repeat domain*528-577*E:8.1e-05 PF01535.17*PPR*PPR repeat*531-558*E:4.1e-07 PF01535.17*PPR*PPR repeat*603-627*E:0.0023 PF14432.3*DYW_deaminase*DYW family of nucleic acid deaminases*702-826*E:7.8e-35	1	0.007	0.132	2.615	0.017	4.834	0	5.714	1	-0.595 PP377_ARATH	Putative pentatricopeptide repeat-containing protein At5g13230, mitochondrial	PCMP-H89 At5g13230 T31B5_50	Arabidopsis thaliana (Mouse-ear cress)			
SRR346596_TR30964_c0_g2_i5_len=2491	NA	NA	NA	NA	NA	PF01699.21*Na_Ca_ex*Sodium/calcium exchanger protein*76-244*E:4.6e-07 PF13499.3*EF-hand_7*EF-hand domain pair*293-357*E:5.3e-10 PF13202.3*EF-hand_5*EF hand*295-318*E:4.9e-05 PF01699.21*Na_Ca_ex*Sodium/calcium exchanger protein*418-556*E:4.2e-05	0.814	0.116	0.892	-0.052	0.038	0.97	0	2.128	0.472	-0.738 .	.	.	.			
SRR346596_TR33708_c1_g1_i5_len=501	NA	NA	NA	NA	NA	.	0.013	0.656	0.021	0.513	0.005	0.636	0	1.083	0.022	0.569 .	.	.	.			
SRR346604_TR3399_c0_g1_i1_len=1474	BUP1_DICDI	Q:209-1360;H:5-390	62.69%ID	E:2e-167	Beta-ureidopropionase	PF00795.19*CN_hydrolase*Carbon-nitrogen hydrolase*146-417*E:1.8e-52	0.066	5.226	0.003	2.881	0.002	2.489	0	2.89	0.56	0.727 BUP1_DICDI	Beta-ureidopropionase (EC 3.5.1.6) (Beta-alanine synthase) (N-carbamoyl-beta-alanine amidohydrolase)	pyd3 bup1 upb1 DDB_G0274123	Dictyostelium discoideum (Slime mold)	PATHWAY: Amino-acid biosynthesis; beta-alanine biosynthesis.		
SRR346604_TR3972_c0_g1_i1_len=1748	ZOG_PHALU	Q:90-1472;H:13-459	55.53%ID	E:3e-169	Zeatin O-glucosyltransferase	PF02201.15*UDPGT*UDP-glucoronosyl and UDP-glucosyl transferase*231-391*E:5.5e-22	1	0.541	0.254	4.356	0.009	5.201	0	6.974	1	-1.478 ZOG_PHALU	Zeatin O-glucosyltransferase (EC 2.4.1.203) (Trans-zeatin O-beta-D-glucosyltransferase)	ZOG1	Phaseolus lunatus (Lima bean) (Phaseolus limensis)			
SRR346604_TR9559_c0_g1_i3_len=2157	AAP3_ARATH	Q:1733-306;H:3-476	79.62%ID	E:0	Amino acid permease 3	PF01490.15*Aa_trans*Transmembrane amino acid transporter protein*40-472*E:7.7e-118	0.013	1.454	0.076	2.46	0.007	1.379	0	1.756	1	-0.006 AAP3_ARATH	Amino acid permease 3 (Amino acid transporter AAP3)	AAP3 At1g77380 F2P24.9	Arabidopsis thaliana (Mouse-ear cress)			
SRR346604_TR10280_c1_g4_i2_len=2417	C81E8_MEDTR	Q:1123-2415;H:43-475	45.52%ID	E:4e-126	Cytochrome P450 81E8 (ECO:0000303|PubMed:14617078)	PF00067.19*p450*Cytochrome P450*25-277*E:2.6e-68	0.629	1.065	0.132	2.038	0.002	4.25	0	6.78	1	1.291 C81E8_MEDTR	Cytochrome P450 81E8 (EC 1.14.13.-)	CYP81E8	Medicago truncatula (Barrel medic) (Medicago tribuloides)			
SRR346604_TR12851_c0_g1_i1_len=2260	MASY_RICCO	Q:1837-176;H:13-567	88.47%ID	E:0	Malate synthase, glyoxysomal	PF10274.19*Malate_synthase*Malate synthase*26-556*E:8.6e-221	1	-0.572	1	-0.574	0.226	1.802	0.001	3.268	1	0.83 MASY_RICCO	Malate synthase, glyoxysomal (EC 2.3.3.9)	Ricinus communis (Castor bean)	PATHWAY: Carbohydrate metabolism; glyoxylate cycle; (S)-malate from isocitrate: step 2/2.			
SRR346604_TR14310_c0_g3_i3_len=2558	COP1_ARATH	Q:393-2288;H:46-674	77.06%ID	E:0	E3 ubiquitin-protein ligase COP1	PF13920.3*zf-C3HC4_3*Zinc finger, C3HC4 type (RING finger)*54-96*E:9.8e-07 PF13923.3*zf-C3HC4_2*Zinc finger, C3HC4 type (RING finger)*57-94*E:5.1e-10 PF00097.22*zf-C3HC4*Zinc finger, C3HC4 type (RING finger)*57-94*E:8.4e-08 PF13445.3*zf-RING_UBOX*RING-type zinc-finger*57-92*E:3.5e-05 PF00400.29*WD40*WD domain, G-beta repeat*462-499*E:0.0022 PF00400.29*WD40*WD domain, G-beta repeat*549-584*E:0.00014	0.365	0.518	0.84	-0.326	0.025

							465*E:6.2e-27																				
SRR924147_TR34893_c0_g1_i1_len=934	Y5278_ARATH	Q:545-267;H:76-168	53.76%ID	E:1e-31	Uncharacterized protein PAM68-like	PF11947.5*DUF3464*Protein of unknown function (DUF3464)*66-187*E:5.1e-39	0.252	-0.272	0.001	-0.795	0.003	0.922	0	1.276	0.572	-0.14	Y5278_ARATH	Uncharacterized protein PAM68-like	At5g52780 F6N7.27	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Membrane; Reference proteome; Transmembrane; Transmembrane helix
SRR924148_TR589_c0_g1_i1_len=2266	KELP_ARATH	Q:120-596;H:13-565	40.85%ID	E:2e-27	RNA polymerase II transcriptional coactivator KELP	PF14223.3*Retrotran_gag_2*gag-polypeptide of LTR copia-type*175-310*E:5.6e-16 PF00098.20*zf-CCHC*Zinc knuckle*341-358*E:0.00023	1	-0.393	0.239	1.3	0.299	1.587	0	3.232	1	0.364	KELP_ARATH	RNA polymerase II transcriptional coactivator KELP	KELP At4g10920 F25I24.130 F8M12.6	Arabidopsis thaliana (Mouse-ear cress)		Activator; Complete proteome; DNA-binding; Nucleus; Reference proteome; Transcription; Transcription regulation
SRR924148_TR8016_c0_g1_i1_len=2514	SBIR1_ARATH	Q:420-2258;H:35-639	60.62%ID	E:0	Leucine-rich repeat receptor-like serine/threonine/tyrosine-protein kinase SOBIR1	PF13855.3*LRR_8*Leucine rich repeat*177-236*E:1.4e-06 PF00560.30*LRR_1*Leucine Rich Repeat*201-223*E:1.8 PF00560.30*LRR_1*Leucine Rich Repeat*272-289*E:1.9 PF00069.22*PKinase*Protein kinase domain*425-703*E:3.5e-44 PF07714.14*Pkinase_Tyr*Protein tyrosine kinase*425-654*E:3.2e-35	0.444	0.473	0.016	1.46	0.017	2.344	0	2.976	1	0.108	SBIR1_ARATH	Leucine-rich repeat receptor-like serine/threonine/tyrosine-protein kinase SOBIR1 (EC 2.7.10.1) (EC 2.7.11.1) (Protein EVERSHED) (Protein SUPPRESSOR OF BIR1-1)	SOBIR1 EVR At2g31880 F20M17.8	Arabidopsis thaliana (Mouse-ear cress)		ATP-binding; Cell membrane; Complete proteome; Glycosylation; Kinase; Leucine-rich repeat; Membrane; Nucleotide-binding; Plant defense; Receptor; Reference proteome; Repeat; Serine/threonine-protein kinase; Signal; Transferase; Transmembrane; Transmembrane helix; Tyrosine-protein kinase
SRR924148_TR21803_c1_g1_i1_len=726	DV4H_CATRO	Q:104-517;H:24-159	70.21%ID	E:3e-58	Deacetoxyvindoline 4-hydroxylase	PF14226.3*DIOX_N*non-haem dioxygenase in morphine synthesis N-terminal*68-324*E:2e-12	0.003	1.25	0.001	1.69	0.011	1.13	0	1.689	0.389	0.371	DV4H_CATRO	Deacetoxyvindoline 4-hydroxylase (EC 1.14.11.20)	D4H	Catharanthus roseus (Madagascar periwinkle) (Vinca rosea)	PATHWAY: Alkaloid biosynthesis; vindoline biosynthesis; vindoline from tabersonine: step 5/6.	Cytoplasm; Dioxygenase; Direct protein sequencing; Iron; Metal-binding; Oxidoreductase; Vitamin C
SRR924148_TR31225_c1_g2_i1_len=829	NA	NA	NA	NA	NA	-	1	0.199	0.299	1.327	1	0.69	0	4.497	0	-3.286	.	-	-	-		-
SRR924148_TR32921_c0_g1_i2_len=1481	RCE1_ARATH	Q:362-910;H:1-184	83.7%ID	E:2e-110	NEDD8-conjugating enzyme Ubc12	PF00179.23*UQ_con*Ubiquitin-conjugating enzyme*33-167*E:4.2e-38	0.887	-0.062	0.136	0.528	0.002	1.277	0.001	1.357	0.883	-0.07	RCE1_ARATH	NEDD8-conjugating enzyme Ubc12 (EC 6.3.2.-) (RUB1 carrier protein 1) (RUB1-conjugating enzyme 1) (RUB1-protein ligase 1)	RCE1 At4g36800 C7A10.560	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Protein modification; protein neddylation.	ATP-binding; Alternative splicing; Complete proteome; Ligase; Nucleotide-binding; Reference proteome; Ubl conjugation pathway
SRR924148_TR37722_c0_g1_i1_len=957	NA	NA	NA	NA	NA	-	0.559	0.418	0.839	0.098	1	0.588	0	2.459	0.178	-0.628	.	-	-	-		-
SRR924148_TR37795_c0_g1_i1_len=952	PCR2_ARATH	Q:639-208;H:6-152	63.27%ID	E:2e-59	Protein PLANT CADMIUM RESISTANCE 2	PF04749.14*PLAC8*PLAC8 family*55-153*E:9.7e-29	0.298	0.737	0.326	0.55	0.01	1.16	0	1.757	1	-0.201	PCR2_ARATH	Protein PLANT CADMIUM RESISTANCE 2 (AtPCR2)	PCR2 At1g14870 F10B6.27	Arabidopsis thaliana (Mouse-ear cress)		Cell membrane; Complete proteome; Membrane; Reference proteome; Transmembrane; Transmembrane helix

Supplemental Table S2

Description of transcripts down-regulated upon challenge with M. sexta found in the intersections between lists of each experiment.

Core
Mx1wk
Mx6h
Mx8h
MxDamage24h
MxDamage24h_MxInact24h
MxInact24h

Core

Transcript (CDF97)	Uniprot homolog	BLASTX Position	BLASTX %Identity	BLASTX evalue	Uniprot descr	Pfam	PValue_Mx6h	logFC_Mx6h	PValue_Mx8h	logFC_Mx8h	PValue_MxDamage24h	logFC_MxDamage24h	PValue_MxInact24h	logFC_MxInact24h	PValue_Mx1wk	logFC_Mx1wk	Entry.name	Protein names	Gene names	Organism	Pathway	Keywords
SRR911446334_TR39822_c0_g2_i1_len=510	RUXG_ARATH	Q:107-346;H:1-80	90%ID	E:3e-48	Probable small nuclear ribonucleoprotein G	.	0	-1.001	0.781	-0.092	0.349	0.365	0.793	-0.107	0	-1.015	RUXG_ARATH	Probable small nuclear ribonucleoprotein G (snRNP-G) (Sm protein G) (Sm-G) (SmG)	At2g23930 T29E15.13	Arabidopsis thaliana (Mouse-ear cress)		Alternative splicing; Complete proteome; Nucleus; RNA-binding; Reference proteome; Ribonucleoprotein; Spliceosome; mRNA processing; mRNA splicing
SRR1222338_TR62384_c3_g1_i4_len=752	RL321_ARATH	Q:605-213;H:3-133	86.26%ID	E:1e-70	60S ribosomal protein L32-1	PF01655.15*Ribosomal_L32e*Ribosomal protein L32*16-122*E:2.1e-50	0	-1.235	0.391	-0.22	0.639	0.151	0.256	-0.402	0	-1.025	RL321_ARATH	60S ribosomal protein L32-1	RPL32A At4g18100 F15J5.70	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Reference proteome; Ribonucleoprotein; Ribosomal protein
SRR1222338_TR75230_c0_g1_i1_len=855	RL12_PRUAR	Q:767-270;H:1-166	92.17%ID	E:5e-104	60S ribosomal protein L11	PF03946.11*Ribosomal_L11_N*Ribosomal protein L11, N-terminal domain*15-70*E:6.1e-23 PF00298.16*Ribosomal_L11*Ribosomal protein L11, RNA binding domain*75-144*E:1.5e-19	0	-0.932	0.687	-0.103	0.4	0.24	0.904	0.046	0	-1.243	RL12_PRUAR	Prunus armeniaca (Apricot) (Armeniaca vulgaris)	RPL12	Prunus armeniaca (Apricot) (Armeniaca vulgaris)		RNA-binding; Ribonucleoprotein; Ribosomal protein; rRNA-binding
SRR1222338_TR83917_c0_g1_i1_len=621	RL37A_ORYSJ	Q:498-223;H:1-92	96.74%ID	E:3e-57	60S ribosomal protein L37a	PF01780.16*Ribosomal_L37ae*Ribosomal L37ae protein family*45-129*E:2.9e-39	0	-1.058	0.386	0.223	1	-0.003	0.633	-0.167	0	-1.357	RL37A_ORYSJ	60S ribosomal protein L37a	Os01g0679700 LOC_Os01g48770 B1144G04.40-1; Os05g0557600 LOC_Os05g48320 OJ1214_E03.13 Osj_018715	Oryza sativa subsp. japonica (Rice)		3D-structure; Complete proteome; Metal-binding; Reference proteome; Ribonucleoprotein; Ribosomal protein; Zinc; Zinc-finger
SRR342019_TR27032_c0_g1_i1_len=1711	NA	NA	NA	NA	NA	-	0	-6.648	1	-0.019	1	-1.533	1	-1.978	0	-5.597	.	-	-	-		-
SRR342022_TR21159_c0_g3_i1_len=2114	EP1G_DAUCA	Q:385-1501;H:5-373	48.58%ID	E:3e-98	Epidermis-specific secreted glycoprotein EP1	PF01453.21*B_lectin*D-mannose binding lectin*112-208*E:6.1e-26 PF08276.8*PAN_2*PAN-like domain*424-453*E:3.4e-05 PF14295.3*PAN_4*PAN domain*427-445*E:0.38	0	-1.159	0.01	-0.875	0.507	0.256	0.003	0.952	0	-1.16	EP1G_DAUCA	Epidermis-specific secreted glycoprotein EP1 (52/54 KDa medium protein)	EP1	Daucus carota (Wild carrot)		Direct protein sequencing; Glycoprotein; Lectin; Secreted; Signal
SRR342023_TR8921_c1_g1_i2_len=778	R27A3_ARATH	Q:131-568;H:1-146	89.04%ID	E:3e-89	60S ribosomal protein L27a-3	PF00828.16*Ribosomal_L27A*Ribosomal proteins 50S-L15, 50S-L18e, 60S-L27A*71-186*E:6.6e-23	0	-1.097	0.117	-0.368	0.657	0.122	0.528	-0.18	0	-1.271	R27A3_ARATH	60S ribosomal protein L27a-3	RPL27AC At1g70600 F24J13.17 F5A18.22	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Reference proteome; Ribonucleoprotein; Ribosomal protein
SRR6488707_TR10026_c0_g2_i1_len=2229	PMG1_ARATH	Q:210-1850;H:1-557	89.05%ID	E:0	2,3-bisphosphoglycerate-independent phosphoglycerate mutase	PF16176.15*Metalloenzyme*Metalloenzyme superfamily*22-545*E:4.7e-101 PF06415.10*iPGM_N*BPG-independent PGAM N-terminus (iPGM_N)*102-322*E:6.4e-59	0.001	-2.284	0	2.743	0.006	1.921	0.001	2.244	0	-2.869	PMG1_MESCR	2,3-bisphosphoglycerate-independent phosphoglycerate mutase (BPG-independent PGAM) (Phosphoglyceromutase) (EC 5.4.2.12) (PGAM-I)	PGM1	Mesembryanthemum crystallinum (Common ice plant) (Cryophytum crystallinum)	PATHWAY: Carbohydrate degradation; glycolysis; pyruvate from D-glyceraldehyde 3-phosphate: step 3/5.	Cytoplasm; Glycolysis; Isomerase; Manganese; Metal-binding; Stress response
SRR6488707_TR24657_c0_g1_i1_len=1073	R10A3_ARATH	Q:171-821;H:1-217	91.71%ID	E:3e-129	60S ribosomal protein L10a-3	PF00687.18*Ribosomal_L1*Ribosomal protein L1p/L10e family*21-211*E:1.1e-44	0	-1.091	0.608	-0.127	0.463	0.211	0.259	-0.33	0	-11.816	R10A3_ARATH	60S ribosomal protein L10a-3	RPL10AC At5g22440 MWD9.24	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Reference proteome; Ribonucleoprotein; Ribosomal protein
SRR924147_TR1989_c1_g1_i6_len=904	RL31_NICGU	Q:136-770;H:99-643	91.67%ID	E:1e-65	60S ribosomal protein L31	.	0.001	-0.822	0.287	-0.257	0.367	0.252	0.796	-0.085	0	-0.942	RL31_NICGU	60S ribosomal protein L31	RPL31	Nicotiana glutinosa (Tobacco)		Ribonucleoprotein; Ribosomal protein
SRR1144634_TR3773_c0_g2_i6_len=2346	THIC_ARATH	Q:136-1770;H:99-643	91.01%ID	E:0	Phosphomethylpyrimidine synthase, chloroplastic	PF01964.15*ThiC_Rad_SAM*Radical SAM ThiC family*79-499*E:4.5e-198	0.68	0.14	0	-1.564	1	0	1	1.674	0	-1.232	THIC_ARATH	Phosphomethylpyrimidine synthase, chloroplastic (EC 4.1.99.17) (Hydroxymethylpyrimidine phosphate synthase) (HMP-P synthase) (HMP-phosphate synthase) (HMPP synthase) (Protein PYRIMIDINE REQUIRING) (Thiamine biosynthesis protein ThiC) (Protein THIAMINE C)	THIC PY At2g29630 T27A16.27	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Cofactor biosynthesis; thiamine diphosphate biosynthesis.	3D-structure; 4Fe-4S; Chloroplast; Complete proteome; Iron; Iron-sulfur; Lyase; Metal-binding; Plastid; Reference proteome; Sadenosyl-L-methionine; Thiamine biosynthesis; Transit peptide; Zinc
SRR1222338_TR7314_c0_g1_i4_len=1143	XTH9_ARATH	Q:122-994;H:10-289	72.16%ID	E:3e-158	Xyloglucan endotransglucosylase-hydrolase protein 9	PF00722.18*Glyco_hydro_16*Glycosyl hydrolases family 16*63-239*E:3.2e-57 PF06935.9*XET_C*Xyloglucan endo-transglycosylase (XET) C-terminus*281-326*E:1.8e-17	0.002	-0.822	0	-3.848	0.611	0.417	1	0.148	0	-0.848	XTH9_ARATH	Xyloglucan endotransglucosylase-hydrolase protein 9 (At-XTH9) (XTH-9) (EC 2.4.1.207)	XTH9 EXGT-A6 XTR16 At4g03210 F4C21.14	Arabidopsis thaliana (Mouse-ear cress)		Alternative splicing; Apoplast; Cell wall; Cell wall biogenesis/degradation; Complete proteome; Disulfide bond; Glycosylation; Glycosidase; Hydrolase; Reference proteome; Secreted; Signal; Transferase
SRR1222338_TR14630_c0_g2_i2_len=1271	GLYM2_FLAPR	Q:1233-289;H:209-517	86.98%ID	E:0	Serine hydroxymethyltransferase 2, mitochondrial	PF00464.16*SHMT*Serine hydroxymethyltransferase*2-240*E:2.9e-122	1	-0.006	0	-0.861	0.034	-0.476	0.005	-0.633	0	-1.614	GLYM2_FLAPR	Serine hydroxymethyltransferase 2, mitochondrial (SHMT2) (EC 2.1.2.1) (Glycine hydroxymethyltransferase 2) (Serine methylase 2)		Flaveria pringlei	PATHWAY: One-carbon metabolism; tetrahydrofolate interconversion.	Mitochondrion; One-carbon metabolism; Pyridoxal phosphate; Transferase; Transit peptide
SRR1222338_TR14140_c0_g1_i1_len=1134	RK3_TOBAC	Q:971-216;H:8-259	82.42%ID	E:2e-123	50S ribosomal protein L3, chloroplastic	PF00297.19*Ribosomal_L3*Ribosomal protein L3*185-272*E:2.2e-17	0.095	-0.738	0.001	-1.614	0.683	0.285	1	0.118	0	-1.172	RK3_TOBAC	50S ribosomal protein L3, chloroplastic (Fragment)	RPL3	Nicotiana tabacum (Common tobacco)		Chloroplast; Plastid; RNA-binding; Ribonucleoprotein; Ribosomal protein; Transit peptide; rRNA-binding
SRR1222338_TR45252_c0_g1_i1_len=1171	RR1_SPIOL	Q:1648-380;H:1-408	81.84%ID	E:0	30S ribosomal protein S1, chloroplastic	PF00575.20*S1*S1 RNA binding domain*109-181*E:1.3e-05 PF00575.20*S1*S1 RNA binding domain*197-261*E:1.8e-08 PF00575.20*S1*S1 RNA binding domain*294-364*E:3.9e-22	0.307	-0.243	0	-0.907	0.013	-0.603	0.083	-0.417	0.001	-0.842	RR1_SPIOL	30S ribosomal protein S1, chloroplastic (CS1)	RPS1	Spinacia oleracea (Spinach)		Chloroplast; Direct protein sequencing; Plastid; RNA-binding; Repeat; Ribonucleoprotein; Ribosomal protein; Transit peptide
SRR1222338_TR45790_c0_g1_i7_len=1429	COL5_ARATH	Q:1243-545;H:149-355	40.59%ID	E:7e-33	Zinc finger protein CONSTANS-LIKE 5	PF06203.11*CCT*CCT motif*182-224*E:4.2e-19	0	-1.06	0	-8.182	0	-7.224	1	4.2	0	-8.413	COL5_ARATH	Zinc finger protein CONSTANS-LIKE 5	COL5 At5g57660 MRI1.1	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Metal-binding; Nucleus; Reference proteome; Repeat; Zinc; Zinc-finger
SRR1222338_TR50273_c0_g1_i13_len=1803	HACD2_BOVIN	Q:1474-1073;H:69-201	39.55%ID	E:2e-21	Very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase 2 (EC0:0000305)	PF04387.11*PTPLA*Protein tyrosine phosphatase-like protein, PTPLA*1-135*E:3.7e-33	0.132	-2.183	0	-6.151	1	-0.768	1	1.252	0	-3.199	HACD2_BOVIN	Very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase 2 (EC 4.2.1.134) (3-hydroxyacyl-CoA dehydratase 2) (HACD2) (Protein-tyrosine phosphatase-like member B)	HACD2 PTPLB	Bos taurus (Bovine)	PATHWAY: Lipid metabolism; fatty acid biosynthesis. (EC0:0000250)UniProtKB:Q6YH2).	Acetylation; Complete proteome; Endoplasmic reticulum; Fatty acid biosynthesis; Fatty acid metabolism; Glycoprotein; Lipid metabolism; Lipid biosynthesis; Lipid metabolism; Lyase; Membrane; Reference proteome; Transmembrane; Transmembrane helix
SRR1222338_TR64958_c0_g1_i3_len=853	CPN81_ARATH	Q:751-387;H:486-600	86.96%ID	E:1e-59	Chaperonin 60 subunit beta 1, chloroplastic	PF00118.21*Cpn60_TCP1*TCP-1/cpn60 chaperonin family*8-69*E:1.2e-23	0.006	-0.685	0	-1.173	0.11	0.537	0.046	0.646	0	-0.849	CPN81_ARATH	Chaperonin 60 subunit beta 1, chloroplastic (CPN-60 beta 1) (60 kDa chaperonin subunit beta 1) (RuBisCO large subunit-binding protein subunit beta, chloroplastic)	CPN60B1 Cpn60-B(3) LEN1 At1g55490 T5A14.11	Arabidopsis thaliana (Mouse-ear cress)		ATP-binding; Chaperone; Complete proteome; Direct protein sequencing; Nucleotide-binding; Phosphoprotein; Plastid; Reference proteome; Transit peptide
SRR1222338_TR83367_c0_g1_i1_len=716	NSA2_HUMAN	Q:661-311;H:144-260	82.91%ID	E:2e-64	Ribosome biogenesis protein NSA2 homolog	.	0.461	1.518	0	-2.445	1	0	0	-5.232	NSA2_HUMAN	Ribosome biogenesis protein NSA2 homolog (Hairy cell leukemia protein 1) (TGF-beta-inducible nuclear protein 1)	NSA2 TINP1 HUSSY-29	Homo sapiens (Human)		Complete proteome; Nucleus; Phosphoprotein; Polymorphism; Reference proteome; Ribonucleoprotein; Ribosome biogenesis; rRNA processing
SRR1221857_TR18303_c0_g1_i1_len=1310	RUB1_BRANA	Q:1131-361;H:292-546	86.38%ID	E:2e-135	RuBisCO large subunit-binding protein subunit alpha, chloroplastic	PF00118.21*Cpn60_TCP1*TCP-1/cpn60 chaperonin family*25-242*E:1.8e-42	0.133	-1.161	0	-3.912	1	-1.038	1	-1.083	0	-3.863	RUB1_BRANA	RuBisCO large subunit-binding protein subunit alpha, chloroplastic (60 kDa chaperonin subunit alpha) (CPN-60 alpha) (Fragment)		Brassica napus (Rape)		Chloroplast; Complete proteome; DNA-binding; Disulfide bond; Hydrolase; Protease; Reference proteome; Signal
SRR1221858_TR1414_c0_g1_i1_len=1581	DHEB_NICPL	Q:351-108;H:22-103	89.94%ID	E:0	Glutamate dehydrogenase B	PF02812.15*ELFV_dehydrog_N*Glu/Leu/Phe/Val dehydrogenase, dimerisation domain*6-91*E:7.1e-31 PF00208.18*ELFV_dehydrog*Glutamate/Leucine/Phenylalanine/Valine dehydrogenase*108-340*E:6.3e-73	0.147	0.906	0	-1.543	0.781	0.47	1	0.287	0.001	-1.893	DHEB_NICPL	Glutamate dehydrogenase B (GDH B) (EC 1.4.1.3)	GDHB	Nicotiana plumbaginifolia (Leadwort-leaved tobacco) (Tex-Mex tobacco)		NAD; Oxidoreductase
SRR1221858_TR55352_c0_g1_i2_len=1138	PISK9_ARATH	Q:94-667;H:554-812	75.57%ID	E:9e-129	Phosphatidylinositol 4-phosphate 5-kinase 9	PF15054.15*PIP5K*Phosphatidylinositol-4-phosphate 5-Kinase*1-247*E:1.4e-50	0.017	-5.869	0.001	-1.884	1	-0.404	0.129	-4.919	0	-2.721	PISK9_ARATH	Phosphatidylinositol 4-phosphate 5-kinase 9 (AtPIPSK9) (EC 2.7.1.68) (1-phosphatidylinositol-4-phosphate kinase 9) (PtdIns(4)P-5-kinase 9)	PIPSK9 At3g09920 F8A24.2	Arabidopsis thaliana (Mouse-ear cress)		ATP-binding; Complete proteome; Kinase; Membrane; Nucleotide-binding; Nucleus; Reference proteome; Repeat; Transferase
SRR1221858_TR60176_c0_g1_i1_len=1053	VATA_ARATH	Q:390-593;H:556-623	89.71%ID	E:5e-31	V-type proton ATPase catalytic subunit A	.	1	0.417	0	-3.54	1	-0.953	1	-0.769	0	-2.964	VATA_ARATH	V-type proton ATPase catalytic subunit A (VATPase subunit A) (EC 3.6.3.14) (VATPase 69 kDa subunit) (Vacuolar H(+)-ATPase subunit A) (Vacuolar proton pump subunit alpha)	VHA-A At1g78900 F9K20.5	Arabidopsis thaliana (Mouse-ear cress)		ATP-binding; Complete proteome; Hydrogen-ion transport; Hydrolase; Ion transport; Membrane; Nucleotide-binding; Reference proteome; Transport; Vacuole
SRR1221859_TR14946_c0_g3_i5_len=638	CB2D_SOLLC	Q:608-276;H:6-116	93.69%ID	E:4e-70	Chlorophyll a-b binding protein 1D	.	0.458	0.155	0	-2.667	0	1.036	0.004	0.613	0	-3.844	CB2D_SOLLC	Chlorophyll a-b binding protein 1D (LHCII type I CAB-1D) (LHCP) (Fragment)	CAB1D	Solanum lycopersicum (Tomato) (Lycopersicon esculentum)		Chloroplast; Complete proteome; Photosynthesis; Photosystem I; Photosystem II; Plastid; Reference proteome; Thylakoid; Transmembrane; Transmembrane helix
SRR1221859_TR59502_c0_g2_i1_len=668	CLPP6_ARATH	Q:143-334;H:208-271	87.5%ID	E:8e-33	ATP-dependent Clp protease proteolytic subunit 6, chloroplastic (EC0:0000303)PubMed:11299370)	.	0.068	1.067	0	-1.94	0.177	0.747	1	0.052	0	-1.577	CLPP6_ARATH	ATP-dependent Clp protease proteolytic subunit 6, chloroplastic (EC 3.4.21.92) (Endopeptidase ClpP6) (nClpP6) (nClpP1)	CLPP6 NCLPP1 NCLPP6 At1g11750 F25C20.10	Arabidopsis thaliana (Mouse-ear cress)		3D-structure; Alternative splicing; Chloroplast; Complete proteome; Direct protein sequencing; Hydrolase; Plastid; Protease; Reference proteome; Serine protease; Transit peptide
SRR1221859_TR12177_c0_g2_i5_len=870	EDL16_ARATH	Q:157-634;H:368-479	56.73%ID	E:4e-35	Sugar transporter ERD6-like 16	PF00083.21*Sugar_tr*Sugar (and other) transporter*38-115*E:2.5e-13	0.043	-1.279	0	-2.46	0.001	-3.175	0.001	-3.684	0	-1.642	EDL16_ARATH	Sugar transporter ERD6-like 16	At5g18840 F17K4.90	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Membrane; Reference proteome; Sugar transport; Transmembrane; Transmembrane helix; Transport
SRR1221859_TR28887_c0_g1_i4_len=1649	GDI2_ARATH	Q:263-1054;H:173-436	87.12%ID	E:2e-167	Guanosine nucleotide dissociation inhibitor 2	PF00996.15*GDI*GDP dissociation inhibitor*1-226*E:1.9e-113	0	1.893	0	-3.533	1	0.088	1	-0.57	0	-2.56	GDI2_ARATH	Guanosine nucleotide dissociation inhibitor 2 (AtGDI2)	GDI2 At3g59920 F24G16.190	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; GTPase activation; Reference proteome
SRR342017_TR7756_c1_g3_i3_len=811	PSBP_SPIOL	Q:76-567;H:104-267	83.54%ID	E:1e-96	Oxygen-evolving enhancer protein 2, chloroplastic	PF01789.13*PsbP*PsbP*26-188*E:1.6e-38	1	-0.31	0	-7.903	0.629	1.248	0.043	2.619	0	-2.658	PSBP_SPIOL	Oxygen-evolving enhancer protein 2, chloroplastic (OEE2) (23 kDa subunit of oxygen evolving system of photosystem II) (23 kDa thylakoid membrane protein) (OEC 23 kDa subunit)	PSBP	Spinacia oleracea (Spinach)		3D-structure; Chloroplast; Direct protein sequencing; Membrane; Photosynthesis; Photosystem II; Plastid; Thylakoid; Transit peptide
SRR342017_TR3199_c0_g5_i1_len=1156	NA	NA	NA	NA	NA	.	0.365	0.568	0	-1.631	0.001	6.552	1	0	0	-1.919	.	-	-	-		-
SRR342017_TR24038_c0_g1_i3_len=1877	XTH9_ARATH	Q:639-211;H:157-289	71.33%ID	E:9e-87	Xyloglucan endotransglucosylase-hydrolase protein 9	.	0.001	-1.162	0	-3.189	0.299	-1.786	0.034	-3.573	0	-1.069	XTH9_ARATH	Xyloglucan endotransglucosylase-hydrolase protein 9 (At-XTH9) (XTH-9) (EC 2.4.1.207)	XTH9 EXGT-A6 XTR16 At4g03210 F4C21.14	Arabidopsis thaliana (Mouse-ear cress)		Alternative splicing; Apoplast; Cell wall; Cell wall biogenesis/degradation; Complete proteome; Disulfide bond; Glycosylation; Glycosidase; Hydrolase; Reference proteome; Secreted; Signal; Transferase
SRR342017_TR26185_c0_g2_i3_len=833	CBSX5_ARATH	Q:90-659;H:193-389	52.79%ID	E:2e-42	CBS domain-containing protein CBSX5	.	0.129	-5.153	0	-8.119	1	0	1	0	0	-1.632	CBSX5_ARATH	CBS domain-containing protein CBSX5	CBSX5 At4g27460 F27G19.60	Arabidopsis thaliana (Mouse-ear cress)		CBS domain; Complete proteome; Reference proteome; Repeat
SRR342017_TR30787_c0_g2_i2_len=1214	EP1G_DAUCA	Q:333-629;H:263-373	48.65%ID	E:2e-25	Epidermis-specific secreted glycoprotein EP1	PF08276.8*PAN_2*PAN-like domain*59-88*E:2.2e-06 PF00024.23*PAN_1*PAN domain*60-88*E:0.00014	1	-1.051	0	-5.341	1	-1.282	1	1.492	0	-3.325	EP1G_DAUCA	Epidermis-specific secreted glycoprotein EP1 (52/54 KDa medium protein)	EP1	Daucus carota (Wild carrot)		Direct protein sequencing; Glycoprotein; Lectin; Secreted; Signal
SRR342019_TR19968_c3_g12_i11_len=818	VICHY_VICSN	Q:148-525;H:384-509	61.11%ID	E:9e-46	Vicianin hydrolase (EC0:0000312)EMBL:ABD03937.1)	PF00232.15*Glyco_hydro_1*Glycosyl hydrolase family 1*3-128*E:3e-38	0.76	0.747	0	-3.14	1	-3.165	1	-3.165	0	-1.648	VICHY_VICSN	Vicianin hydrolase (VH) (EC 3.2.1.119) (Fragment)		Vicia sativa subsp. nigra (Common vetch) (Vicia angustifolia)		Direct protein sequencing; Disulfide bond; Glycoprotein; Glycosidase; Hydrolase; Signal
SRR342019_TR25267_c2_g1_i2_len=663	PGKH_WHEAT	Q:610-371;H:390-469	96.25%ID	E:3e-33	Phosphoglycerate kinase, chloroplastic	PF00162.16*PGK*Phosphoglycerate kinase*18-89*E:5.7e-29	1	0.164	0	-1.913	0.892	-0.152	0.675	-0.305	0	-4.904	PGKH_WHEAT	Phosphoglycerate kinase, chloroplastic (EC 2.7.2.3)		Triticum aestivum (Wheat)	PATHWAY: Carbohydrate biosynthesis; Calvin cycle.	ATP-binding; Calvin cycle; Chloroplast; Complete proteome; Kinase; Nucleotide-binding; Plastid; Reference proteome; Stroma; Transferase; Transit peptide
SRR342019_TR27500_c1_g2_i3_len=1179	EFTA_TOBAC	Q:1113-517;H:238-436	97.99%ID	E:3e-135	Elongation factor 1-alpha	PF03144.22*GTP_EFTU_D2*Elongation factor Tu domain 2*7-50*E:2.2e-07 PF03143.14*GTP_EFTU_D3*Elongation factor Tu C-terminal domain*59-168*E:5.5e-39	0.003	-0.893	0	-1.413	0	0.967	0.576	0.17	0	-2.412	EFTA_TOBAC	Elongation factor 1-alpha (EF-1-alpha) (Vitronectin-like adhesion protein 1) (PVN1)		Nicotiana tabacum (Common tobacco)		Cytoplasm; Elongation factor; GTP-binding; Nucleotide-binding; Phosphoprotein; Protein biosynthesis
SRR342019_TR35318_c0_g1_i1_len=928	NA	NA	NA	NA	NA	.	0.791	-0.087	0	-1.183	0.18	-0.472	0.31	-0.37	0	-6.178	.	-	-	-		-
SRR342019_TR38162_c5_g11_i3_len=817	TIP1_ARATH	Q:76-373;H:121-251	82.44%ID	E:8e-62	Aquaporin TIP1-1	PF00230.17*MIP*Major intrinsic protein*1-84*E:5.9e-31	0.798	0.49	0	-3.05	0.206	0.752	0.458	0.493	0	-4.155	TIP1_ARATH	Aquaporin TIP1-1 (Aquaporin TIP) (Gamma-tonoplast intrinsic protein) (Gamma-TIP) (Tonoplast intrinsic protein 1-1) (AtTIP1;1) (Tonoplast intrinsic protein, root-specific RB7) [Cleaved into: Aquaporin TIP1-1, N-terminally processed]	TIP1-1 AQP1 At2g36830 T12I8.1	Arabidopsis thaliana (Mouse-ear cress)		Acetylation; Complete proteome; Membrane; Reference proteome; Repeat; Transmembrane; Transmembrane helix; Transport; Vacuole
SRR342022_TR24849_c2_g7_i1_len=3139	GLGB1_PEA	Q:2542-1037;H:342-846	85.74%ID	E:0	1,4-alpha-glucan-branching enzyme 1, chloroplastic/amyloplastic	PF00128.21*Alpha-amylase*Alpha amylase, catalytic domain*15-86*E:9.1e-13 PF02806.15*Alpha-amylase_C*Alpha amylase, C-terminal all-beta domain*404-498*E:1.9e-25	0.534	-0.402	0	-2.129	0.593	-0.671	0.239	-1.135	0	-4.28	GLGB1_PEA	1,4-alpha-glucan-branching enzyme 1, chloroplastic/amyloplastic (EC 2.4.1.18) (Starch branching enzyme I)	SBE1	Pisum sativum (Garden pea)	PATHWAY: Glycan biosynthesis; starch biosynthesis.	Amyloplast; Chloroplast; Direct protein sequencing; Plastid; Transferase; Transit peptide
SRR342022_TR24889_c4_g1_i1_len=565	NA	NA	NA	NA	NA	.	0.812	-0.187	0	-5.712	0.131	-0.496	0.011	-0.861	0	-3.916	.	-	-	-		-
SRR342022_TR27316_c4_g3_i1_len=1414	SYNC1_ARATH	Q:532-1218;H:342-672	74.46%ID	E:2e-119	Asparagine--tRNA ligase, cytoplasmic 1 (EC0:0000305)	PF00152.17*tRNA-synt_2*tRNA synthetases class II (D, K and N)*1-199*E:2e-41	0.629	1.285	0	-2.

SRR648707_TR22461_c0_g1_i2_len=1674	DXS2_ORYSJ	Q:102-1394,H:283-713	82.6%ID	E:0	Probable 1-deoxy-D-xylulose-5-phosphate synthase 2, chloroplastic	PF13292.3^DXP_synthase_N^1-deoxy-D-xylulose-5-phosphate synthase^6-51^E:6.9e-11 PF00275.21^Transket_pyr^Transketolase, pyrimidine binding domain^88-249^E:2.8e-43 PF02780.17^Transketolase_C^Transketolase, C-terminal domain^267-350^E:2.2e-31	0.107	0.576	0.001	-1.757	0.326	-0.556	0	-3.052	0.257	-0.308 DXS2_ORYSJ	Probable 1-deoxy-D-xylulose-5-phosphate synthase 2, chloroplastic (1-deoxyxylulose-5-phosphate synthase) (DXP synthase) (DXPS) (EC 2.2.1.7)	Oxo07g0190000 LOC_Oo07g09190 Os2_23394 OSJNBb0002L09.31 OSJNBb0003E08.7	Oryza sativa subsp. japonica (Rice)	PATHWAY: Metabolic intermediate biosynthesis; 1-deoxy-D-xylulose 5-phosphate biosynthesis; 1-deoxy-D-xylulose 5-phosphate from D-glyceraldehyde 3-phosphate and pyruvate: step 1/1.	Chloroplast; Complete proteome; Isoprene biosynthesis; Magnesium; Metal-binding; Plastid; Reference proteome; Thiamine biosynthesis; Thiamine pyrophosphate; Transferase; Transit peptide
SRR924147_TR21947_c2_g1_i1_len=1264	MTDH_APIGR	Q:1262-2243,H:17-359	57.73%ID	E:4e-130	Mannitol dehydrogenase	PF00840.9^ADH_N^Alcohol dehydrogenase GroES-like domain^22-131^E:3e-23 PF02826.16^2-Hacid_dh_C^D-isomer specific 2-hydroxyacid dehydrogenase, NAD binding domain^162-212^E:2.8e-06 PF00107.23^ADH_zinc_N^Zinc-binding dehydrogenase^175-298^E:5e-14	0.48	-0.153	0	-1.666	0.006	-0.617	0	-0.912	0.021	-0.922 MTDH_APIGR	Mannitol dehydrogenase (EC 1.1.1.255) (NAD-dependent mannitol dehydrogenase)	MTD	Apium graveolens (Celery)	-	Cytoplasm; Metal-binding; NAD; Oxidoreductase; Zinc
SRR342017_TR10068_c0_g1_i1_len=877	R10A1_ARATH	Q:235-878,H:1-214	90.19%ID	E:5e-126	60S ribosomal protein L10a-1	PF00687.18^Ribosomal_L1^Ribosomal protein L1p/L10e family^23-210^E:5.6e-44	0	-8.353	1	3.301	0	-6.845	0.854	-0.25	0.502	-4.155 R10A1_ARATH	60S ribosomal protein L10a-1	RPL10A At1g08360 T27G7.6	Arabidopsis thaliana (Mouse-ear cress)	-	Complete proteome; Reference proteome; Ribonucleoprotein; Ribosomal protein
SRR342017_TR11303_c0_g1_i1_len=1129	NA	NA	NA	NA	NA	-	0.001	-0.896	0.681	-0.165	0.001	-0.983	0.026	-0.631	0.001	1.294	-	-	-	-	-
SRR342023_TR12969_c4_g2_i2_len=506	G3PA_TOBAC	Q:200-505,H:9-109	86.27%ID	E:3e-45	Glyceraldehyde-3-phosphate dehydrogenase A, chloroplastic	PF00044.21^Gp_dh_N^Glyceraldehyde 3-phosphate dehydrogenase, NAD binding domain^69-119^E:1.9e-13	0	-1.22	0.08	0.627	0	-1.45	0.026	-0.505	0.009	0.557 G3PA_TOBAC	Glyceraldehyde-3-phosphate dehydrogenase A, chloroplastic (EC 1.2.1.13) (NADP-dependent glyceraldehydephosphate dehydrogenase subunit A) (Fragment)	GAPA	Nicotiana tabacum (Common tobacco)	PATHWAY: Carbohydrate biosynthesis; Calvin cycle.	Calvin cycle; Chloroplast; NADP; Oxidoreductase; Plastid; Transit peptide
SRR646572_TR8076_c0_g1_i1_len=820	NA	NA	NA	NA	NA	-	0	-2.078	0.704	0.161	0.001	-1.145	0.328	-0.299	0.642	0.222	-	-	-	-	-
SRR122236_TR9961_c0_g2_i2_len=816	CB23_TOBAC	Q:319-627,H:163-265	99.03%ID	E:5e-64	Chlorophyll a-b binding protein 36, chloroplastic	-	0.053	-0.49	0	-1.301	0	-1.127	0.01	-0.673	0.001	0.681 CB23_TOBAC	Chlorophyll a-b binding protein 36, chloroplastic (LHCII type I CAB-36) (LHCP)	CAB36	Nicotiana tabacum (Common tobacco)	-	-
SRR122238_TR54680_c0_g2_i2_len=1203	BAS1_ORYSJ	Q:815-228,H:66-401	95.41%ID	E:1e-133	2-Cys peroxiredoxin BAS1, chloroplastic	PF00578.18^AhpC-TSA^AhpC/TSA family^78-211^E:5e-41 PF08534.7^Redoxin^78-213^E:7.1e-15 PF10417.6^1-cysPrx_C^C-terminal domain of 1-Cys peroxiredoxin^232-287^E:5e-11	0.021	-0.503	0	-0.75	0	-0.762	0.014	-0.535	0.062	-0.458 BAS1_ORYSJ	2-Cys peroxiredoxin BAS1, chloroplastic (EC 1.11.1.15) (Thiol-specific antioxidant protein)	BAS1 Os02g0537700 LOC_Os02g33450 OSJNBa0014M172 P0506B05.23	Oryza sativa subsp. japonica (Rice)	-	Antioxidant; Chloroplast; Disease resistance; Direct protein sequencing; Disulfide bond; Hydrogen peroxide; Oxidoreductase; Peroxidase; Plastid; Redoxactive center; Reference proteome; Transit peptide
SRR122238_TR55852_c0_g1_i2_len=930	RBS_MALSP	Q:851-312,H:1-183	81.42%ID	E:2e-107	Ribulose bisphosphate carboxylase small chain, chloroplastic	PF12338.5^RbcS^Ribulose-1,5-bisphosphate carboxylase small subunit^2-42^E:6.5e-21 PF00101.17^RuBisCO_small^Ribulose bisphosphate carboxylase, small chain^69-177^E:1.2e-39	0.097	-0.427	0	-1.073	0	-0.821	0.007	-0.612	0.551	-0.154 RBS_MALSP	Ribulose bisphosphate carboxylase small chain, chloroplastic (RuBisCO small subunit) (EC 4.1.1.39)	RBCS	Malus sp. (Crab apple)	-	Calvin cycle; Carbon dioxide fixation; Chloroplast; Lyase; Monooxygenase; Oxidoreductase; Photorespiration; Photosynthesis; Plastid; Transit peptide
SRR122238_TR76493_c0_g1_i2_len=816	PSAN_ARATH	Q:163-666,H:1-168	69.19%ID	E:9e-61	Photosystem I reaction center subunit N, chloroplastic	PF05479.8^PsaN^Photosystem I reaction centre subunit N (PSAN or PSI-N)^97-225^E:6.7e-68	0.796	-0.055	0	-0.999	0	-0.725	0.005	-0.587	0.981	0.006 PSAN_ARATH	Photosystem I reaction center subunit N, chloroplastic (PSI-N)	PSAN At5g64040 MHJ24.2	Arabidopsis thaliana (Mouse-ear cress)	-	Arabidopsis thaliana; Chloroplast; Direct protein sequencing; Membrane; Photosynthesis; Photosystem I; Plastid; Reference proteome; Thylakoid; Transit peptide
SRR127857_TR6634_c0_g1_i3_len=2761	CP41B_ARATH	Q:1417-2550,H:1-378	85.19%ID	E:0	Chloroplast stem-loop binding protein of 41 kDa b, chloroplastic	PF04321.14^RmlD_sub_bind^RmlD substrate binding domain^55-299^E:9e-05 PF01370.18^Epimerase^NAD dependent epimerase/dehydratase family^56-273^E:1.2e-13 PF13460.3^NAD_binding_10^NAD(P)H-binding^60-212^E:9.6e-09	0.252	-0.299	0	-0.93	0	-0.828	0.01	-0.61	0.324	-0.239 CP41B_ARATH	Chloroplast stem-loop binding protein of 41 kDa b, chloroplastic (CSP41b) (Heteroglycan-interacting protein 1.3) (Protein CHLOROPLAST RNA BINDING) (Protein GbS1)	CSP41B CRB HIP1.3 At1g09340 T31J12.6	Arabidopsis thaliana (Mouse-ear cress)	-	Carbohydrate metabolism; Chloroplast; Direct protein sequencing; Membrane; Photosynthesis; Photosystem I; Plastid; Reference proteome; Polysaccharide degradation; RNA-binding; Reference proteome; Transit peptide; rRNA processing; rRNA-binding
SRR127857_TR8697_c0_g1_i2_len=905	LOG1_ARATH	Q:207-602,H:80-211	90.15%ID	E:3e-80	Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG1	PF03641.11^Lysine_decarbox^Possible lysine decarboxylase^5-90^E:5.6e-35	0.13	-0.642	0	-3.578	0.001	-1.722	0.003	-1.416	0.62	-0.259 LOG1_ARATH	Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG1 (EC 3.2.2.n1) (Protein LONELY GUY 1)	LOG1 At2g28305 T18L18 T3B23.2	Arabidopsis thaliana (Mouse-ear cress)	-	Complete proteome; Cytokinin biosynthesis; Cytoplasm; Hydrolase; Nucleus; Reference proteome
SRR127857_TR18439_c1_g1_i3_len=1505	NA	NA	NA	NA	NA	PF14215.3^bHLH-MYC_N^bHLH-MYC and R2R3-MYB transcription factors N-terminal^13-198^E:5.2e-27	0.24	-0.408	0	-3.185	0.001	-1.687	0.013	-1.224	1	-0.043	-	-	-	-	-
SRR127857_TR20316_c0_g1_i2_len=1988	PSBO_TOBAC	Q:94-988,H:79-332	91.34%ID	E:6e-164	Oxygen-evolving enhancer protein 1, chloroplastic	PF01716.15^MSP^Manganese-stabilising protein / photosystem II polypeptide^1-161^E:1.3e-76	0.923	-0.021	0	-0.64	0.692	-0.672	0.691	PSBO_TOBAC	Oxygen-evolving enhancer protein 1, chloroplastic (OEE1) (33 kDa subunit of oxygen evolving system of photosystem II) (33 kDa thylakoid membrane protein) (OEC 33kDa subunit) (OEC33)	PSBO	Nicotiana tabacum (Common tobacco)	-	Chloroplast; Manganese; Membrane; Photosynthesis; Photosystem II; Plastid; Thylakoid; Transit peptide
SRR127857_TR25644_c0_g1_i1_len=1865	CHLI_SOYBN	Q:1-1475,H:1-421	85.82%ID	E:0	Magnesium-chelatase subunit ChlI, chloroplastic	PF01078.18^Mg_chelatase^Magnesium chelatase, subunit ChlI^198-268^E:2.9e-07 PF00493.20^MCM^MCM2/3/5 family^201-388^E:4.4e-06	0.023	-0.529	0	-1.046	0	-0.936	0.004	-0.664	0.82	0.055 CHLI_SOYBN	Magnesium-chelatase subunit ChlI, chloroplastic (Mg-chelatase subunit I-1) (EC 6.6.1.1) (Mg-protoporphyrin IX chelatase subunit ChlI)	CHLI	Glycine max (Soybean) (Glycine hispida)	PATHWAY: Porphyrin-containing compound metabolism; chlorophyll biosynthesis.	Chloroplast; Direct protein sequencing; Membrane; Metal-binding; Nucleus; Reference proteome; Transit peptide
SRR127857_TR30200_c1_g3_i1_len=1157	CAHC_SPIOL	Q:1074-547,H:144-339	89.2%ID	E:5e-110	Carbonic anhydrase, chloroplastic	PF00484.16^Pro_CA^Carbonic anhydrase^1-158^E:5.6e-40	0.033	-0.641	0	-3.577	0	-1.996	0.095	-0.741	0.118	-1.842 CAHC_SPIOL	Carbonic anhydrase, chloroplastic (EC 4.2.1.1) (Carbonate dehydratase)	-	Spinacia oleracea (Spinach)	-	Chloroplast; Direct protein sequencing; Lyase; Plastid; Transit peptide; Zinc
SRR127858_TR28861_c0_g1_i1_len=1089	APT3_ARATH	Q:896-372,H:7-181	82.86%ID	E:1e-99	Adenine phosphoribosyltransferase 3	PF00156.24^Pribosyltran^Phosphoribosyl transferase domain^44-167^E:6e-20	0.746	-0.11	0	-2.138	0	-2.322	0.002	-1.38	0.444	0.239 APT3_ARATH	Adenine phosphoribosyltransferase 3 (EC 2.4.2.7)	APT3 At4g22570 F7K2.150	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Purine metabolism; AMP biosynthesis via salvage pathway; AMP from adenine: step 1/1.	Complete proteome; Cytoplasm; Glycosyltransferase; Purine salvage; Reference proteome; Transferase
SRR127858_TR8859_c1_g4_i3_len=1797	MTDH_APIGR	Q:117-603,H:33-359	57.49%ID	E:2e-118	Mannitol dehydrogenase	PF00840.9^ADH_N^Alcohol dehydrogenase GroES-like domain^5-92^E:2.8e-17 PF02826.16^2-Hacid_dh_C^D-isomer specific 2-hydroxyacid dehydrogenase, NAD binding domain^123-172^E:3.3e-06 PF00107.23^ADH_zinc_N^Zinc-binding dehydrogenase^136-259^E:3.8e-14	0.294	0.523	0	-2.758	0.001	-1.793	0.004	-1.403	0.147	-0.938 MTDH_APIGR	Mannitol dehydrogenase (EC 1.1.1.255) (NAD-dependent mannitol dehydrogenase)	MTD	Apium graveolens (Celery)	-	Cytoplasm; Metal-binding; NAD; Oxidoreductase; Zinc
SRR342017_TR8869_c0_g2_i1_len=978	NDADA_ARATH	Q:79-351,H:1-93	87.41%ID	E:1e-86	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13-A	PF06212.9^GRIM-19^GRIM-19 protein^20-138^E:2.2e-42	0.43	0.688	0	-2.208	0	-2.772	0.019	-1.271	1	0 NDADA_ARATH	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13-A (Protein MATERNAL EFFECT EMBRYO ARREST 4)	MEE4 At1g04630 T1G11.12	Arabidopsis thaliana (Mouse-ear cress)	-	Complete proteome; Electron transport; Membrane; Mitochondrion; Mitochondrion inner membrane; Reference proteome; Respiratory chain; Transmembrane; Transmembrane helix; Transport
SRR342017_TR10762_c4_g2_i5_len=3443	LACS2_ARATH	Q:91-2145,H:3-661	64.97%ID	E:0	Long chain acyl-CoA synthetase 2	PF00501.25^AMP-binding^AMP-binding enzyme^52-621^E:3.3e-99	0.451	-0.31	0.001	-1.954	0	-1.742	0.007	-1.141	0.095	0.729 LACS2_ARATH	Long chain acyl-CoA synthetase 2 (EC 6.2.1.3) (Protein Botrytis resistant 1) (Protein LATERAL ROOT DEVELOPMENT 2)	LACS2 BRE1 LRD2 SMA4 At1g49430 F13F21.14	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Lipid metabolism; fatty acid metabolism.	Complete proteome; Endoplasmic reticulum; Fatty acid metabolism; Ligase; Lipid metabolism; Magnesium; Nucleotide-binding; Reference proteome
SRR342017_TR2730_c0_g2_i1_len=846	NA	NA	NA	NA	NA	-	0.816	-0.109	0	-3.51	0.001	-2.094	0.021	-1.242	0.258	-0.499	-	-	-	-	-
SRR342017_TR32028_c2_g3_i3_len=2023	HEM3_PEA	Q:651-1649,H:40-369	83.53%ID	E:0	Porphobilinogen deaminase, chloroplastic	PF01379.17^Porphobil_deam^Porphobilinogen deaminase, dipyrromethane cofactor binding domain^73-284^E:1.5e-72 PF03900.12^Porphobil_deamC^Porphobilinogen deaminase, C-terminal domain^298-370^E:3.6e-13	0.005	-0.725	0	-1.189	0.001	-1.151	0.024	-0.733	0.666	-0.113 HEM3_PEA	Porphobilinogen deaminase, chloroplastic (PBG) (EC 2.5.1.61) (Hydroxymethylbilane synthase) (HMBS) (Pre-uroporphyrinogen synthase)	HEMC	Pisum sativum (Garden pea)	PATHWAY: Porphyrin-containing compound metabolism; protoporphyrin-IX biosynthesis; coproporphyrinogen-III from 5-aminolevulinate: step 2/4.; PATHWAY: Porphyrin-containing compound metabolism; chlorophyll biosynthesis.	Chlorophyll biosynthesis; Chloroplast; Direct protein sequencing; Plastid; Porphyrin biosynthesis; Transferase; Transit peptide
SRR342019_TR17507_c0_g10_i1_len=1488	NA	NA	NA	NA	NA	-	0.395	-0.306	0	-2.96	0	-1.889	0.002	-1.71	0.004	-1.214	-	-	-	-	-
SRR342019_TR19760_c0_g1_i1_len=1781	DCVR_CUCSA	Q:211-1455,H:1-419	75.18%ID	E:0	Divinyl chlorophyllide a 8-vinyl-reductase, chloroplastic	PF05368.10^NmrA^NmrA-like family^84-323^E:4.3e-13 PF03720.18^Epimerase^NAD dependent epimerase/dehydratase family^84-203^E:1e-08 PF01073.16^3Beta_HSD^3-beta hydroxysteroid dehydrogenase/isomerase family^85-20^E:8e-06 PF13460.3^NAD_binding_10^NAD(P)H-binding^88-296^E:4.6e-19	0.158	-0.458	0	-1.203	0	-1.082	0.003	-0.81	0.337	0.28 DCVR_CUCSA	Divinyl chlorophyllide a 8-vinyl-reductase, chloroplastic (EC 1.3.1.75)	DVR	Cucumis sativus (Cucumber)	PATHWAY: Porphyrin-containing compound metabolism; chlorophyll biosynthesis.	Chlorophyll biosynthesis; Chloroplast; NADP; Oxidoreductase; Plastid; Transit peptide
SRR342019_TR21621_c2_g1_i1_len=1884	Y4744_ARATH	Q:1447-401,H:49-387	42.13%ID	E:4e-86	Uncharacterized protein At4g06744	PF13516.3^LRR_6^Leucine Rich repeat^29-293^E:1.2	0.068	-0.436	0	-2.041	0	-1.178	0.003	-0.927	0.012	-0.621 Y4744_ARATH	Uncharacterized protein At4g06744	At4g06744 F15N16	Arabidopsis thaliana (Mouse-ear cress)	-	Complete proteome; Leucine-rich repeat; Reference proteome; Repeat; Secreted; Signal
SRR342019_TR30363_c1_g4_i2_len=3294	HEM6_TOBAC	Q:1378-164,H:1-397	76.85%ID	E:0	Oxygen-dependent coproporphyrinogen-III oxidase, chloroplastic	-	0.033	-0.641	0	-1.164	0	-1.102	0.003	-0.889	0.377	-0.29 HEM6_TOBAC	Oxygen-dependent coproporphyrinogen-III oxidase, chloroplastic (Coprogen oxidase) (Coproporphyrinogenase) (EC 1.3.3.3)	CPX	Nicotiana tabacum (Common tobacco)	PATHWAY: Porphyrin-containing compound metabolism; protoporphyrin-IX biosynthesis; protoporphyrinogen-IX from coproporphyrinogen-III (O2 route): step 1/1.	Chlorophyll biosynthesis; Chloroplast; Heme biosynthesis; Oxidoreductase; Plastid; Porphyrin biosynthesis; Transit peptide
SRR342019_TR38174_c0_g1_i6_len=904	RR13_ARATH	Q:163-615,H:4-154	74.17%ID	E:1e-71	30S ribosomal protein S13, chloroplastic	PF00416.19^Ribosomal_S13^Ribosomal protein S13/S18^45-149^E:2.8e-32	0.366	-0.21	0	-1.006	0	-0.824	0.003	-0.704	0.032	-0.472 RR13_ARATH	30S ribosomal protein S13, chloroplastic (CS13)	RPS13 At5g14320 F18O22_110	Arabidopsis thaliana (Mouse-ear cress)	-	Alternative splicing; Chloroplast; Complete proteome; Plastid; RNA-binding; Reference proteome; Ribonucleoprotein; Ribosomal protein; Transit peptide; rRNA-binding
SRR342022_TR25676_c0_g3_i1_len=2187	PLY18_ARATH	Q:1579-434,H:27-408	86.13%ID	E:0	Probable pectate lyase 18	PF15044.3^CLU_N^Mitochondrial function, CLU-N term^49-120^E:3e-08 PF12807.4^eIF3_p135^Translation initiation factor eIF3 subunit 135^726-867^E:5.6e-25 PF13424.3^TPR_12^Tetratricopeptide repeat^907-968^E:2e-08 PF13424.3^TPR_12^Tetratricopeptide repeat^937-1007^E:5.5e-13 PF13374.3^TPR_10^Tetratricopeptide repeat^937-978^E:9.3e-09 PF13181.3^TPR_8^Tetratricopeptide repeat^938-969^E:0.11 PF13424.3^TPR_12^Tetratricopeptide repeat^1021-1095^E:1e-10 PF13374.3^TPR_10^Tetratricopeptide repeat^1021-1060^E:1e-06	0.862	0.067	0	-1.839	0	-1.018	0.032	-0.586	0.226	2.285 PLY18_ARATH	Probable pectate lyase 18 (EC 4.2.2.2) (Pectate lyase A10)	At4g24780 F22K18.20	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Glycan metabolism; pectin degradation; 2-dehydro-3-deoxy-D-gluconate from pectin: step 2/5.	Signal
SRR342022_TR28271_c1_g1_i1_len=6054	CLU_ARATH	Q:2492-378,I:H:788-1258	38.87%ID	E:3e-89	Clustered mitochondria protein	PF15044.3^CLU_N^Mitochondrial function, CLU-N term^48-117^E:1.5e-08 PF12807.4^eIF3_p135^Translation initiation factor eIF3 subunit 135^734-877^E:2.5e-23 PF13424.3^TPR_12^Tetratricopeptide repeat^947-1017^E:2.8e-13 PF13374.3^TPR_10^Tetratricopeptide repeat^947-987^E:2.5e-08 PF13181.3^TPR_8^Tetratricopeptide repeat^949-979^E:0.19 PF13424.3^TPR_12^Tetratricopeptide repeat^1031-1105^E:1.6e-11 PF13374.3^TPR_10^Tetratricopeptide repeat^1031-1070^E:1.9e-06	1	-0.128	0	-8.831	0	-0.906	0.006	-0.687	1	0 CLU_ARATH	Clustered mitochondria protein (Friendly mitochondria protein)	FMT CLU At3g52140 FAF15.250	Arabidopsis thaliana (Mouse-ear cress)	-	Alternative splicing; Complete proteome; Cytoplasm; Reference proteome; Repeat; TPR repeat
SRR342023_TR3519_c2_g1_i1_len=1064	PLAS_SOLLC	Q:219-695,H:11-170	76.54%ID	E:3e-67	Plastocyanin, chloroplastic	-	0.249	-0.244	0	-2.18	0	-0.788	0.007	-0.563	0	0.951 PLAS_SOLLC	Plastocyanin, chloroplastic	PETE	Solanum lycopersicum (Tomato) (Lycopersicon esculentum)	-	Chloroplast; Complete proteome; Copper; Electron transport; Membrane; Metal-binding; Plastid; Reference proteome; Thylakoid; Transit peptide; Transport
SRR342023_TR8761_c0_g3_i1_len=1004	NA	NA	NA	NA	NA	-	0.074	-0.942	0	-1.785	0	-3.297	0.004	-2.038	1	-0.064	-	-	-	-	-
SRR342023_TR18283_c3_g6_i1_len=860	NA	NA	NA	NA	NA	-	0.807	0.167	0	-1.723	0.001	-1.478	0.025	-0.893	0.848	0.333	-	-	-	-	-
SRR646596_TR18300_c0_g1_i1_len=1635	FENR1_TOBAC	Q:344-1348,H:29-362	89.85%ID	E:0	Ferredoxin--NADP reductase, leaf-type isozyme, chloroplastic	PF03970.21^FAD_binding_8^Oxidoreductase FAD-binding domain^118-204^E:0.00016 PF00175.18^NAD_binding_1^Oxidoreductase NAD-binding domain^218-333^E:8e-30 PF13738.3^Pyr_redox_3^Pyridine nucleotide-disulphide oxidoreductase^8-774^E:2.8e-16 PF07714.14^Pkinase_Tyr^Protein tyrosine kinase^815-894^E:7.5e-06	0.618	-0.114	0	-0.835	0	-0.777	0.006	-0.584	0.019	-0.502 FENR1_TOBAC	Ferredoxin--NADP reductase, leaf-type isozyme, chloroplastic (FNR) (EC 1.18.1.2)	PETH	Nicotiana tabacum (Common tobacco)	PATHWAY: Energy metabolism; photosynthesis.	Chloroplast; Electron transport; FAD; Flavoprotein; Membrane; NADP; Oxidoreductase; Photosynthesis; Plastid; Thylakoid; Transit peptide; Transport
SRR646604_TR2290_c0_g1_i1_len=1657	CP41A_ARATH	Q:1329-346,H:78-405	82.93%ID	E:0	Chloroplast stem-loop binding protein of 41 kDa a, chloroplastic	PF04321.14^RmlD_sub_bind^RmlD substrate binding domain^55-299^E:9e-05 PF01370.18^Epimerase^NAD dependent epimerase/dehydratase family^88-298^E:5.9e-08 PF13460.3^NAD_binding_10^NAD(P)H-binding^88-246^E:2.4e-06	0.008	-1.343	0	-2.682	0	-1.471	0.005	-1.038	1	0.066 CP41A_ARATH	Chloroplast stem-loop binding protein of 41 kDa a, chloroplastic (CSP41a)	CSP41A At3g63140 T20O10.240	Arabidopsis thaliana (Mouse-ear cress)	-	Chloroplast; Complete proteome; Direct protein sequencing; Membrane; Photosynthesis; Photosystem I; Plastid; Reference proteome; Thylakoid; Transit peptide; rRNA processing; rRNA-binding
SRR646604_TR5735_c0_g1_i1_len=2479	PSAO_ARATH	Q:258-596,H:28-140	87.61%ID	E:4e-61	Photosystem I subunit O	PF03715.25^Cyb5^Cytochrome b5like Heme/Steroid binding domain^9-77^E:6.5e-24 PF00487.21^FA_desaturase^Fatty acid desaturase^137-223^E:4.8e-11	0.832	-0.332	0	-2.81	0	-2.475	0.001	-2.035	0.581	0.395 PSAO_ARATH	Photosystem I subunit O (PSI-O)	PSAO At1g08380 T27G7	Arabidopsis thaliana (Mouse-ear cress)	-	Chloroplast; Direct protein sequencing; Membrane; Photosynthesis; Photosystem I; Plastid; Reference proteome; Thylakoid; Transit peptide; Transmembrane helix
SRR646604_TR5839_c0_g1_i12_len=3706	PHOT2_ARATH	Q:2929-335,H:64-915	74.89%ID	E:0	Phototropin-2	PF13426.4^PAS_9^PAS domain^176-272^E:4.1e-19 PF00989.22^PAS^PAS fold^182-267^E:1.5e-08 PF08447.9^PAS_3^PAS fold^183-266^E:8e-08 PF13426.4^PAS_9^PAS domain^446-538^E:2e-19 PF00989.22^PAS^PAS fold^449-538^E:2.2e-08 PF00989.22^PAS^Protein kinase domain^626-815^E:4e-60 PF07714.14^Pkinase_Tyr^Protein tyrosine kinase^628-774^E:2.8e-16 PF07714.14^Pkinase_Tyr^Protein tyrosine kinase^815-894^E:7.5e-06	0.341	-0.419	0	-2.464	0	-1.09	0.002	-0.818	0.24	0.398 PHOT2_ARATH	Phototropin-2 (EC 2.7.11.1) (Defective in chloroplast avoidance protein 1) (Non-phototropic hypocotyl 1-like protein 1) (ANK/ITP) (NPH1-like protein 1)	PHOT2 CAV1 KIN7 NPL1 At5g58140 K21L19.6	Arabidopsis thaliana (Mouse-ear cress)	-	3D-structure; ATP-binding; Alternative splicing; Cell membrane; Chromophore; Complete proteome; FMN; Flavoprotein; Kinase; Membrane; Nucleotide-binding; Phosphoprotein; Photoreceptor protein; Reference proteome; Repeat; Sensory transduction; Serine/threonine-protein kinase; Transferase
SRR646604_TR16056_c0_g4_i3_len=1773	PX24B_DICDI	Q:855-1439,H:1-182	31.28%ID	E:2e-24	PXMP2/4 family protein 2	PF04117.9^Mpv17_PMP22^Mpv17 / PMP22 family^129-189^E:1.2e-15	0.33	-0.366	0	-2.718	0.001	-1.987	0.008	-1.451	0.23	0.464 PX24B_DICDI	PXMP2/4 family protein 2	DDB_G0278529	Dictyostelium discoideum (Slime mold)	-	Complete proteome; Membrane; Reference proteome; Transmembrane; Transmembrane helix
SRR646604_TR17949_c0_g1_i1_len=1768	CB4A_ARATH	Q:1441-626,H:14-287	86.5%ID	E:1e-161	Chlorophyll a-b binding protein CP29.1, chloroplastic	PF00504.18^Chloroa_b-bind^Chlorophyll A-B binding protein^60-256^E:1.5e-49	0.953	0.014	0	-1.479	0	-0.816	0.002	-0.652	0.274	0.253 CB4A_ARATH	Chlorophyll a-b binding protein CP29.1, chloroplastic (LHCB4.1) (LHCIII protein 4.1)	LHCB4.1 At5g01530 F7A7_50	Arabidopsis thaliana (Mouse-ear cress)	-	Chlorophyll; Chloroplast; Chromophore; Complete proteome; Membrane; Metal-binding; Phosphoprotein; Photosynthesis; Photosystem I; Photosystem II; Plastid; Reference proteome; Thylakoid; Transit peptide; Transmembrane; Transmembrane helix
SRR648707_TR19129_c1_g1_i1_len=1022	RBS_MALSP	Q:795-256,H:1-183	81.42%ID	E:5e-107	Ribulose bisphosphate carboxylase small chain, chloroplastic	PF12338.5^RbcS^Ribulose-1,5-bisphosphate carboxylase small subunit^2-42^E:6.5e-21 PF00101.17^RuBisCO_small^Ribulose bisphosphate carboxylase, small chain^69-177^E:1.2e-39 PF00269.22^Pkinase^Protein kinase domain^1-211^E:3e-29 PF07714.14^Pkinase_Tyr^Protein tyrosine kinase^2-123^E:5.3e-08	0.513	-0.135	0	-0.724	0	-0.87	0.002	-0.654	0.213	-0.257 RBS_MALSP	Ribulose bisphosphate carboxylase small chain, chloroplastic (RuBisCO small subunit) (EC 4.1.1.39)	RBCS	Malus sp. (Crab apple)	-	Calvin cycle; Carbon dioxide fixation; Chloroplast; Lyase; Monooxygenase; Oxidoreductase; Photorespiration; Photosynthesis; Plastid; Transit peptide
SRR924147_TR37530_c0_g2_i2_len=2375	AFC2_ARATH	Q:1186-542,H:212-425	80.09%ID	E:3e-116	Serine/threonine-protein kinase AFC2	PF00069.22^Pkinase^Protein kinase domain^1-211^E:3e-29 PF07714.14^Pkinase_Tyr^Protein tyrosine kinase^2-123^E:5.3e-08	0.155	-1.15	0	-6.876	0	-7.317	0.014	-1.801	1	0 AFC2_ARATH	Serine/threonine-protein kinase AFC2 (EC 2.7.12.1)	AFC2 At4g24740 F22K18.60	Arabidopsis thaliana (Mouse-ear cress)	-	ATP-binding; Alternative splicing; Complete proteome; Kinase; Nucleotide-binding; Reference proteome; Serine/threonine-protein kinase; Transferase
SRR924148_TR23282_c0_g1_i1_len=1579	PRXQ_GENTR	Q:217-1217,H:1-217	77.42%ID	E:1e-112	Peroxiredoxin Q, chloroplastic	PF08534.7^Redoxin^Redoxin^74-206^E:3.4e-26 PF00578.18^AhpC-TSA^AhpC/TSA family^75-193^E:4.5e-41	0.583	-0.174	0	-1.177	0	-0.972	0.006	-0.748	0.635	0.387 PRXQ_GENTR	Peroxiredoxin Q, chloroplastic (EC 1.11.1.15) (Thioredoxin reductase)	AFP1	Gentiana triflora (Clustered gentian)	-	Antioxidant; Chloroplast; Disulfide bond; Oxidoreductase; Peroxidase; Plastid; Redox-active center; Thylakoid; Transit peptide
SRR342022_TR6161_c1_g4_i7_len=1903	PGKH_TOBAC	Q:1723-308,H:1-472	91.31%ID	E:0	Phosphoglycerate kinase, chloroplastic	PF00162.16^PGK^Phosphoglycerate kinase^146-524^E:3.9e-161	0.421	-0.182	0.107	-0.35	0	-1.044	0.001	-0.692	0	-3.32 PGKH_TOBAC	Phosphoglycerate kinase, chloroplastic (EC 2.7.2.3)	CB23 At1g56190 T10O22.21	Nicotiana tabacum (Common tobacco)	PATHWAY: Carbohydrate biosynthesis; Calvin cycle.	ATP-binding; Calvin cycle; Chloroplast; Kinase; Nucleotide-binding; Plastid; Transferase; Transit peptide
SRR342022_TR28030_c0_g3_i1_len=1265	CB23_TOBAC	Q:161-955,H:1-265	92.45%ID	E:4e-180	Chlorophyll a-b binding protein 36, chloroplastic	PF00504.18^Chloroa_b-bind^Chlorophyll A-B binding protein^66-231^E:5.2e-50	0.249	0.374	0.027	-0.619	0	-1.777	0.02	-0.638	0	-3.315 CB23_TOBAC	Chlorophyll a-b binding protein 36, chloroplastic (LHCII type I CAB-36) (LHCP)	CAB36	Nicotiana tabacum (Common tobacco)	-	Chlorophyll; Chloroplast; Chromophore; Membrane; Metal-binding; Phosphoprotein; Photosynthesis; Photosystem I; Photosystem II; Plastid; Thylakoid; Transit peptide; Transmembrane; Transmembrane helix
SRR122238_TR32454_c2_g1_i1_len=738	GASA4_ARATH	Q:154-411,H:20-106	70.45%ID	E:3e-34	Gibberellin-regulated protein 4	PF02704.11^GASA^Gibberellin regulated protein^47-106^E:3.7e-22	0.001	-0.872	0	-3.035	0	-1.456	0.003	-1.054	0.016	-0.672 GASA4_ARATH	Gibberellin-regulated protein 4 (GAST1 protein

SRR342019_TR1262_c0_g1_i1_len=411	NA	NA	NA	NA	NA	.	1	0.056	0	-3.196	0	-2.375	0	-1.935	0.094	1.107	.	.	.	.	.	.	.
SRR342019_TR1943_c7_g2_i6_len=1601	CAHC_TOBAC	Q:1496-610,H:1-321	77.27%ID	E:2e-157	Carbonic anhydrase, chloroplastic	PF00484.16*Pro_CA*Carbonic anhydrase*156-313*E:2.5e-39	0.285	-0.239	0	-0.957	0	-1.496	0	-1.577	0.018	-0.796 CAHC_TOBAC	Carbonic anhydrase, chloroplastic (EC 4.2.1.1) (Carbonate dehydratase)	Nicotiana tabacum (Common tobacco)	Chloroplast; Lyase; Plastid; Transit peptide; Zinc
SRR342019_TR17300_c1_g4_i2_len=668	PSAO_ARATH	Q:38-137,H:28-111	84.52%ID	E:3e-43	Photosystem I subunit O	.	0.805	0.065	0	-1.054	0	-1.073	0	-0.952	0.101	0.461 PSAO_ARATH	Photosystem I subunit O (PSI-O)	PSAO At1g08380 T27G7	Arabidopsis thaliana (Mouse-ear cress)	Chloroplast; Complete proteome; Direct protein sequencing; Membrane; Photosynthesis; Photosystem I; Plastid; Reference proteome; Thylakoid; Transit peptide; Transmembrane; Transmembrane helix
SRR342019_TR18410_c0_g8_i1_len=573	CB4A_SOLLC	Q:346-2,H:1-111	82.61%ID	E:2e-49	Chlorophyll a/b binding protein CP24 10A, chloroplastic	PF00504.18*Chloro_b-bind*Chlorophyll A/B binding protein*72-115*E:2.4e-19	0.082	-0.428	0	-1.127	0	-1.532	0	-1.29	0.016	0.672 CB4A_SOLLC	Chlorophyll a/b binding protein CP24 10A, chloroplastic (CAB-10A) (LHCP)	CAP10A	Solanum lycopersicum (Tomato) (Lycopersicon esculentum)	Chlorophyll; Chloroplast; Chromophore; Complete proteome; Membrane; Photosynthesis; Photosystem II; Plastid; Reference proteome; Thylakoid; Transit peptide; Transmembrane; Transmembrane helix
SRR342019_TR20493_c2_g1_i1_len=2112	NA	NA	NA	NA	NA	.	0.352	0.313	0	-1.261	0.001	-1.022	0	-1.302	1	1.059	.	.	.	.	.	.	.
SRR342019_TR21154_c4_g3_i1_len=943	PB27A_ARATH	Q:638-246,H:41-237	70.37%ID	E:3e-58	Photosystem II repair protein PSB27-H1, chloroplastic	PF13326.3*PSII_Pbs27*Photosystem II Pbs27*42-171*E:5.7e-31	0.039	-0.505	0	-1.573	0	-0.958	0.001	-0.761	0.798	-0.47 PB27A_ARATH	Photosystem II repair protein PSB27-H1, chloroplastic (Psb27-H1) (Thylakoid lumenal protein PSB27-H1)	PSB27-1 At1g03600 F21B7.14 F21B7.21 F21B7.22 F21B7_140	Arabidopsis thaliana (Mouse-ear cress)	Chloroplast; Complete proteome; Direct protein sequencing; Membrane; Phosphoprotein; Plastid; Reference proteome; Thylakoid; Transit peptide
SRR342019_TR22648_c0_g2_i2_len=1741	DAAA_ARATH	Q:1164-265,H:70-373	59.47%ID	E:9e-125	3-amino-acid transaminase, chloroplastic (ECO:0000303|PubMed:18318836)	PF01063.16*Aminotran_4*Amino-transferase class IV*77-301*E:1.9e-40	0.002	-1.271	0	-2.057	0	-2.34	0	-1.979	1	0.097 DAAA_ARATH	3-amino-acid transaminase, chloroplastic (EC 2.6.1.21) (EC 4.1.3.38) (Aminodeoxychorismate lyase) (ADACL) (Branched-chain-amino-acid aminotransferase-like protein 3)	DAAT BCAL3 At5g57850 MTI20.10	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Cofactor biosynthesis; tetrahydrofolate biosynthesis; 4-aminobenzoate from chorismate: step 2/2.
SRR342019_TR23916_c4_g1_i2_len=1152	CB22_TOBAC	Q:90-484,H:1-265	93.96%ID	E:0	Chlorophyll a/b binding protein 21, chloroplastic	PF00504.18*Chloro_b-bind*Chlorophyll A/B binding protein*65-231*E:1.6e-50	0.531	-0.139	0	-2.022	0	-0.804	0	-0.937	0.447	0.157 CB22_TOBAC	Chlorophyll a/b binding protein 21, chloroplastic (LHCII type I CAB-21) (LHCP)	CAB21	Nicotiana tabacum (Common tobacco)	Acetylation; Chloroplast; Chromophore; Magnesium; Membrane; Metal-binding; Phosphoprotein; Photosystem I; Photosystem II; Plastid; Thylakoid; Transit peptide; Transmembrane; Transmembrane helix
SRR342019_TR23916_c4_g1_i3_len=1251	CB22_TOBAC	Q:90-484,H:1-265	93.96%ID	E:0	Chlorophyll a/b binding protein 21, chloroplastic	PF00504.18*Chloro_b-bind*Chlorophyll A/B binding protein*65-231*E:1.6e-50	0.211	-0.257	0	-0.902	0	-0.967	0	-0.771	0.384	0.178 CB22_TOBAC	Chlorophyll a/b binding protein 21, chloroplastic (LHCII type I CAB-21) (LHCP)	CAB21	Nicotiana tabacum (Common tobacco)	Acetylation; Chloroplast; Chromophore; Magnesium; Membrane; Metal-binding; Phosphoprotein; Photosystem I; Photosystem II; Plastid; Thylakoid; Transit peptide; Transmembrane; Transmembrane helix
SRR342019_TR27542_c2_g1_i1_len=1526	CB5_ARATH	Q:460-1038,H:5-194	78.87%ID	E:1e-106	Chlorophyll a/b binding protein CP26, chloroplastic	PF00504.18*Chloro_b-bind*Chlorophyll A/B binding protein*94-202*E:2.4e-24	1	0.004	0	-2.127	0	-1.339	0	-1.796	0.337	0.357 CB5_ARATH	Chlorophyll a/b binding protein CP26, chloroplastic (LHCB5) (LHCIIc) (Light-harvesting complex II protein 5)	LHCB5 At4g10340 F24G24.140	Arabidopsis thaliana (Mouse-ear cress)	Chloroplast; Complete proteome; Chromophore; Complete proteome; Magnesium; Membrane; Metal-binding; Phosphoprotein; Photosynthesis; Photosystem I; Photosystem II; Plastid; Reference proteome; Thylakoid; Transit peptide; Transmembrane; Transmembrane helix
SRR342019_TR27542_c2_g1_i5_len=1425	CB5_ARATH	Q:460-1296,H:5-280	82.86%ID	E:7e-138	Chlorophyll a/b binding protein CP26, chloroplastic	PF00504.18*Chloro_b-bind*Chlorophyll A/B binding protein*94-255*E:5.4e-46	0.983	0.005	0	-1.089	0	-0.929	0	-0.845	0.556	-0.123 CB5_ARATH	Chlorophyll a/b binding protein CP26, chloroplastic (LHCB5) (LHCIIc) (Light-harvesting complex II protein 5)	LHCB5 At4g10340 F24G24.140	Arabidopsis thaliana (Mouse-ear cress)	Chloroplast; Chromophore; Complete proteome; Magnesium; Membrane; Metal-binding; Phosphoprotein; Photosynthesis; Photosystem I; Photosystem II; Plastid; Reference proteome; Thylakoid; Transit peptide; Transmembrane; Transmembrane helix
SRR342019_TR27782_c0_g3_i1_len=1930	CHLP_TOBAC	Q:204-1580,H:1-460	87.83%ID	E:0	Geranylgeranyl diphosphate reductase, chloroplastic	PF01134.19*GIDA*Glucose inhibited division protein A*121-155*E:0.00011	0.09	-0.411	0	-1.71	0	-1.299	0	-0.937	0.025	0.495 CHLP_TOBAC	Geranylgeranyl diphosphate reductase, chloroplastic (EC 1.3.1.83) (Geranylgeranyl reductase)	CHLP	Nicotiana tabacum (Common tobacco)	PATHWAY: Porphyrin-containing compound metabolism; chlorophyll biosynthesis.; PATHWAY: Cofactor biosynthesis; tocopherol biosynthesis.
SRR342019_TR27808_c0_g1_i3_len=1457	CRR60_ARATH	Q:1218-526,H:35-259	62.77%ID	E:8e-80	Cysteine-rich repeat secretory protein 60	PF10657.14*Stress-antifung*Salt stress response/antifungal*31-125*E:5e-20 |PF10657.14*Stress-antifung*Salt stress response/antifungal*174-231*E:9.5e-09	0.059	-0.623	0	-2.201	0	-1.674	0	-1.754	0.843	-0.102 CRR60_ARATH	Cysteine-rich repeat secretory protein 60 (Plasmodesmata-located protein 7) (PDLP7)	CRRSP60 At5g37660 K12B20.12	Arabidopsis thaliana (Mouse-ear cress)	
SRR342019_TR30724_c0_g2_i2_len=1607	PSAK_ARATH	Q:970-1275,H:29-130	87.25%ID	E:3e-41	Photosystem I reaction center subunit psaK, chloroplastic	.	0.922	0.071	0	-1.675	0	-1.454	0	-1.45	0.147	0.453 PSAK_ARATH	Photosystem I reaction center subunit psaK, chloroplastic (PSI-K) (Photosystem I subunit X)	PSAK At1g30380 T4K22.2	Arabidopsis thaliana (Mouse-ear cress)	Chloroplast; Complete proteome; Membrane; Photosynthesis; Photosystem I; Plastid; Reference proteome; Thylakoid; Transit peptide; Transmembrane; Transmembrane helix
SRR342019_TR31144_c1_g1_i2_len=775	FER_CAPAN	Q:119-556,H:1-144	73.29%ID	E:7e-60	Ferredoxin, chloroplastic	PF00111.24*Fer2*2Fe-2S iron-sulfur cluster binding domain*99-170*E:1.4e-19	0.051	-0.409	0	-1.084	0	-1.125	0	-0.255	1	FER_CAPAN	Ferredoxin, chloroplastic (PFLP)	AP1	Capsicum annum (Bell pepper)	2Fe-2S; Chloroplast; Electron transport; Iron; Iron-sulfur; Metal-binding; Phosphoprotein; Plastid; Transit peptide; Transport
SRR342019_TR31716_c0_g1_i3_len=1330	NA	NA	NA	NA	NA	PF14547.3*Hydrophob_seed*Hydrophobic seed protein*167-250*E:4.6e-27	0.019	-0.555	0	-2.672	0	-1.624	0	-1.2	0.92	-0.035	.	.	.	.
SRR342019_TR37554_c0_g1_i9_len=867	NA	NA	NA	NA	NA	.	0.729	0.208	0	-2.962	0	-2.674	0	-2.675	0.655	-0.237	.	.	.	.
SRR342022_TR2829_c2_g1_i1_len=2246	G3PB_PEA	Q:450-1874,H:10-451	81.47%ID	E:0	Glyceraldehyde-3-phosphate dehydrogenase B, chloroplastic	PF00044.21*Gp_dh_N*Glyceraldehyde 3-phosphate dehydrogenase, NAD binding domain*2-105*E:3.3e-33 |PR02600.17*Gp_dh_C*Glyceraldehyde 3-phosphate dehydrogenase, C-terminal domain*110-267*E:1.1e-65 |PR02672.12*CP12*CP12 domain*296-317*E:2.3e-05	0.543	-0.201	0	-1.039	0	-1.25	0.001	-0.734	0.285	0.263 G3PB_PEA	Glyceraldehyde-3-phosphate dehydrogenase B, chloroplastic (EC 1.2.1.13) (NADP-dependent glyceraldehydephosphate dehydrogenase subunit B)	GAPB GPB1	Pisum sativum (Garden pea)	PATHWAY: Carbohydrate biosynthesis; Calvin cycle.
SRR342022_TR4115_c1_g2_i2_len=2017	POR_DAUCA	Q:173-1366,H:1-398	79.45%ID	E:0	Protochlorophyllide reductase, chloroplastic	PF03658.7*KR*KR domain*96-185*E:9.7e-07 |PF00106.22*adh_short*short chain dehydrogenase*88-230*E:3.4e-19 |PF13561.3*adh_short_C2*Enoyl-(Acyl carrier protein) reductase*92-229*E:6.9e-11	0.019	-0.544	0	-1.645	0	-1.254	0	-0.841	1	-0.819 POR_DAUCA	Protochlorophyllide reductase, chloroplastic (EC 1.3.1.33) (NADPH-protochlorophyllide oxidoreductase) (POR)	POR1	Daucus carota (Wild carrot)	PATHWAY: Porphyrin-containing compound metabolism; chlorophyll biosynthesis.
SRR342022_TR4209_c2_g2_i2_len=1887	PLY1_ARATH	Q:1052-1885,H:62-339	91.73%ID	E:0	Probable pectate lyase 1	PF00544.16*Pec_lyase_C*Pectate lyase*8-177*E:7e-22 |PF13229.3*Beta_helix*Right handed beta helix region*27-146*E:3.7e-07	0.886	-0.062	0	-2.087	0	-2.443	0	-1.983	1	-0.996 PLY1_ARATH	Probable pectate lyase 1 (EC 4.2.2.2) (Pectate lyase A1)	At1g04680 T1G11.7 T1G11_6	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Glycan metabolism; pectin degradation; 2-dehydro-3-deoxy-D-gluconate from pectin: step 2/5.
SRR342022_TR7524_c6_g4_i8_len=1411	CB12_PETHY	Q:267-1037,H:1-268	60.45%ID	E:2e-105	Chlorophyll a/b binding protein, chloroplastic	PF00504.18*Chloro_b-bind*Chlorophyll A/B binding protein*63-229*E:4.1e-50	0.05	-0.485	0	-1.423	0	-1.431	0	-1.281	0.282	-0.259 CB12_PETHY	Chlorophyll a/b binding protein, chloroplastic (LHCI type II CAB)	Petunia hybrida (Petunia)		Chlorophyll; Chloroplast; Chromophore; Magnesium; Membrane; Metal-binding; Phosphoprotein; Photosynthesis; Photosystem I; Photosystem II; Plastid; Thylakoid; Transit peptide; Transmembrane; Transmembrane helix
SRR342022_TR7773_c0_g1_i2_len=870	NA	NA	NA	NA	NA	.	0.175	-0.987	0.001	-2.473	0	-2.832	0	-2.874	1	-0.029	.	.	.	.
SRR342022_TR13446_c0_g2_i1_len=809	NA	NA	NA	NA	NA	.	0.875	0.064	0	-5.807	0.001	-2.644	0	-3.435	0.25	-0.393	.	.	.	.
SRR342022_TR16646_c3_g3_i4_len=1490	YAB1_ARATH	Q:970-353,H:21-229	65.12%ID	E:2e-81	Axial regulator YABBY 1	PF04690.10*YABBY*YABBY protein*32-195*E:7.7e-72	0.024	-0.721	0	-2.327	0	-1.883	0	-1.676	0.038	-0.679 YAB1_ARATH	Axial regulator YABBY 1 (FI-54) (Protein ABNORMAL FLORAL ORGANS) (Protein FILAMENTOUS FLOWER) (Protein antherless)	YAB1 AFO AT FIL At2g45190 F4L23.30	Arabidopsis thaliana (Mouse-ear cress)	Complete proteome; DNA-binding; Developmental protein; Metal-binding; Nucleus; Reference proteome; Zinc; Zinc-finger
SRR342022_TR18094_c3_g1_i1_len=617	NA	NA	NA	NA	NA	.	0.088	-0.595	0	-3.132	0	-1.447	0	-1.615	0.907	-0.04	.	.	.	.
SRR342022_TR18117_c1_g3_i1_len=1173	PDF1_ARATH	Q:698-1021,H:191-302	68.75%ID	E:2e-21	Protodermal factor 1	.	0.086	-0.512	0	-4.895	0	-2.809	0	-3.93	0.799	0.083 PDF1_ARATH	Protodermal factor 1	PDF1 At2g42840 F7D19.16	Arabidopsis thaliana (Mouse-ear cress)	Complete proteome; Reference proteome; Signal
SRR342022_TR18636_c4_g4_i3_len=2040	NA	NA	NA	NA	NA	.	0.089	-0.558	0	-1.545	0	-1.857	0	-1.913	1	0.251	.	.	.	.
SRR342022_TR20089_c0_g3_i1_len=1263	NA	NA	NA	NA	NA	.	0.932	-0.037	0	-2.302	0	-2.051	0	-1.369	1	0.219	.	.	.	.
SRR342022_TR20209_c3_g5_i2_len=2978	PP213_ARATH	Q:1168-2742,H:76-599	63.05%ID	E:0	Pentatricopeptide repeat-containing protein At3g04760, chloroplastic	PF01535.17*PPR*PPR repeat*71-94*E:0.25 |PF13812.3*PPR_3*Pentatricopeptide repeat domain*87-144*E:0.0004 |PF12854.4*PPR_1*PPR repeat*131-181*E:3.8e-09 |PF13812.3*PPR_3*Pentatricopeptide repeat domain*131-180*E:3.5e-08 |PF13041.3*PPR_2*PPR repeat family*132-181*E:4.2e-18 |PF01535.17*PPR*PPR repeat*136-185*E:1.8e-08 |PF13812.3*PPR_3*Pentatricopeptide repeat domain*152-212*E:7.1e-12 |PF12854.4*PPR_1*PPR repeat*183-194*E:2.4e-10 |PF13041.3*PPR_2*PPR repeat family*167-213*E:4.3e-15 |PF01535.17*PPR*PPR repeat*170-220*E:4.3e-06 |PF12854.4*PPR_1*PPR repeat*199-250*E:2.3e-06 |PF01535.17*PPR*PPR repeat*203-235*E:0.00061 |PF13041.3*PPR_2*PPR repeat family*218-251*E:1.2e-10 |PF13812.3*PPR_3*Pentatricopeptide repeat domain*225-282*E:4.9e-10 |PF12854.4*PPR_1*PPR repeat*233-281*E:2e-12 |PF01535.17*PPR*PPR repeat*240-269*E:3.4e-06 |PF13041.3*PPR_2*PPR repeat family*241-284*E:3.9e-12 |PF13041.3*PPR_2*PPR repeat family*272-321*E:1e-13 |PF01535.17*PPR*PPR repeat*275-302*E:0.0092 |PF17177.1*PPR_long*Pentatricopeptide-repeat region of PROPR*291-416*E:2.9e-12 |PF13812.3*PPR_3*Pentatricopeptide repeat domain*295-354*E:9.5e-08 |PF12854.4*PPR_1*PPR repeat*304-335*E:1.8e-11 |PF01535.17*PPR*PPR repeat*310-340*E:1.9e-07 |PF13041.3*PPR_2*PPR repeat family*316-356*E:1.7e-09 |PF13812.3*PPR_3*Pentatricopeptide repeat domain*332-391*E:4.2e-08 |PF12854.4*PPR_1*PPR repeat*338-370*E:1.5e-09 |PF01535.17*PPR*PPR repeat*345-375*E:0.00041 |PF13812.3*PPR_3*Pentatricopeptide repeat domain*370-424*E:1.3e-10 |PF12854.4*PPR_1*PPR repeat*374-404*E:1.3e-10 |PF13041.3*PPR_2*PPR repeat family*377-424*E:3.8e-15 |PF01535.17*PPR*PPR repeat*381-410*E:1.4e-06 |PF13812.3*PPR_3*Pentatricopeptide repeat domain*401-458*E:5.1e-08 |PF13041.3*PPR_2*PPR repeat family*412-461*E:4.7e-11 |PF01535.17*PPR*PPR repeat*415-444*E:0.088 |PF17177.1*PPR_long*Pentatricopeptide-repeat region of PROPR*437-528*E:6e-10 |PF12854.4*PPR_1*PPR repeat*443-478*E:2.1e-14 |PF13041.3*PPR_2*PPR repeat family*447-496*E:1.5e-15 |PF01535.17*PPR*PPR repeat*450-480*E:2.1e-10 |PF13812.3*PPR_3*Pentatricopeptide repeat domain*471-528*E:3e-09 |PF12854.4*PPR_1*PPR repeat*479-511*E:1.5e-08 |PF13041.3*PPR_2*PPR repeat family*483-528*E:1.2e-13 |PF01535.17*PPR*PPR repeat*485-515*E:3.7e-07 |PF14363.2*LTF_2*Probable lipid transfer*9-99*E:2.5e-11 |PR00234.19*Tryp_alpha_amyl*Protease inhibitor/seed storage/LTP family*27-101*E:3e-07	0.125	-0.513	0.001	-1.302	0.001	-1.031	0.001	-1.016	0.089	0.574 PP213_ARATH	Pentatricopeptide repeat-containing protein At3g04760, chloroplastic	At3g04760 F7O18.25	Arabidopsis thaliana (Mouse-ear cress)	Chloroplast; Complete proteome; Plastid; Reference proteome; Repeat; Transit peptide
SRR342022_TR28986_c0_g2_i1_len=745	NA	NA	NA	NA	NA	.	0.003	1.147	0	-5.396	0.001	-1.085	0	-1.999	0.832	-0.254	.	.	.	.
SRR342022_TR32151_c0_g5_i4_len=749	NA	NA	NA	NA	NA	.	0.016	-0.546	0	-2.767	0	-2.51	0	-3.065	1	-0.927	.	.	.	.
SRR342023_TR161_c2_g2_i7_len=2055	RUS5_ARATH	Q:1612-362,H:80-604	64.32%ID	E:4e-136	Protein root UVB sensitive 5 (ECO:0000303|PubMed:19515790)	PF04884.11*DUF647*Vitamin B6 photo-protection and homoeostasis*44-282*E:7.3e-67	0.237	-0.471	0	-1.41	0	-1.718	0	-1.855	0.832	-0.258 RUS5_ARATH	Protein root UVB sensitive 5	RUS5 At5g01510 F7A7.30	Arabidopsis thaliana (Mouse-ear cress)	Complete proteome; Reference proteome
SRR342023_TR2846_c0_g5_i2_len=1227	ABP20_PRUPE	Q:258-782,H:28-202	69.89%ID	E:3e-72	Auxin-binding protein ABP20	PF00190.19*Cupin_1*Cupin*54-199*E:4.1e-32	0	1.428	0	-3.732	0	-2.648	0	-1.69	0.615	0.105 ABP20_PRUPE	Auxin-binding protein ABP20	ABP20	Prunus persica (Peach) (Amygdalus persica)	Apoplast; Auxin signaling pathway; Cell wall; Disulfide bond; Glycoprotein; Manganese; Metal-binding; Receptor; Secreted; Signal
SRR342023_TR7356_c3_g3_i3_len=1225	CB11_SOLLC	Q:907-200,H:1-236	86.02%ID	E:5e-135	Chlorophyll a/b binding protein 6A, chloroplastic	PF00504.18*Chloro_b-bind*Chlorophyll A/B binding protein*56-210*E:3.5e-46	0.142	-0.323	0	-1.327	0	-1.12	0	-0.915	0.82	0.054 CB11_SOLLC	Chlorophyll a/b binding protein 6A, chloroplastic (LHCI type I CAB-6A) (Light-harvesting complex I 26 kDa protein)	CAB6A	Solanum lycopersicum (Tomato) (Lycopersicon esculentum)	Chlorophyll; Chloroplast; Chromophore; Complete proteome; Membrane; Metal-binding; Phosphoprotein; Photosynthesis; Photosystem I; Photosystem II; Plastid; Reference proteome; Thylakoid; Transit peptide; Transmembrane; Transmembrane helix
SRR342023_TR8133_c1_g4_i1_len=1447	PUMP3_ARATH	Q:183-521,H:15-236	54.7%ID	E:2e-27	Mitochondrial uncoupling protein 3	.	0.11	-0.533	0	-1.485	0	-1.686	0	-2.145	0.204	-0.423 PUMP3_ARATH	Mitochondrial uncoupling protein 3 (AtPUMP3)	PUMP3 UCP3 At1g14140 F7A19.22	Arabidopsis thaliana (Mouse-ear cress)	Complete proteome; Membrane; Mitochondrion; Mitochondrion inner membrane; Reference proteome; Repeat; Stress response; Transmembrane; Transmembrane helix; Transport
SRR342023_TR8775_c0_g2_i4_len=634	ARG7_VIGRR	Q:159-446,H:1-90	56.25%ID	E:4e-30	Indole-3-acetic acid-induced protein ARG7	.	0.099	-0.849	0	-3.356	0	-2.431	0	-2.01	0.003	-1.032 ARG7_VIGRR	Indole-3-acetic acid-induced protein ARG7	ARG7	Vigna radiata var. radiata (Mung bean) (Phaseolus aureus)	
SRR342023_TR9121_c7_g10_i2_len=1422	HIDM_GLYEC	Q:202-1140,H:16-327	45.34%ID	E:1e-87	2-hydroxyisoflavanone dehydratase	PF00135.25*Coesterase*Carboxylesterase family*63-119*E:3.8e-06 |PF07859.10*Abhydrolase_3*alpha/beta hydrolase fold*77-291*E:3.1e-33	0.008	-0.577	0	-2.663	0	-2.058	0	-1.793	0.126	0.339 HIDM_GLYEC	2-hydroxyisoflavanone dehydratase (EC 3.1.1.1) (EC 4.2.1.105) (Carboxylesterase HIDM)	HIDM	Glycyrrhiza echinata (Licorice)	PATHWAY: Secondary metabolite biosynthesis; flavonoid biosynthesis.
SRR342023_TR10990_c0_g5_i2_len=981	CB12_SOLLC	Q:979-230,H:21-270	89.2%ID	E:5e-166	Chlorophyll a/b binding protein 7, chloroplastic	PF00504.18*Chloro_b-bind*Chlorophyll A/B binding protein*54-220*E:7.8e-52	0.673	-0.089	0	-1.648	0	-0.951	0	-0.859	0.581	0.371 CB12_SOLLC	Chlorophyll a/b binding protein 7, chloroplastic (LHCI type II CAB-7)	CAB7	Solanum lycopersicum (Tomato) (Lycopersicon esculentum)	Chlorophyll; Chloroplast; Chromophore; Complete proteome; Magnesium; Membrane; Metal-binding; Phosphoprotein; Photosynthesis; Photosystem I; Photosystem II; Plastid; Reference proteome; Thylakoid; Transit peptide; Transmembrane; Transmembrane helix
SRR342023_TR12272_c0_g1_i1_len=1032	NA	NA	NA	NA	NA	.	0.01	-1.13	0	-3.367	0	-2.44	0	-2.466	0.193	-0.652	.	.	.	.
SRR342023_TR12898_c7_g3_i9_len=1759	PAP12_ARATH	Q:1428-394,H:62-407	68.5%ID	E:2e-173	Probable plastid-lipid-associated protein 12, chloroplastic	PF04755.9*PAP_fibrillin*PAP_fibrillin*85-259*E:9.3e-43	0.699	0.141	0	-2.173	0	-1.303	0	-1.097	0.443	0.287 PAP12_ARATH	Probable plastid-lipid-associated protein 12, chloroplastic (Fibrillin-10)	PAP12 FBN10 FIB10 At1g51110/At1g51115 F23H24.16/F23H24.17	Arabidopsis thaliana (Mouse-ear cress)	Chloroplast; Complete proteome; Plastid; Reference proteome; Thylakoid; Transit peptide
SRR342023_TR15719_c0_g2_i1_len=1696	CUT1A_ARATH	Q:647-303,H:50-164	73.04%ID	E:6e-51	Protein CURVATURE THYLAKOID 1A, chloroplastic	PF14159.3*CAAD*CAAD domains of cyanobacterial aminoacyl-tRNA synthetase*36-119*E:1.6e-32	0.374	-0.192	0	-0.84	0	-1.002	0	-0.928	0.6	0.135 CUT1A_ARATH	Protein CURVATURE THYLAKOID 1A, chloroplastic	CUR1 At4g01150 A_IG002N01.18 F2N1.18	Arabidopsis thaliana (Mouse-ear cress)	
SRR342023_TR16454_c2_g4_i2_len=1411	GEDH1_OCIBA	Q:778-1404,H:33-244	57.55%ID	E:2e-72	Geraniol dehydrogenase 1	PF08240.9*ADH_N*Alcohol dehydrogenase GroES-like domain*5-92*E:9.8e-18 |PF02826.16*2-Hacid_dh_C*D-isomer specific 2-hydroxyacid dehydrogenase, NAD binding domain*133-172*E:1e-06 |PF12796.4*Ank_2*Ankyrin repeats (3 copies)*130-216*E:8.8e-10 |PF13637.3*Ank_4*Ankyrin repeats (many copies)*165-198*E:5.5e-07 |PF13857.3*Ank_5*Ankyrin repeats (many copies)*173-228*E:8.6e-12 |PF13606.3*Ank_3*Ankyrin repeat*188-214*E:0.0049 |PR00023.27*Ank*Ankyrin repeat*188-213*E:0.005 |PR03385.21*Chromo*Chromo (CHRomatin Organisation MOdifier) domain*316-360*E:2.2e-09	0.521	-0.148	0	-1.065	0	-1.198	0	-1.328	0.089	0.363 GEDH1_OCIBA	Geraniol dehydrogenase 1 (ObaGEDH) (EC 1.1.1.183)	GEDH1	Ocimum basilicum (Sweet basil)	
SRR342023_TR18007_c0_g1_i1_len=1626	SR43C_ARATH	Q:1169-281,H:83-369	67.01%ID	E:4e-134	Signal recognition particle 43 kDa protein, chloroplastic	.	0.084	-0.468	0	-1.33	0	-1.155	0	-1.177	0.482	0.197 SR43C_ARATH	Signal recognition particle 43 kDa protein, chloroplastic (Chromo protein SRP43) (CpSRP43)	CAO CPSRP43 At2g47450 T30B22.25	Arabidopsis thaliana (Mouse-ear cress)	3D-structure; ANK repeat; Chloroplast; Coiled coil; Complete proteome; Metal-binding; Plastid; Reference proteome; Repeat; Ribonucleoprotein; Signal recognition particle; Transit peptide
SRR342023_TR18091_c1_g1_i1_len=763	NA	NA	NA	NA	NA	.	0.004	-0.657	0	-2.205	0	-2.698	0	-2.35	1	-0.472	.	.	.	.
SRR342023_TR19865_c1_g1_i3_len=1788	NA	NA	NA	NA	NA	.	0.729	-0.209	0	-2.276	0	-2.29	0	-3.21	1	-0.211	.	.	.	.
SRR342023_TR19865_c1_g1_i7_len=1482	NA	NA	NA	NA	NA	PF00403.23*HMA*Heavy-metal-associated domain*36-92*E:5.1e-10 |PF00403.23*HMA*Heavy-metal-associated domain*142-194*E:1.6e-12	0.009	-0.654	0	-2.328	0	-1.041	0	-1.157	1	0	.	.	.	.
SRR342023_TR20116_c0_g1_i1_len=534	NA	NA	NA	NA	NA	.	0.534	0.186	0	-1.758	0	-2.049	0	-2.412	0.001	1.176	.	.	.	.
SRR342023_TR20176_c2_g5_i1_len=761	CB4A_ARATH	Q:648-1,H:57-272	92.13%ID	E:4e-145	Chlorophyll a/b binding protein CP29.1, chloroplastic	PF00504.18*Chloro_b-bind*Chlorophyll A/B binding protein*45-241*E:9.9e-50	0.863	-0.037	0	-1.15	0	-1.036	0	-0.932	0.794	0.056 CB4A_ARATH	Chlorophyll a/b binding protein CP29.1, chloroplastic (LHCB4.1) (LHCII protein 4.1)	LHCB4.1 At5g01530 F7A7_50	Arabidopsis thaliana (Mouse-ear cress)	Chloroplast; Complete proteome; Direct protein sequencing; Membrane; Magnesium; Metal-binding; Phosphoprotein; Photosynthesis; Photosystem I; Photosystem II; Plastid; Reference proteome; Thylakoid; Transit peptide; Transmembrane; Transmembrane helix
SRR342023_TR24219_c2_g1_i3_len=527	GDL79_ARATH	Q:3-266,H:275-362	79.55%ID	E:6e-48	GDSL esterase/lipase At5g33370	.	0.047	-0.43	0	-2.098	0	-1.426	0	-1.775	1	-0.031 GDL79_ARATH	GDSL esterase/lipase At5g33370 (EC 3.1.1.-) (Extracellular lipase At5g33370)	At5g33370 F19N2.90	Arabidopsis thaliana (Mouse-ear cress)	Alternative splicing; Complete proteome; Glycoprotein; Hydrolase; Lipid degradation; Lipid metabolism; Reference proteome; Secreted; Signal
SRR342023_TR27072_c0_g1_i1_len=2757	3MG1_ECOLI	Q:1717-1187,H:3-179	42.46%ID	E:7e-41	DNA-3-methyladenine glycosylase 1	PF03352.10*Adenine_glyco*Methyladenine glycosylase*219-390*E:2.7e-62	0.077	-0.468	0	-2.977	0	-1.764	0	-1.617	1	0.103 3MG1_ECOLI	DNA-3-methyladenine glycosylase 1 (EC 3.2.2.20) (3-methylarenine-DNA glycosylase I, constitutive) (TAG I) (DNA-3-methylarenine glycosidase I) (DNA-3-methyladenine glycosylase I)	tag b3549 JW3518	Escherichia coli (strain K12)	3D-structure; Complete proteome; DNA damage; DNA repair; Direct protein sequencing; Hydrolase; Metal-binding; Reference proteome; Zinc
SRR342023_TR28132_c0_g2_i1_len=646	NA	NA	NA	NA	NA	.	0.18	-0.805	0	-1.702	0	-2.787	0	-2.646	1	-2.774	.	.	.	.
SRR342023_TR28931_c0_g1_i1_len=696	NA	NA	NA	NA	NA	.	0.969	-0.021	0	-1.135	0.001	-1.04	0	-1.265	0.268	0.313	.	.	.	.
SRR346552_TR22428_c0_g1_i1_len=1365	FER_CAPAN	Q:352-789,H:1-144	73.29%ID	E:1e-57	Ferredoxin, chloroplastic	PF00111.24*Fer2*2Fe-2S iron-sulfur cluster binding domain*60-131*E:7.8e-20	0.026	-2.118	0	-4.129	0	-5.084	0	-3.752	1	-1.08 FER_CAPAN	Ferredoxin, chloroplastic (PFLP)	AP1	Capsicum annum (Bell pepper)	2Fe-2S; Chloroplast; Electron transport; Iron; Iron-sulfur; Metal-binding; Phosphoprotein; Plastid; Transit peptide; Transport
SRR346596_TR7673_c0_g1_i2_len=4622	CHLH_ARATH	Q:4005-442,H:193-1381	89.57%ID	E:0	Magnesium-chelatase subunit ChlH, chloroplastic	PF02514.13*CobN-Mg_chel*CobN/Magnesium Chelatase*31-1148*E:0	0.165	-0.373	0	-1.62	0	-1.178	0	-0.902	0.047

SRR1271858_TR48478_c0_g1_i1_len=650	H32_WHEAT	Q:528-121,H:1-136	99.26%ID	E:3e-77	Histone H3.2	PF00125.21*Histone*Core histone H2A/H2B/H3/H4*1-132*E:8.3e-55	0	-1,684	0	-4,424	0,377	-0,692	0,045	-1,482	1	-0,46	H32_WHEAT	Histone H3.2				Triticum aestivum (Wheat)			Acetylation; Chromosome; Complete proteome; DNA-binding; Direct protein sequencing; Methylation; Nucleosome core; Nucleus; Phosphorylation; Reference proteome
SRR1271859_TR26446_c2_g4_i4_len=945	H2A1_MEDTR	Q:717-394,H:26-132	93.52%ID	E:1e-47	Probable histone H2A.1	PF00125.21*Histone*Core histone H2A/H2B/H3/H4*20-97*E:6.9e-13*PF16211.2*Histone_H2A_C*C-terminus of histone H2A*100-132*E:2.7e-18	0	-1,019	0	-1,505	0,505	0,438	0,86	0,2	0,025	0,812	H2A1_MEDTR	Probable histone H2A.1		MtrDRAFT_AC149210g1v1		Medicago truncatula (Barrel medic) (Medicago tribuloides)			Chromosome; DNA-binding; Nucleosome core; Nucleus
SRR1271859_TR26579_c1_g1_i6_len=1242	XTH9_ARATH	Q:101-544,H:10-156	72.97%ID	E:1e-118	Xyloglucan endotransglucosylase/hydrolase protein 9	PF00722.18*Glyco_hydro_16*Glycosyl hydrolases family 16*56-180*E:8.7e-39	0	-1,277	0	-3,151	1	0,057	0,581	-0,493	0,038	-1,756	XTH9_ARATH	Xyloglucan endotransglucosylase/hydrolase protein 9 (At-XTH9) (XTH-9) (EC 2.4.1.207)	XTH9 EXGT-A6 XTR16 At4g03210 FAC21,14			Arabidopsis thaliana (Mouse-ear cress)			Complete proteome; Disulfide bond; Glycosylation; Glycosidase; Hydrolase; Reference proteome; Secreted; Signal; Transferase
SRR1271859_TR33596_c0_g1_i2_len=560	H4_SOYBN	Q:247-480,H:22-99	100%ID	E:2e-47	Histone H4	PF15511.3*CENP-T_C*Centromere kinetochore component CENP-T histone fold*35-96*E:1.4e-08*PF02969.14*TAF*TATA box binding protein associated factor (TAF)*35-92*E:0.00016	0	-1,58	0	-1,809	0,312	0,556	0,874	0,108	0,076	-0,396	H4_SOYBN	Histone H4				Glycine max (Soybean) (Glycine hispida)			Chromosome; Complete proteome; DNA-binding; Methylation; Nucleosome core; Nucleus; Reference proteome
SRR342017_TR4662_c1_g6_i2_len=913	NA	NA	NA	NA	NA	PF10249.5*DUF3531*Protein of unknown function (DUF3531)*87-227*E:4.7e-55	0	-3,566	0	-3,933	1	-0,073	1	-2,396	0,418	0,317									
SRR342017_TR9810_c0_g2_i1_len=881	RUBB_PEA	Q:881-60,H:318-591	93.07%ID	E:1e-159	RuBisCO large subunit-binding protein subunit beta, chloroplastic	PF00118.21*Cpn60_TCP1*TCP-1/cpn60 chaperonin family*16-258*E:2.9e-49	0,001	-0,958	0	-1,143	0,099	0,553	0,192	0,447	1	0,071	RUBB_PEA	RuBisCO large subunit-binding protein subunit beta, chloroplastic (60 kDa chaperonin subunit beta) (CPN-60 beta)				Pisum sativum (Garden pea)			ATP-binding; Chaperone; Chloroplast; Direct protein sequencing; Nucleotide-binding; Plastid; Transit peptide
SRR342017_TR16448_c0_g1_i6_len=793	H2B1_MEDTR	Q:505-230,H:57-148	98.91%ID	E:2e-57	Probable histone H2B.1	PF00125.21*Histone*Core histone H2A/H2B/H3/H4*2-128*E:1.3e-22*PF00808.20*CBFD_NFYB_HMF*Histone-like transcription factor (CBF/NF-Y) and archaeal histone*70-126*E:0.00028	0	-1,228	0	-2,359	1	0,08	0,34	0,47	0,52	0,45	H2B1_MEDTR	Probable histone H2B.1				Medicago truncatula (Barrel medic) (Medicago tribuloides)			Chromosome; DNA-binding; Isopeptide bond; Nucleosome core; Nucleus; Ubl conjugation
SRR342017_TR16982_c0_g1_i1_len=533	H32_LILLO	Q:38-216,H:1-58	100%ID	E:5e-31	Histone H3.2	PF00125.21*Histone*Core histone H2A/H2B/H3/H4*49-109*E:1.4e-10	0	-1,865	0	-3,354	0,732	0,666	1	0,462	0,671	-0,133	H32_LILLO	Histone H3.2	YAH3			Lilium longiflorum (Trumpet lily)			Acetylation; Chromosome; DNA-binding; Direct protein sequencing; Methylation; Nucleosome core; Nucleus; Phosphoprotein
SRR342017_TR20766_c0_g1_i3_len=679	NIFU1_ARATH	Q:509-18,H:66-230	77.58%ID	E:4e-65	NifU-like protein 1, chloroplastic	PF0106.14*NifU/NifU-like domain*2-69*E:7.4e-23*PF01106.14*NifU/NifU-like domain*81-137*E:3.2e-05	0	-6,96	0	-2,828	1	-0,803	0,037	0,958	0,502	-3,927	NIFU1_ARATH	NifU-like protein 1, chloroplastic (AtCNfu1) (AtCnfU-IVb)	NIFU1 CNFU1 NFU1 At4g01940 T7B11.20			Arabidopsis thaliana (Mouse-ear cress)			Chloroplast; Complete proteome; Disulfide bond; Plastid; Reference proteome; Transit peptide
SRR342017_TR22430_c1_g1_i21_len=674	RL291_ARATH	Q:202-384,H:1-61	81.97%ID	E:1e-26	60S ribosomal protein L29-1	-	0	-1,675	0	-2,104	0,592	-0,205	0,226	-0,466	0,12	-0,441	RL291_ARATH	60S ribosomal protein L29-1	RPL29A At3g06700 F3E22.16 T8E24.8			Arabidopsis thaliana (Mouse-ear cress)			Complete proteome; Phosphoprotein; Reference proteome; Ribonucleoprotein; Ribosomal protein
SRR342017_TR24038_c0_g1_i2_len=1157	XTH9_ARATH	Q:936-211,H:58-289	76.45%ID	E:7e-138	Xyloglucan endotransglucosylase/hydrolase protein 9	PF00722.18*Glyco_hydro_16*Glycosyl hydrolases family 16*3-116*E:5.4e-39*PF06955.9*XET_C*Xyloglucan endo-transglycosylase (XET) C-terminus*158-203*E:8.7e-18	0	-0,929	0	-3,345	0,133	0,617	0,754	0,194	0,452	-0,56	XTH9_ARATH	Xyloglucan endotransglucosylase/hydrolase protein 9 (At-XTH9) (XTH-9) (EC 2.4.1.207)	XTH9 EXGT-A6 XTR16 At4g03210 FAC21,14			Arabidopsis thaliana (Mouse-ear cress)			Complete proteome; Disulfide bond; Glycosylation; Glycosidase; Hydrolase; Reference proteome; Secreted; Signal; Transferase
SRR342019_TR18511_c2_g5_i3_len=1003	H32_WHEAT	Q:826-419,H:1-136	99.26%ID	E:1e-75	Histone H3.2	PF00125.21*Histone*Core histone H2A/H2B/H3/H4*1-132*E:8.3e-55	0	-1,493	0	-3,562	1	-0,465	0,299	-1,391	0,006	-0,807	H32_WHEAT	Histone H3.2				Triticum aestivum (Wheat)			Acetylation; Chromosome; Complete proteome; DNA-binding; Direct protein sequencing; Methylation; Nucleosome core; Nucleus; Phosphoprotein; Reference proteome
SRR342019_TR24957_c0_g2_i1_len=897	NA	NA	NA	NA	NA	-	0	-1,889	0	-4,213	1	0,439	1	0,413	1	0									
SRR342019_TR28229_c0_g1_i1_len=1357	SODF3_ARATH	Q:997-341,H:45-263	77.63%ID	E:2e-128	Superoxide dismutase [Fe] 3, chloroplastic	PF00081.19*Sod_Fe_N*Iron/manganese superoxide dismutases, alpha-hairpin domain*55-140*E:2.9e-21*PF02777.15*Sod_Fe_C*Iron/manganese superoxide dismutases, C-terminal domain*150-250*E:1.2e-35	0,001	-0,931	0	-1,816	0,5	-0,792	0,832	-0,36	0,281	-0,299	SODF3_ARATH	Superoxide dismutase [Fe] 3, chloroplastic (EC 1.15.1.1) (Protein FE SUPEROXIDE DISMUTASE 3)	FSD3 At5g23310 MKD15.17			Arabidopsis thaliana (Mouse-ear cress)			Chloroplast; Complete proteome; Iron; Metal-binding; Oxidoreductase; Plastid; Reference proteome; Thylakoid; Transit peptide
SRR342019_TR28386_c1_g1_i1_len=1347	EPI1G_DAUCA	Q:1181-294,H:8-309	48.71%ID	E:7e-84	Epidermis-specific secreted glycoprotein EP1	PF10453.21*B_lectin*D-mannose binding lectin*86-179*E:1.8e-26	0	-0,918	0	-1,669	1	0,065	1	0,135	0,126	-0,35	EPI1G_DAUCA	Epidermis-specific secreted glycoprotein EP1 (52/54 kDa medium protein)	EP1			Daucus carota (Wild carrot)			Direct protein sequencing; Glycoprotein; Lectin; Secreted; Signal
SRR342019_TR33798_c0_g2_i1_len=846	PSAEA_NICSY	Q:604-242,H:21-246	69.92%ID	E:4e-36	Photosystem I reaction center subunit IV A, chloroplastic	PF02427.14*PSI_PsaE*Photosystem I reaction centre subunit IV / PsaE*141-250*E:4.7e-30	0	-1,596	0	-1,187	0,009	-0,583	0,02	-0,519	0,891	0,058	PSAEA_NICSY	Photosystem I reaction center subunit IV A, chloroplastic (PSI-E A) [Cleaved into: Photosystem I reaction center subunit IV A isoform 2]	PSAEA			Nicotiana sylvestris (Wood tobacco) (South American tobacco)			Chloroplast; Direct protein sequencing; Membrane; Photosynthesis; Photosystem I; Plastid; Thylakoid; Transit peptide
SRR342022_TR4553_c9_g3_i4_len=812	H2B1_MEDTR	Q:525-250,H:57-148	98.91%ID	E:6e-58	Probable histone H2B.1	PF00125.21*Histone*Core histone H2A/H2B/H3/H4*37-163*E:2.5e-22	0	-1,132	0	-1,996	0,429	0,466	0,623	0,35	0,005	-1,05	H2B1_MEDTR	Probable histone H2B.1				Medicago truncatula (Barrel medic) (Medicago tribuloides)			Acetylation; Chromosome; DNA-binding; Isopeptide bond; Nucleosome core; Nucleus; Ubl conjugation
SRR342022_TR6932_c1_g2_i3_len=1899	GSA_TOBAC	Q:1671-268,H:18-478	83.55%ID	E:0	Glutamate-1-semialdehyde 2,1-aminomutase, chloroplastic	PF00202.18*Aminotran_3*Aminotransferase class-III*84-466*E:1.5e-69	0	-0,917	0	-1,074	0,029	-0,65	0,485	-0,211	1	3,367	GSA_TOBAC	Glutamate-1-semialdehyde 2,1-aminomutase, chloroplastic (GSA) (EC 5.4.3.8) (Glutamate-1-semialdehyde aminotransferase) (GSA-AT)	GSA		PATHWAY: Porphyrin-containing compound metabolism; protoporphyrin-IX biosynthesis; 5-aminolevulinate from L-glutamyl-tRNA(Glu); step 2/2 ; PATHWAY: Porphyrin-containing compound metabolism; chlorophyll biosynthesis	Nicotiana tabacum (Common tobacco)			Chlorophyll biosynthesis; Chloroplast; Isomerase; Plastid; Porphyrin biosynthesis; Pyridoxal phosphate; Transit peptide
SRR342022_TR15174_c6_g3_i1_len=643	CP2B_ARATH	Q:486-37,H:1-153	55.48%ID	E:3e-33	-	PF00160.18*Pro_isomerase*Cyclophilin type peptidyl-prolyl cis-trans isomerase/CLD*146-203*E:1.1e-14	0	-0,868	0	-0,974	0,02	-1,099	0,14	-0,68	1	-0,287	PNSL5_ARATH	Photosynthetic NDH subunit of lumenal location 5, chloroplastic (Cyclophilin of 20 kDa 2) (Peptidyl-prolyl cis-trans isomerase CYP20-2) (EC 5.2.1.8) (Rotamase CYP20-2) (Thylakoid lumen PPIase of 20 kDa) (TLP20)	PNSL5 CYP20-2 At5g13120 T19L5_80			Arabidopsis thaliana (Mouse-ear cress)			Chloroplast; Complete proteome; Cytoplasm; Cytoplasmic; Cyclophilin; Direct protein sequencing; Disulfide bond; Isomerase; Membrane; Plastid; Reference proteome; Rotamase; Thylakoid; Transit peptide; Transport
SRR342022_TR18762_c3_g4_i2_len=1984	CCNA4_DAUCA	Q:441-1436,H:11-331	61.26%ID	E:5e-136	G2/mitotic-specific cyclin C13-1	PF00134.20*Cyclin_N*Cyclin, N-terminal domain*107-235*E:3e-43*PF02984.16*Cyclin_C*Cyclin, C-terminal domain*238-360*E:8.9e-32	0	-1,569	0	-4,589	1	-0,307	1	-1,123	1	0,61	CCNA4_DAUCA	G2/mitotic-specific cyclin C13-1 (A-like cyclin) (Fragment)				Daucus carota (Wild carrot)			Cell cycle; Cell division; Cyclin; Mitosis
SRR342022_TR32140_c0_g1_i1_len=822	CCD32_ARATH	Q:107-727,H:168-367	46.76%ID	E:2e-57	Cyclin-D3-2	PF02984.16*Cyclin_C*Cyclin, C-terminal domain*16-125*E:1.1e-23	0	-1,85	0	-5,184	1	0	0,254	4,691	0,07	-0,728	CCD32_ARATH	Cyclin-D3-2 (G1/S-specific cyclin-D3-2) (CycD3;2)	CYCD3-2 At5g67260 K3G17.2			Arabidopsis thaliana (Mouse-ear cress)			Cell cycle; Cell division; Complete proteome; Cyclin; Reference proteome
SRR342023_TR7541_c0_g3_i1_len=664	RL111_ARATH	Q:1-663,H:1-168	95.83%ID	E:7e-107	60S ribosomal protein L11-1	PF00298.18*Ribosomal_L5*Ribosomal protein L5*62-155*E:1.4e-20*PF00673.18*Ribosomal_L5_C*ribosomal L5P family C-terminus*119-213*E:1.4e-20	0	-1,485	0	-1,737	0,317	-0,487	0,634	-0,274	0,051	-0,839	RL111_ARATH	60S ribosomal protein L11-1 (L18A)	RPL11A RPL18A At2g42740 F7D19.26			Arabidopsis thaliana (Mouse-ear cress)			Complete proteome; Cytoplasm; RNA-binding; Reference proteome; Ribonucleoprotein; Ribosomal protein; rRNA-binding
SRR342023_TR11135_c0_g1_i4_len=607	H2B1_MEDTR	Q:301-576,H:57-148	98.91%ID	E:2e-58	Probable histone H2B.1	PF00125.21*Histone*Core histone H2A/H2B/H3/H4*2-96*E:1.3e-22*PF00808.20*CBFD_NFYB_HMF*Histone-like transcription factor (CBF/NF-Y) and archaeal histone*70-126*E:0.00028	0	-1,341	0	-0,99	1	-0,027	0,037	-0,676	0,014	-0,542	H2B1_MEDTR	Probable histone H2B.1				Medicago truncatula (Barrel medic) (Medicago tribuloides)			Acetylation; Chromosome; DNA-binding; Isopeptide bond; Nucleosome core; Nucleus; Ubl conjugation
SRR342023_TR12524_c0_g5_i1_len=2310	CCD31_ARATH	Q:1845-1093,H:53-300	55.43%ID	E:3e-80	Cyclin-D3-1	PF00134.20*Cyclin_N*Cyclin, N-terminal domain*76-203*E:2.5e-26*PF02984.16*Cyclin_C*Cyclin, C-terminal domain*205-331*E:3e-19	0	-1,372	0	-3,874	0,132	-1,451	0,008	-2,897	0,285	-0,345	CCD31_ARATH	Cyclin-D3-1 (Cyclin-delta-3) (Cyclin-d3) (G1/S-specific cyclin-D3-1) (CycD3;1)	CYCD3-1 CYCD3 At4g34160 F28A23.80			Arabidopsis thaliana (Mouse-ear cress)			Cell cycle; Cell division; Complete proteome; Cyclin; Mitosis; Reference proteome
SRR646572_TR17837_c0_g1_i1_len=3147	POR_DAUCA	Q:2971-1796,H:1-398	84.67%ID	E:0	Protochlorophyllide reductase, chloroplastic	PF08659.7*KR*KR domain*80-175*E:8e-09*PF00106.22*adh_short*short chain dehydrogenase*82-224*E:6.5e-21*PF13561.3*adh_short_C2*Enoyl-(Acyl carrier protein) reductase*86-223*E:1.5e-12	0	-0,812	0	-2,568	0,037	-1,189	0,241	-0,697	0,016	0,585	POR_DAUCA	Protochlorophyllide reductase, chloroplastic (PCR) (EC 1.3.1.33) (NADPH-protochlorophyllide oxidoreductase) (POR)	POR1		PATHWAY: Porphyrin-containing compound metabolism; chlorophyll biosynthesis	Daucus carota (Wild carrot)			Chlorophyll biosynthesis; Chloroplast; NADP; Oxidoreductase; Photosynthesis; Plastid; Transit peptide
SRR648705_TR25739_c0_g2_i1_len=813	H32_WHEAT	Q:206-613,H:1-136	99.26%ID	E:2e-76	Histone H3.2	PF00125.21*Histone*Core histone H2A/H2B/H3/H4*1-132*E:8.3e-55	0,001	-1,252	0	-3,548	1	-0,328	1	-0,518	0,008	-0,712	H32_WHEAT	Histone H3.2				Triticum aestivum (Wheat)			Acetylation; Chromosome; Complete proteome; DNA-binding; Direct protein sequencing; Methylation; Nucleosome core; Nucleus; Phosphoprotein; Reference proteome
SRR648705_TR34697_c0_g1_i1_len=1268	NA	NA	NA	NA	NA	PF00538.16*Linker_histone*linker histone H1 and H5 family*27-87*E:5.8e-09*PF02178.16*AT_hook*AT hook motif*122-130*E:25*PF02178.16*AT_hook*AT hook motif*151-162*E:0.18*PF02178.16*AT_hook*AT hook motif*188-199*E:0.55	0	-1,424	0	-3,574	0,073	-2,034	0,025	-2,74	0,033	-0,753									
SRR648705_TR37418_c0_g2_i3_len=1382	KITH_ORYSJ	Q:935-579,H:67-188	74.17%ID	E:3e-76	Thymidine kinase	PF00265.15*TK*Thymidine kinase*22-145*E:2e-31	0,001	-1,211	0	-3,473	0,732	0,574	1	0,012	0,021	-0,937	KITH_ORYSJ	Thymidine kinase (EC 2.7.1.21)	TK Os03g0113100 LOC_Os03g02200 OSJNBa0090O10.3			Oryza sativa subsp. japonica (Rice)			ATP-binding; Alternative splicing; Complete proteome; DNA synthesis; Kinase; Metal-binding; Nucleotide-binding; Reference proteome; Transferase; Zinc
SRR648707_TR18549_c0_g2_i1_len=649	H32_WHEAT	Q:622-215,H:1-136	99.26%ID	E:1e-77	Histone H3.2	PF00125.21*Histone*Core histone H2A/H2B/H3/H4*10-141*E:1.1e-54	0	-1,447	0	-4,24	0,564	0,29	0,798	-0,226	0,004	-0,671	H32_WHEAT	Histone H3.2				Triticum aestivum (Wheat)			Acetylation; Chromosome; Complete proteome; DNA-binding; Direct protein sequencing; Methylation; Nucleosome core; Nucleus; Phosphoprotein; Reference proteome
SRR648707_TR26172_c0_g1_i1_len=745	H2B1_MEDTR	Q:30-578,H:57-148	98.91%ID	E:4e-58	Probable histone H2B.1	PF00125.21*Histone*Core histone H2A/H2B/H3/H4*46-168*E:2.6e-22	0	-1,239	0	-1,853	0,173	0,461	0,316	0,355	0,005	-0,645	H2B1_MEDTR	Probable histone H2B.1				Medicago truncatula (Barrel medic) (Medicago tribuloides)			Acetylation; Chromosome; DNA-binding; Isopeptide bond; Nucleosome core; Nucleus; Ubl conjugation
SRR324147_TR4550_c0_g2_i2_len=845	H32_WHEAT	Q:722-315,H:1-136	99.26%ID	E:4e-77	Histone H3.2	PF00125.21*Histone*Core histone H2A/H2B/H3/H4*42-173*E:2.1e-54	0	-1,383	0	-6,521	1	-0,216	0,066	-5,389	0,01	-1,135	H32_WHEAT	Histone H3.2				Triticum aestivum (Wheat)			Acetylation; Chromosome; Complete proteome; DNA-binding; Direct protein sequencing; Methylation; Nucleosome core; Nucleus; Phosphoprotein; Reference proteome
SRR324147_TR7895_c0_g1_i1_len=880	NA	NA	NA	NA	NA	PF10249.5*DUF3531*Protein of unknown function (DUF3531)*40-180*E:2.4e-55	0	-3,12	0	-5,242	1	1,538	1	0,004	0,004	-3,021									
SRR324147_TR27771_c0_g2_i2_len=810	H2A4_ORYSJ	Q:184-607,H:30-137	92.59%ID	E:1e-48	Probable histone H2A.4	PF00125.21*Histone*Core histone H2A/H2B/H3/H4*20-97*E:6.9e-13*PF16211.2*Histone_H2A_C*C-terminus of histone H2A*100-132*E:1.6e-18	0	-1,214	0	-1,784	0,299	0,44	1	-0,006	0,006	-0,692	H2A4_ORYSJ	Probable histone H2A.4	Os05g0461400 LOC_Os05g38640 OJ1281_H05.14 OJ1525_A02.1 Osj_018061			Oryza sativa subsp. japonica (Rice)			Chromosome; Complete proteome; DNA-binding; Nucleosome core; Nucleus; Reference proteome
SRR324148_TR4114_c0_g3_i1_len=1065	H2A1_SOLLC	Q:723-358,H:22-146	86.4%ID	E:3e-50	Histone H2A.1	PF00125.21*Histone*Core histone H2A/H2B/H3/H4*17-94*E:9.2e-13*PF16211.2*Histone_H2A_C*C-terminus of histone H2A*97-129*E:2e-18	0	-1,332	0	-2,814	0,811	0,811	1	-0,312	0,044	-0,811	H2A1_SOLLC	Histone H2A.1 (LeH2A-1)				Solanum lycopersicum (Tomato) (Lycopersicon esculentum)			Acetylation; Chromosome; Complete proteome; DNA-binding; Nucleosome core; Nucleus; Reference proteome
SRR324148_TR26974_c1_g1_i1_len=814	H4_SOYBN	Q:627-382,H:22-103	100%ID	E:6e-49	Histone H4	PF15511.3*CENP-T_C*Centromere kinetochore component CENP-T histone fold*35-96*E:1.4e-08*PF02969.14*TAF*TATA box binding protein associated factor (TAF)*35-92*E:0.00016	0	-1,401	0	-2,463	1	0,001	0,306	-0,442	0,004	-0,782	H4_SOYBN	Histone H4				Glycine max (Soybean) (Glycine hispida)			Chromosome; Complete proteome; DNA-binding; Methylation; Nucleosome core; Nucleus; Reference proteome
SRR324148_TR35599_c0_g2_i1_len=1604	FTSZ1_ARATH	Q:1033-285,H:36-397	87.29%ID	E:5e-171	Cell division protein FtsZ homolog 1, chloroplastic	PF00091.22*Tubulin*Tubulin/FtsZ family, GTPase domain*64-224*E:2.4e-42*PF12327.5*FtsZ_C*FtsZ family, C-terminal domain*273-366*E:8.8e-30	0	-7,253	0	-6,68	0	6,834	1	0	0,37	0,432	FTSZ1_ARATH	Cell division protein FtsZ homolog 1, chloroplastic (AtFtsZ1) (AtFtsZ1-1) (Chloroplast FtsZ) (CpFtsZ) (Protein ACCUMULATION AND REPLICATION OF CHLOROPLASTS 10) (Protein PLASTID MOVEMENT IMPAIRED4)	FTSZ1 ARC10 FTSZ1-1 PMI4 At5g55280 MCO15.23			Arabidopsis thaliana (Mouse-ear cress)			Acetylation; Cell cycle; Chloroplast; Complete proteome; GTP-binding; Membrane; Nucleotide-binding; Plastid; Reference proteome; Thylakoid; Transit peptide

Ms1wk

Transcript (CDF97)	Uniprot homolog	BLASTX Position	BLASTX %Identity	BLASTX evalue	Uniprot descr	Pfam	PValue_Ms6h	logFC_Ms6h	PValue_Ms8h	logFC_Ms8h	PValue_MsDamage24h	logFC_MsDamage24h	PValue_MsInstact24h	logFC_MsInstact24h	PValue_Ms1wk	logFC_Ms1wk	Entry.name	Protein names	Gene names	Organism	Pathway	Keywords
SRR1144633_TR5470_c0_g1_i1_len=2288	YHKF_SCHPO	Q:784-1293,H:159-329	38.01%ID	E:3e-32	Uncharacterized RNA-binding protein C660.15	PF00076.19*RRM_1*RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)*6-66*E:4e-13*PF00076.19*RRM_1*RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)*94-151*E:4.4e-11*PF00076.19*RRM_1*RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)*244-297*E:3.6e-13	1	-0,487	0,76	0,59	1	-0,259	0,017	-5,782	0	-3,19	YHKF_SCHPO	Uncharacterized RNA-binding protein C660.15	SPBC660.15	Schizosaccharomyces pombe (strain 972 / ATCC 24843) (Fission yeast)		Complete proteome; Nucleus; RNA-binding; Reference proteome; Repeat
SRR1144633_TR5687_c0_g2_i1_len=2266	RD21A_ARATH	Q:1992-763,H:23-434	68.67%ID	E:0	Cysteine proteinase RD21a	PF08246.9*Inhibitor_I29*Cathepsin propeptide inhibitor domain (I29)*116-173*E:1.2e-16*PF00112.20*Peptidase_C1*Papain family cysteine protease*204-419*E:2e-84*PF00396.15*Granulin*Granulin*453-499*E:9.2e-11	0,123	0,792	0,204	0,586	0,629	2,121	1	1,322	0	-7,253	RD21A_ARATH	Cysteine proteinase RD21a (RD21) (EC 3.4.22.-)	RD21A At1g47128 F2G19.31	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Disulfide bond; Glycoprotein; Hydrolase; Protease; Reference proteome; Signal; Thiol protease; Zymogen
SRR1144633_TR13566_c0_g2_i3_len=680	Y475T_DICDI	Q:609-166,H:608-766	37.11%ID	E:4e-23	OTU domain-containing protein DDB_G0284757	PF02338.16*OTU*OTU-like cysteine protease*53-142*E:7.9e-11	1	0,627	1	-0,16	1	0	0,001	-5,554	Y475T_DICDI	OTU domain-containing protein DDB_G0284757 (EC 3.1.2.-)	DDB_G0284757	Dictyostelium discoideum (Slime mold)		Complete proteome; Hydrolase; Protease; Reference proteome; Thiol protease
SRR1144633_TR19396_c0_g2_i1_len=1200	HS154_ARATH	Q:844-447,H:1-134	51.45%ID	E:3e-37	15.4 kDa class V heat shock protein	PF00011.18*HSP20*Hsp20/alpha crystallin family*33-112*E:1.6e-15	0,803	-0,085	0,909	-0,048	0,798	0,512	0,187	1,221	1	-1,438	HS154_ARATH	15.4 kDa class V heat shock protein (15.4 kDa heat shock protein) (AtHsp15.4)	HSP15.4 At4g21870 T8O5.80	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Cytoplasm; Reference proteome; Stress response
SRR1144633_TR23247_c0_g3_i1_len=610	NA	NA	NA	NA	NA	-	0,454	0,326	0,555	0,315	0,626	0,286	1	0,018	0	-1,426						
SRR1144633_TR27825_c0_g4_i2_len=5814	POLX_TOBAC	Q:2260-5787,H:1-1161	40.27%ID	E:0	Retrovirus-related Pol polyprotein from transposon TNT 1-94	PF14223.3*Retrotran_gag_2*gag-polypeptide of LTR copia-type*59-187*E:1.8e-33*PF00098.20*zf-CCHC*Zinc knuckle*227-242*E:0.00069*PF13976.3*gag_pre-integrs*GAG-pre-integrase domain*397-464*E:2.9e-14*PF00665.23*rve*Integrase core domain*480-594*E:6.3e-26*PF07727.11*RVT_2*Reverse transcriptase (RNA-dependent DNA polymerase)*854-1101*E:1.2e-91	0,502	3,981	1	-2,771	1	1	0	1	0	-6,243	POLX_TOBAC	Retrovirus-related Pol polyprotein from transposon TNT 1-94 [Includes: Protease (EC 3.4.23.-); Reverse transcriptase (EC 2.7.7.49); Endonuclease]		Nicotiana tabacum (Common tobacco)		Aspartyl protease; Endonuclease; Hydrolase; Metal-binding; Nuclease; Nucleotidyltransferase; Protease; RNA-directed DNA polymerase; Transferase; Transposable element; Zinc; Zinc-finger
SRR1144633_TR27911_c0_g1_i1_len=851	NDK1_TOBAC	Q:198-639,H:1-148	95.95%ID	E:3e-89	Nucleoside diphosphate kinase 1	-	1	0	1	0	1	0	1	0	1	0	-0,871	NDK1_TOBAC	Nucleoside diphosphate kinase 1 (EC 2.7.4.6) (Nucleoside diphosphate kinase I) (NDK I) (NDP kinase I) (NDPK I)		Nicotiana tabacum (Common tobacco)		ATP-binding; Kinase; Magnesium; Metal-binding; Nucleotide metabolism; Nucleotide-binding; Phosphoprotein; Transferase
SRR1144634_TR11817_c0_g1_i2_len=864	PS83B_ARATH	Q:172-755,H:17-204	93.09%ID	E:2e-127	Proteasome subunit beta type-3-B	PF00227.23*Proteasome*Proteasome subunit*3-108*E:8.1e-22	1	-0,023	1	-0,354	0,461	1,315	1	-0,013	0	-3,971	PS83B_ARATH	Proteasome subunit beta type-3-B (EC 3.4.25.1) (20S proteasome beta subunit C-2)	PBC2 At1g77440 T5M16.3	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Cytoplasm; Hydrolase; Nucleus; Protease; Proteasome; Reference proteome; Threonine protease; Zymogen
SRR1144634_TR12619_c0_g1_i1_len=1897	NA	NA	NA	NA	NA	-	0,429	0,476	0	1,981	0,09	-0,581	0,371	-0,31	0	-1,071						
SRR1144634_TR22915_c0_g1_i1_len=571	CVIF1_ARATH	Q:163-501,H:26-138	41.59%ID	E:2e-22	Cell wall / vacuolar inhibitor of fructosidase 1	PF04043.12*PMEI*Plant invertase/pectin methylesterase inhibitor*54-187*E:1e-13	0	1,217	0	1,991	0	1,233	0,932	-0,046	0	-7,8	CVIF1_ARATH	Cell wall / vacuolar inhibitor of fructosidase 1 (AtC/VIF1)	C/VIF1 CIF1 VIF1 At1g47960 T2J15.13	Arabidopsis thaliana (Mouse-ear cress)		Alternative splicing; Complete proteome; Disulfide bond; Glycoprotein; Reference proteome; Signal; Vacuole
SRR1144634_TR23693_c0_g1_i1_len=980	NA	NA	NA	NA	NA	PF00515.19*RCC1*Regulator of chromosome condensation (RCC1) repeat*24-82*E:3.1e-05*PF13540.3*RCC1_2*Regulator of chromosome condensation (RCC1) repeat*28-58*E:3.5e-09*PF00415.15*RCC1*Regulator of chromosome condensation (RCC1) repeat*45-103*E:1.8e-10*PF13540.3*RCC1_2*Regulator of chromosome condensation (RCC1) repeat*81-120*E:4.1e-08	1	-0,145	0,133	-1,124	0,118	2,087	0,502	-3,875	0,001	-6,586						
SRR1144634_TR38687_c0_g1_i2_len=645	SP1L1_ARATH	Q:113-433,H:1-110	67.57%ID	E:1e-29	Protein SPIRAL1-like 1	-	0,08	-0,613	0,552	-0,242	0,594	0,27	0,826	0,162	0	-1,059	SP1L1_ARATH	Protein SPIRAL1-like 1	SP1L1 At1g26355 T1K7.26	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Microtubule; Phosphoprotein; Reference proteome
SRR1144634_TR38813_c0_g1_i1_len=549	NA	NA	NA	NA	NA	-	0	0	1	0	1	0	1	0	0	-6,781						
SRR1122236_TR4154_c0_g1_i1_len=1464	MTDH_FRAAN	Q:121-1182,H:4-357	70.34%ID	E:2e-159	Probable mannitol dehydrogenase	PF08240.9*ADH_N*Alcohol dehydrogenase GroES-like domain*39-152*E:1.2e-27*PF00107.23*ADH_zinc_N*Zinc-binding dehydrogenase*195-317*E:2e-18	0,009	6,062	0,349	0,395	0,066	5,245	0	7,238	0	-9,752	MTDH_F

SRR1271857_TR12669_c0_g2_i1_len=503	NA	NA	NA	NA	NA		.	1	0	1	0	1	0	1	0	0	-5.232	.	.	.	.	.	.	.
SRR1271857_TR15938_c3_g1_i1_len=1535	NA	NA	NA	NA	NA		.	1	-0.635	1	-0.467	1	0	1	0	0	-7.091	.	.	.	.	.	.	.
SRR1271857_TR18439_c1_g1_i2_len=1600	NA	NA	NA	NA	NA		PF14215.3*bHLH-MYC_N*bHLH-MYC and R2R3-MYB transcription factors N-terminal*65-196*E:5.2e-20	1	0	1	0	1	0	1	0	0	-7.442	.	.	.	.	.	.	.
SRR1271857_TR18439_c1_g1_i6_len=1589	NA	NA	NA	NA	NA		PF14215.3*bHLH-MYC_N*bHLH-MYC and R2R3-MYB transcription factors N-terminal*13-136*E:3.7e-14	1	-0.189	0.017	-5.88	0.129	-4.976	0.129	-3.804	0	-7.07	.	.	.	.	.	.	.
SRR1271857_TR21426_c0_g2_i2_len=2739	DADIS_PANGI	Q:72-2456,H:1-763	71.21%ID	E:0	Dammarenediol II synthase		PF13249.3*SQHop_cyclase_N*Squalene-hopene cyclase N-terminal domain*103-361*E:3.8e-39 PF00432.18*Prenyltrans*Prenyltransferase and squalene oxidase repeat*149-191*E:3.4e-09 PF13243.3*SQHop_cyclase_C*Squalene-hopene cyclase C-terminal domain*415-722*E:9.3e-38 PF00432.18*Prenyltrans*Prenyltransferase and squalene oxidase repeat*592-632*E:7.6e-07 PF00432.18*Prenyltrans*Prenyltransferase and squalene oxidase repeat*641-691*E:1.7e-07	0.62	-0.501	1	-0.464	0.798	-0.42	0.239	-1.429	0	-2.351	DADIS_PANGI	Dammarenediol II synthase (EC 4.2.1.125)	PNA DDS	Panax ginseng (Korean ginseng)	.	.	Isomerase; Lyase; Membrane; Repeat; Transmembrane; Transmembrane helix
SRR1271857_TR21502_c0_g3_i5_len=1074	VATL_KALDA	Q:837-343,H:1-165	98.18%ID	E:3e-69	V-type proton ATPase 16 kDa proteolipid subunit	PF00137.18*ATP-synt_C*ATP synthase subunit C*17-76*E:6.3e-14 PF00137.18*ATP-synt_C*ATP synthase subunit C*97-155*E:6.7e-21	.	1	-0.125	1	0.557	1	0.567	1	0.732	0	-6.984	VATL_KALDA	V-type proton ATPase 16 kDa proteolipid subunit (V-ATPase 16 kDa proteolipid subunit) (V-type H(+)-ATPase 16 kDa subunit) (Vacuolar proton pump 16 kDa proteolipid subunit)	Kalanchoe daigremontiana (Devil's backbone) (Bryophyllum daigremontianum)	.	.	.	Hydrogen ion transport; Ion transport; Membrane; Transmembrane; Transmembrane helix; Transport; Vacuole
SRR1271857_TR22544_c0_g3_i1_len=725	NA	NA	NA	NA	NA		.	0.719	0.138	0.108	-0.542	0.352	-0.745	1	-0.005	0	-4.11	.	.	.	.	.	.	.
SRR1271857_TR27540_c2_g2_i1_len=649	NA	NA	NA	NA	NA		.	0.732	-0.741	0.254	-3.635	1	1.419	1	0.767	0	-3.109	.	.	.	.	.	.	.
SRR1271857_TR35081_c0_g2_i1_len=2246	GSH1_SOLLC	Q:248-1984,H:1-523	74.31%ID	E:0	Glutamate--cysteine ligase, chloroplastic	PF04107.10*GCS2*Glutamate-cysteine ligase family 2(GCS2)*147-391*E:7.3e-81	0.793	-0.201	0.707	0.371	0.395	0.587	0.25	0.782	0	-8.02	GSH1_SOLLC	Glutamate--cysteine ligase, chloroplastic (EC 6.3.2.2) (Gamma-ECS) (GCS) (Gamma-glutamylcysteine synthetase)	GSH1	Solanum lycopersicum (Tomato) (Lycopersicon esculentum)	PATHWAY: Sulfur metabolism; glutathione biosynthesis; glutathione from L-cysteine and L-glutamate: step 1/2.	.	ATP-binding; Chloroplast; Complete proteome; Disulfide bond; Glutathione biosynthesis; Ligase; Nucleotide-binding; Plastid; Reference proteome; Transit peptide
SRR1271857_TR38062_c0_g3_i1_len=523	NA	NA	NA	NA	NA		.	0.121	-0.845	0.029	-1.097	1	0.347	1	0.069	0	-1.392	.	.	.	.	.	.	.
SRR1271857_TR43231_c0_g3_i4_len=3639	RVE6_ARATH	Q:3565-2605,H:1-314	58.01%ID	E:7e-84	Protein REVEILLE 6		.	0.729	-0.162	0.906	0.119	1	0.02	0.783	-0.176	0	-2.546	RVE6_ARATH	Protein REVEILLE 6	RVE6 At5g52660 F6N7.15	Arabidopsis thaliana (Mouse-ear cress)	.	.	Alternative splicing; Complete proteome; DNA-binding; Nucleus; Reference proteome; Transcription; Transcription regulation
SRR1271858_TR1911_c0_g2_i2_len=609	NA	NA	NA	NA	NA		PF13650.3*Asp_protease_2*Aspartyl protease*97-192*E:5.4e-06	0.798	0.544	1	-0.584	1	1.001	1	0.09	0.001	-3.822	.	.	.	.	.	.	.
SRR1271858_TR2802_c0_g1_i1_len=1319	POL3_DROME	Q:1312-644,H:370-590	39.56%ID	E:3e-37	Retrovirus-related Pol polyprotein from transposon 17.6		0.38	0.49	1	-0.776	0.629	1.004	0.629	1.168	0.001	-4.458	POL3_DROME	Retrovirus-related Pol polyprotein from transposon 17.6 [Includes: Protease (EC 3.4.23.-); Reverse transcriptase (EC 2.7.7.49); Endonuclease]	pol	Drosophila melanogaster (Fruit fly)	.	.	.	Aspartyl protease; Endonuclease; Hydrolase; Nuclease; Nucleotidyltransferase; Protease; RNA-directed DNA polymerase; Transferase; Transposable element
SRR1271858_TR4441_c0_g1_i1_len=626	NA	NA	NA	NA	NA		.	0.013	-1.544	0.009	-5.963	1	0.845	1	1.009	0.001	-1.18	.	.	.	.	.	.	.
SRR1271858_TR25211_c0_g2_i1_len=675	NA	NA	NA	NA	NA		.	0	1.292	0	6.744	0	8.539	0.129	4.207	0	-2.021	.	.	.	.	.	.	.
SRR1271858_TR30562_c1_g1_i7_len=3536	GCL1_ARATH	Q:2318-3229,H:164-435	64.14%ID	E:4e-124	LanC-like protein GCL1		PF05147.10*LANC_like*Lanthionine synthetase C-like protein*71-156*E:1.6e-14	1	0.4	1	0.586	1	0	1	0	0	-7.855	GCL1_ARATH	LanC-like protein GCL1 (G protein-coupled receptor 2-like protein 1) (Protein GCR2-like 1)	GCL1 At5g65280 MQN23.23	Arabidopsis thaliana (Mouse-ear cress)	.	.	Complete proteome; Reference proteome
SRR1271858_TR33754_c0_g2_i1_len=840	NA	NA	NA	NA	NA		.	0.62	0.732	0	3.277	0	3.166	0.001	2.819	0	-2.698	.	.	.	.	.	.	.
SRR1271858_TR41562_c0_g2_i1_len=2082	ASPG1_ARATH	Q:594-1787,H:177-500	28.07%ID	E:2e-26	Protein ASPARTIC PROTEASE IN GUARD CELL 1		PF14543.3*TAXI_N*Xylanase inhibitor N-terminal*81-263*E:4.1e-28 PF00026.20*Asp*Eukaryotic aspartyl protease*88-489*E:2.5e-07 PF14543.3*TAXI_C*Xylanase inhibitor C-terminal*307-437*E:5.7e-29	1	0.789	1	2.294	1	0.4	1	0.61	0	-2.923	ASPG1_ARATH	Protein ASPARTIC PROTEASE IN GUARD CELL 1 (AtASPG1) (EC 3.4.23.-)	ASPG1 At3g18490 MYF24.22	Arabidopsis thaliana (Mouse-ear cress)	.	.	Aspartyl protease; Complete proteome; DNA-binding; Disulfide bond; Endoplasmic reticulum; Hydrolase; Protease; Reference proteome; Signal
SRR1271858_TR46393_c0_g2_i1_len=720	NA	NA	NA	NA	NA		.	0.221	-0.594	0.644	-0.182	0.154	0.767	0.87	0.16	0.001	-1.321	.	.	.	.	.	.	.
SRR1271858_TR55841_c0_g2_i6_len=1175	SC31B_ARATH	Q:171-773,H:93-1104	65.85%ID	E:2e-60	Protein transport protein SEC31 homolog B (ECO:0000305)		PF07304.8*SRA1*Steroid receptor RNA activator (SRA1)*49-187*E:9.8e-06	0.719	-0.327	0.014	-0.892	0.052	1.478	0.111	1.74	0	-1.493	SC31B_ARATH	Protein transport protein SEC31 homolog B (SEC31-like protein B)	SEC31B At3g63460 MAA21.90	Arabidopsis thaliana (Mouse-ear cress)	.	.	Alternative splicing; Complete proteome; ER-Golgi transport; Endoplasmic reticulum; Golgi apparatus; Phosphoprotein; Protein transport; Reference proteome; Repeat; Transport; WD repeat
SRR1271858_TR57655_c0_g1_i1_len=1188	PPSP1_ARATH	Q:959-306,H:16-236	56.56%ID	E:3e-94	Inorganic pyrophosphatase 1	PF06888.9*Put_Phosphatase*Putative Phosphatase*7-235*E:8e-90 PF12710.4*HAD*haloacid dehalogenase-like hydrolase*7-183*E:4.5e-09	0.895	0.134	0.105	0.988	0.006	1.429	0.025	1.215	0	-7.217	PPSP1_ARATH	Inorganic pyrophosphatase 1 (AtPPaPase1) (PPi phosphatase 1) (Pyrophosphate-specific phosphatase 1) (EC 3.6.1.1) (Protein PHOSPHATE STARVATION-INDUCED GENE 2) (AIPS2)	PS2 At1g73010 F3N23.21	Arabidopsis thaliana (Mouse-ear cress)	.	.	Complete proteome; Hydrolase; Magnesium; Metal-binding; Reference proteome
SRR1271858_TR58517_c0_g1_i1_len=528	NA	NA	NA	NA	NA		.	1	0	1	0	1	1.335	1	0	0	-2.087	.	.	.	.	.	.	.
SRR1271858_TR66514_c0_g1_i1_len=713	NA	NA	NA	NA	NA		.	0.774	0.126	0	2.337	0.03	0.709	0.01	0.821	0	-1.268	.	.	.	.	.	.	.
SRR1271859_TR156_c0_g1_i2_len=788	RUXG_ARATH	Q:249-488,H:1-80	90%ID	E:5e-44	Probable small nuclear ribonucleoprotein G		.	0.581	-0.456	0.412	-0.52	0.189	1.841	1	0.771	0	-8.63	RUXG_ARATH	Probable small nuclear ribonucleoprotein G (snRNP-G) (Sm protein G) (Sm-G) (SmG)	At2g23930 T29E15.13	Arabidopsis thaliana (Mouse-ear cress)	.	.	Alternative splicing; Complete proteome; Nucleus; RNA-binding; Reference proteome; Ribonucleoprotein; Spliceosome; mRNA processing; mRNA splicing
SRR1271859_TR1028_c0_g1_i2_len=1019	NA	NA	NA	NA	NA		.	1	0	1	0.716	1	0	1	0	0	-6.707	.	.	.	.	.	.	.
SRR1271859_TR2483_c1_g1_i9_len=1301	RAE1C_ARATH	Q:193-798,H:1-216	93.07%ID	E:7e-117	Ras-related protein RABE1c		PF00025.18*ArfADP-ribosylation factor family*16-163*E:2.1e-15 PF00071.19*Ras*Ras family*17-178*E:1.6e-66 PF08477.10*Roc*Ras of Complex, Roc, domain of DAPkinase*17-132*E:4.6e-35 PF04670.9*Gtr1_RagA*Gtr1/RagA G protein conserved region*17-132*E:4.5e-05 PF01926.20*MMR_HSR1*50.5 ribosome-binding GTPase*18-128*E:4.7e-05	0.811	0.335	0.16	-0.589	0	8.307	0	7.859	0	-3.996	RAE1C_ARATH	Ras-related protein RABE1c (AtRABE1c) (Ras-related protein Ara-3) (Ras-related protein Rab8A) (AtRab8A)	RABE1C ARA-3 RAB8A At3g46060 F12M12.30	Arabidopsis thaliana (Mouse-ear cress)	.	.	Cell membrane; Complete proteome; GTP-binding; Golgi apparatus; Lipoprotein; Membrane; Nucleotide-binding; Prenylation; Protein transport; Reference proteome; Transport
SRR1271859_TR6453_c0_g2_i1_len=768	PDCB3_ARATH	Q:535-762,H:1-80	69.74%ID	E:1e-34	PLASMODESMATA CALLOSE-BINDING PROTEIN 3		.	0.282	-0.969	0.623	0.434	0.226	2.062	0.629	1.041	0	-2.266	PDCB3_ARATH	PLASMODESMATA CALLOSE-BINDING PROTEIN 3 (AtPDCB3)	PDCB3 At1g18650 F25I16.1	Arabidopsis thaliana (Mouse-ear cress)	.	.	Cell junction; Cell membrane; Complete proteome; Disulfide bond; GPI-anchor; Glycoprotein; Lipoprotein; Membrane; Reference proteome; Signal
SRR1271859_TR9840_c0_g1_i2_len=2451	ENO_SOLLC	Q:1605-277,H:1-444	93.24%ID	E:0	Enolase		PF03952.13*Enolase_N*Enolase, N-terminal domain*4-139*E:2.7e-56 PF00113.19*Enolase_C*Enolase, C-terminal TIM barrel domain*148-439*E:3.7e-161 PF13378.3*MR_MLE_C*Enolase C-terminal domain-like*275-403*E:9.1e-09 PF01976.8*MAAL_C*Methylaspartate ammonia/glase C-terminus*297-400*E:1.3e-05	0.161	-0.344	0.531	-0.167	0.14	0.414	0.218	0.352	0	-2.1	ENO_SOLLC	Enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (2-phosphoglycerate dehydratase)	PGH1	Solanum lycopersicum (Tomato) (Lycopersicon esculentum)	PATHWAY: Carbohydrate degradation; glycolysis; pyruvate from D-glyceraldehyde 3-phosphate: step 4/5.	.	Complete proteome; Cytoplasm; Glycolysis; Lyase; Magnesium; Metal-binding; Reference proteome
SRR1271859_TR10078_c0_g1_i3_len=1503	DPM1_HUMAN	Q:697-1215,H:88-260	69.94%ID	E:9e-79	Dolichol-phosphate mannosyltransferase subunit 1		PF00535.23*Glycos_transf_2*Glycosyl transferase family 2*17-124*E:1.7e-19 PF13641.3*Glyco_transf_2_3*Glycosyltransferase like family 2*23-155*E:1.4e-06 PF13506.3*Glyco_transf_21*Glycosyl transferase family 21*29-124*E:3.7e-07	1	0.755	0	1.59	0	2.085	0	1.819	0	-1.753	MIRA_SYNDU	Dolichol-phosphate mannosyltransferase subunit 1 (EC 2.4.1.83) (Dolichol-phosphate mannose synthase subunit 1) (DPM synthase subunit 1) (Mannosyltransferase 1) (Protein beta-D-mannosyltransferase subunit 1) (Mannose-P-dolichol synthase subunit 1) (MPD synthase subunit 1)	DPM1	Homo sapiens (Human)	PATHWAY: Protein modification; protein glycosylation.	.	Acetylation; Complete proteome; Congenital disorder of glycosylation; Congenital muscular dystrophy; Disease mutation; Dolichol pathway; Endoplasmic reticulum; Glycosyltransferase; Hydrolase; Membrane; Phosphoprotein; Reference proteome; Transferase
SRR1271859_TR12356_c0_g2_i1_len=584	MIRA_SYNDU	Q:44-379,H:103-216	59.13%ID	E:6e-37	Miraculin		PF00197.15*Kunitz_legume*Trypsin and protease inhibitor*2-108*E:1.3e-26	0.003	0.755	0	1.59	0	2.085	0	1.819	0	-1.753	MIRA_SYNDU	Miraculin (MIR)	Synsepalum dulcificum (Miracle fruit) (Richadella dulcifica)	.	.	.	Direct protein sequencing; Disulfide bond; Glycoprotein; Signal; Taste-modifying protein
SRR1271859_TR1834_c0_g1_i1_len=512	NA	NA	NA	NA	NA		.	0	1.376	0	8.288	0.066	5.219	1	2.21	0	-2.11	.	.	.	.	.	.	.
SRR1271859_TR20089_c0_g1_i3_len=1800	SPDE_COFAR	Q:1064-657,H:116-251	94.12%ID	E:3e-84	Spermidine synthase	PF01564.14*Spermine_synth*Spermine/spermidine synthase*1-120*E:6.6e-39	1	-0.498	0.692	0.921	1	-0.169	1	-0.65	0	-4.839	SPDE_COFAR	Spermidine synthase (SPDSY) (EC 2.5.1.16) (Putrescine aminopropyltransferase)	Coffea arabica (Arabian coffee)	PATHWAY: Amine and polyamine biosynthesis; spermidine biosynthesis; spermidine from putrescine: step 1/1.	.	.	Polyamine biosynthesis; Spermidine biosynthesis; Transferase
SRR1271859_TR20141_c0_g3_i2_len=1412	SKP1A_ARATH	Q:1224-760,H:2-160	77.99%ID	E:5e-69	SKP1-like protein 1A	PF03931.12*Skp1_POZ*Skp1 family, tetramerisation domain*5-64*E:1.5e-30 PF01466.16*Skp1*Skp1 family, dimerisation domain*108-155*E:2e-30	0.933	0.025	0.873	0.061	0.004	0.869	0.028	0.678	0	-2.409	SKP1A_ARATH	SKP1-like protein 1A (SKP1-like 1) (UFO-binding protein 1)	SKP1A ASK1 SKP1 UIP1 At1g75950 T4O12.17	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Protein modification; protein ubiquitination.	.	3D-structure; Auxin signaling pathway; Chromosome partition; Complete proteome; Cytoplasm; Cytoskeleton; Developmental protein; Ethylene signaling pathway; Host-virus interaction; Nucleus; Reference proteome; Ubl conjugation pathway
SRR1271859_TR23354_c0_g2_i1_len=1562	NA	NA	NA	NA	NA		PF00257.16*Dehydrin*Dehydrin*10-178*E:2e-43	0	2.197	0	4.675	0	5.109	0	2.946	0	-2.756	.	.	.	.	.	.	.
SRR1271859_TR24255_c0_g2_i2_len=1652	G3PC_TOBAC	Q:1442-468,H:1-325	93.54%ID	E:0	Glyceraldehyde-3-phosphate dehydrogenase, cytosolic	PF00044.21*Gp_dh_N*Glyceraldehyde 3-phosphate dehydrogenase, NAD binding domain*6-156*E:1.1e-55 PF02800.17*Gp_dh_C*Glyceraldehyde 3-phosphate dehydrogenase, C-terminal domain*161-318*E:2.5e-72	0.152	-0.31	0.44	0.171	0.826	0.048	0.54	0.131	1	0	-7.135	G3PC_TOBAC	Glyceraldehyde-3-phosphate dehydrogenase, cytosolic (EC 1.2.1.12) (Fragment)	GAPC	Nicotiana tabacum (Common tobacco)	PATHWAY: Carbohydrate degradation; glycolysis; pyruvate from D-glyceraldehyde 3-phosphate: step 1/5.	.	Cytoplasm; Glycolysis; NAD; Oxidoreductase
SRR1271859_TR27396_c0_g1_i2_len=1056	Y5T5_SYNY3	Q:539-981,H:40-183	44%ID	E:6e-29	Thylakoid membrane protein sll0575	PF11016.5*DUF2854*Protein of unknown function (DUF2854)*114-264*E:5.9e-50	1	1.691	1	0	1	1.397	1	-0.243	0	-8.037	Y5T5_SYNY3	Thylakoid membrane protein sll0575	sll0575	Synechocystis sp. (strain PCC 6803 / Kazusa)	.	.	Complete proteome; Membrane; Reference proteome; Thylakoid; Transmembrane; Transmembrane helix
SRR1271859_TR27652_c0_g1_i1_len=517	NA	NA	NA	NA	NA		.	0.44	-0.914	0.732	0.584	0.005	6.146	0	7.215	0.001	-6.625	.	.	.	.	.	.	.
SRR1271859_TR29534_c0_g1_i11_len=2746	FLA1_ARATH	Q:78-1107,H:22-331	67.52%ID	E:2e-139	Fasciclin-like arabinogalactan protein 1	PF02469.19*Fasciclin*Fasciclin domain*73-143*E:0.0002 PF02469.19*Fasciclin*Fasciclin domain*235-363*E:1.9e-13	0.917	-0.068	0.623	-0.318	0.014	-1.067	0.01	-1.173	0.001	-3.044	FLA1_ARATH	Fasciclin-like arabinogalactan protein 1	FLA1 At5g55730 MDF20.17	Arabidopsis thaliana (Mouse-ear cress)	.	.	Cell membrane; Complete proteome; GPI-anchor; Glycoprotein; Lipoprotein; Membrane; Proteoglycan; Reference proteome; Repeat; Signal
SRR1271859_TR33494_c0_g1_i2_len=749	URM12_ARATH	Q:6-16-362,H:1-99	81.18%ID	E:1e-42	Ubiquitin-related modifier 1 homolog 2 (ECO:0000255|HAMAP-Rule:MF_03048)	PF09138.8*Urm1*Urm1 (Ubiquitin related modifier)*33-129*E:5.3e-36	0.718	-0.24	0.833	-0.113	0.43	0.706	0.545	0.602	0	-6.475	URM12_ARATH	Ubiquitin-related modifier 1 homolog 2	URM1-2 At3g61113 T20K12	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: tRNA modification; 5methoxycarbonylmethyl-2thiouridine-RNA biosynthesis. (ECO:0000255|HAMAP-Rule:MF_03048).	.	Complete proteome; Cytoplasm; Isopeptide bond; Reference proteome; Ubl conjugation pathway; tRNA processing
SRR1271859_TR35239_c0_g1_i1_len=917	SYP_PLAF7	Q:96-755,H:516-766	44.16%ID	E:7e-52	Proline--tRNA ligase	PF13393.17*HGTP_anticodon*Anticodon binding domain*21-117*E:4.8e-22 PF09180.8*ProRS-C_1*Prolyl-tRNA synthetase, C-terminal*144-217*E:2.8e-26	1	0.58	1	0	0.001	1	0.637	1	0	0	-1.6	SYP_PLAF7	Proline--tRNA ligase (EC 6.1.1.15) (Prolyl-tRNA synthetase) (ProRS)	proRS PfL0670c	Plasmodium falciparum (isolate 3D7)	.	.	3D-structure; ATP-binding; Aminoacyl-tRNA synthetase; Complete proteome; Cytoplasm; Ligase; Nucleotide-binding; Protein biosynthesis; Reference proteome
SRR1271859_TR36883_c0_g1_i9_len=911	DEF1A_SOLLC	Q:827-231,H:68-275	79.33%ID	E:7e-112	Peptide deformylase 1A, chloroplastic	PF01327.18*Pep_deformylase*Polypeptide deformylase*34-189*E:1.3e-46	0.299	-1.484	1	-0.133	0.517	0.946	1	-0.249	0.001	-6.633	DEF1A_SOLLC	Peptide deformylase 1A, chloroplastic (PDF 1A) (EC 3.5.1.88) (Polypeptide deformylase)	PDF1A	Solanum lycopersicum (Tomato) (Lycopersicon esculentum)	.	.	Chloroplast; Complete proteome; Hydrolase; Metal-binding; Plastid; Protein biosynthesis; Reference proteome; Transit peptide; Zinc
SRR1271859_TR37765_c1_g2_i1_len=2034	ARF2_ORYSJ	Q:1865-1323,H:1-181	99.45%ID	E:2e-124	ADP-ribosylation factor 2	PF00025.18*ArfADP-ribosylation factor family*5-177*E:3e-80 PF09439.7*SRPRB*Signal recognition particle receptor beta subunit*16-143*E:8.5e-14 PF08477.10*Roc*Ras of Complex, Roc, domain of DAPkinase*19-129*E:1.1e-13 PF04670.9*Gtr1_RagA*Gtr1/RagA G protein conserved region*19-142*E:2.5e-10 PF01926.20*MMR_HSR1*50.5 ribosome-binding GTPase*19-122*E:4.7e-05 PF00071.19*Ras*Ras family*20-172*E:1e-12	1	-0.404	1	0.653	1	0.059	1	-0.095	0	-3.934	ARF2_ORYSJ	ADP-ribosylation factor 2	ARF Os05g0489600 LOC_Os05g41060 OJ1119_H02.17	Oryza sativa subsp. japonica (Rice)	.	.	Complete proteome; ER-Golgi transport; GTP-binding; Golgi apparatus; Lipoprotein; Myristate; Nucleotide-binding; Protein transport; Reference proteome; Transport
SRR1271859_TR41148_c1_g1_i1_len=697	NA	NA	NA	NA	NA		.	0.721	-0.178	0.002	-1.203	0.249	-0.521	0.058	-0.838	0.001	-1.221	.	.	.	.	.	.	.
SRR1271859_TR42956_c0_g3_i8_len=1513	XTH2_SOYBN	Q:310-1089,H:30-282	67.31%ID	E:2e-122	Xyloglucan endotransglucosylase/hydrolase 2 (ECO:0000250|UniProtKB:Q38857)	PF00722.18*Glycos_hydro_16*Glycosyl hydrolases family 16*29-209*E:4.7e-63 PF06955.9*XET_C*Xyloglucan endo-transglycosylase (XET) C-terminus*242-284*E:1.2e-16	1	-1.022	1	0.135	0.226	-2.007	0.226	-1.834	0	-2.025	XTH2_SOYBN	Xyloglucan endotransglucosylase/hydrolase 2 (EC 2.4.1.207) (Brassinosteroid-regulated protein BRU1)	Glycine max (Soybean) (Glycine hispida)	.	.	.	Apoplast; Cell wall; Complete proteome; Disulfide bond; Glycoprotein; Glycosidase; Hydrolase; Reference proteome; Secreted; Signal; Transferase
SRR1271859_TR43217_c0_g2_i4_len=1598	NA	NA	NA	NA	NA		.	0.847	-0.114	0.35	0.557	0.763	0.24	1	0.134	0	-5.573	.	.	.	.	.	.	.
SRR1271859_TR46622_c0_g3_i1_len=996	NA	NA	NA	NA	NA		.	0.524	-0.524	0.333	0.574	0.748	0.223	0.86	0.276	0	-7.403	.	.	.	.	.	.	.
SRR1271859_TR47131_c1_g2_i3_len=1606	NA	NA	NA	NA	NA		.	1	-0.007	0.25	-0.676	0.299	1.457	0.692	0.876	0	-1.944	.	.	.	.	.	.	.
SRR342017_TR4651_c0_g2_i3_len=1236	CUL1_ARATH	Q:2-985,H:411-738	78.05%ID	E:2e-173	Cullin-1	PF00888.19*Cullin*Cullin family*2-231*E:6.8e-77 PF10557.6*Cullin_Nedd8*Cullin protein neddylation domain*258-320*E:3.1e-26	1	-0.015	0.025	-1.717	0.226	1.775	0.132	2.036	0	-1.995	CUL1_ARATH	Cullin-1	CUL1 At4g02570 T10P11.26	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Protein modification; protein ubiquitination.	.	Auxin signaling pathway; Cell cycle; Complete proteome; Cytoplasm; Cytoskeleton; Developmental protein; Ethylene signaling pathway; Isopeptide bond; Nucleus; Reference proteome; Ubl conjugation; Ubl conjugation pathway
SRR342017_TR7034_c0_g1_i6_len=853	NA	NA	NA	NA	NA		.	1	0	1	0	1	0	1	0	0	-2.316	.	.	.	.	.	.	.
SRR342017_TR7330_c1_g4_i2_len=896	BTL3_DANRE	Q:799-434,H:1-123	58.54%ID	E:3e-41	Transcription factor BTF3 homolog 4	PF01849.15*NAC*NAC domain*36-91*E:5.1e-19	0.629	1.912	1	0.431	0.502	2.802	1	0.948	0	-6.43	BTL3_DANRE	Transcription factor BTF3 homolog 4 (Basic transcription factor 3-like 4)	btf3l4	Danio rerio (Zebrafish) (Brachydanio rerio)	.	.	Complete proteome; Reference proteome
SRR342017_TR7809_c1_g2_i1_len=2995	TCPD_ARATH	Q:1704-2741,H:184-628	92.2%ID	E:0	T-complex protein 1 subunit delta (ECO:0000303|PubMed:11599560)	PF00118.21*Cpn60_TCP1*TCP-1/cpn60 chaperonin family*10-361*E:3.3e-97	0.24	-0.508	0.005	-1.633	0.211	-0.714	0.043	-1.244	0	-1.099	TCPD_ARATH	T-complex protein 1 subunit delta (TCP-1-delta) (CCT-delta) (Chaperonin CCT4)	CCT4 At3g18190 MRC8	Arabidopsis thaliana (Mouse-ear cress)	.	.	ATP-binding; Chaperone; Complete proteome; Cytoplasm; Nucleotide-binding; Reference proteome
SRR342017_TR8701_c1_g2_i2_len=1867	HMG13_ARATH	Q:383-1537,H:58-442	56.85%ID	E:4e-94	High mobility group B protein 13	PF09011.7*HMG_box_2*HMG-box domain*196-257*E:1.1e-09 PF00505.16*HMG_box*HMG (high mobility group) box*198-259*E:4e-17 PF09011.7*HMG_box_2*HMG-box domain*312-379*E:1e-13 PF00505.16*HMG_box*HMG (high mobility group) box*314-380*E:1e-18 PF09011.7*HMG_box_2*HMG-box domain*439-510*E:1.8e-11 PF00505.16*HMG_box*HMG (high mobility group) box*442-510*E:1.3e-17 PF08073.9*CHDNT*CHDNT (NUC034) domain*451-485*E:0.00027	0.058	-0.875	0.016	-2.704	0.692	-0.738	0.692	-0.627	0	-0.998	HMG13_ARATH	High mobility group B protein 13 (Nucleosome/chromatin assembly factor group D 13)	HMGB13 NFD13 At4g11080 F2P3.3 T22B4.60	Arabidopsis thaliana (Mouse-ear cress)	.	.	Complete proteome; DNA-binding; Nucleus; Reference proteome; Repeat
SRR342017_TR9822_c1_g1_i1_len=845	UEV1C_ARATH	Q:624-187,H:1-145	89.73%ID	E:2e-88	Ubiquitin-conjugating enzyme E2 variant 1C	PF00179.23*UQ_con*Ubiquitin-conjugating enzyme*43-136*E:8.3e-15	0.407	0.375	0.881	0.053	0	2.757	0	3.479	0	-4.15	UEV1C_ARATH	Ubiquitin-conjugating enzyme E2 variant 1C (Ubc enzyme variant 1C) (Protein MMS ZWEI HOMOLOG 3)	UEV1C MMZ3 At2g36060 F11F19.3	Arabidopsis thaliana (Mouse-ear cress)	.	.	Alternative splicing; Complete proteome; Reference proteome
SRR342017_TR12675_c1_g2_i3_len=886	GH33_ARATH	Q:288-1,H:446-541	79.17%ID	E:8e-43	Indole-3-acetic acid-amido synthetase GH3.3	.	0.25	-0.868	0.133	0.632	0.212	1.025	0.381	0.805	0	-2.419	GH33_ARATH	Indole-3-acetic acid-amido synthetase GH3.3 (EC 6.3.2.-) (Auxin-responsive GH3-like protein 3) (AtGH3-3)	GH3.3 At2g23170 T20D16.20	Arabidopsis thaliana (Mouse-ear cress)	.	.	Complete proteome; Ligase; Reference proteome
SRR342017_TR13518_c0_g1_i1_len=574	NUD25_ARATH	Q:51-362,H:1-175	72.64%ID	E:3e-49	Nudix hydrolase 25	.	0.16	1.24	0.002	6.311	0.066	5.298	0.002	6.299	0.001	-6.547	NUD25_ARATH	Nudix hydrolase 25 (AtNUDT25) (EC 3.6.1.17) (Bis(5'-nucleosyl)-tetraphosphatase (asymmetrical))	NUDT25 NUDX25 At1g30110 T2H7.9	Arabidopsis thaliana (Mouse-ear cress)	.	.	Complete proteome; Hydrolase; Manganese; Metal-binding; Reference proteome
SRR342017_TR17264_c1_g2_i1_len=762	14KD_DAUCA	Q:277-528,H:54-137	70.24%ID	E:2e-22	14 kDa proline-rich protein DC2.15	.	1	-1.659	1	-1.942	0.129	5.045	0.502	3.937	0	-0.961	14KD_DAUCA	14 kDa proline-rich protein DC2.15	Daucus carota (Wild carrot)	.	.	.	Membrane; Signal; Transmembrane; Transmembrane helix
SRR342017_TR17850_c1_g1_i1_len=1349	FLA8_ARATH	Q:1349-627,H:94-334	75.93%ID	E:5e-115	Fasciclin-like arabinogalactan protein 8	PF02469.19*Fasciclin*Fasciclin domain*105-235*E:5.2e-20	1	-0.346	0.692	-0.907	1	-0.478	1	0.158	0	-8.788	FLA8_ARATH	Fasciclin-like arabinogalactan protein 8 (AtAGP8)	FLA8 At2g45470 F4L23.2	Arabidopsis thaliana (Mouse-ear cress)	.	.	Cell membrane; Complete proteome; GPI-anchor; Glycoprotein; Lipoprotein; Membrane; Proteoglycan; Reference proteome; Repeat; Signal
SRR342017_TR22832_c0_g1_i1_len=694	RS212_ARATH	Q:544-302,H:1-81	81.48%ID	E:4e-44	40S ribosomal protein S21-2

SRR646604_TR8067_c0_g2_i1_len=1041	PER12_ARATH	Q:170-730;H:153-339	66.84%ID	E:8e-86	Peroxidase 12	PF00141.20*peroxidase*Peroxidase*5-151*E:4.5e-38	1	0	1	3.225	1	0	0	0.001	-3.191	PER12_ARATH	Peroxidase 12 (Atperox P12) (EC 1.11.1.7) (ATP4a) (PRXR6)	PER12 P12 At1g71695 F14O23.6 F26A9.5	Arabidopsis thaliana (Mouse-ear cress)		Calcium; Complete proteome; Disulfide bond; Glycoprotein; Heme; Hydrogen peroxide; Iron; Metal-binding; Oxidoreductase; Peroxidase; Reference proteome; Secreted; Signal; Vacuole
SRR646604_TR13798_c0_g2_i1_len=811	SUI1_ORYSJ	Q:560-222;H:1-115	92.17%ID	E:4e-70	Protein translation factor SUI1 homolog	PF01253.19*SUI1*Translation initiation factor SUI1*28-102*E:5.4e-26	0.04	0.467	0.02	0.537	0	1.442	0	1.329	0	-1.392	SUI1_ORYSJ	Protein translation factor SUI1 homolog (Protein GOS2) (Protein eIF1) (Translation initiation factor 1)	GOS2 Os07g0529800 LOC_Os07g34589	Oryza sativa subsp. japonica (Rice)	Complete proteome; Initiation factor; Protein biosynthesis; Reference proteome; Translation regulation
SRR646604_TR16508_c0_g1_i1_len=1479	AVP_VIGRR	Q:245-1336;H:403-764	98.08%ID	E:0	Pyrophosphate-energized vacuolar membrane proton pump	PF03030.13*H_PPase*Inorganic H+ pyrophosphatase*1-273*E:5e-130	0.578	-0.166	0.23	0.376	0.421	0	0.376	0.421	0	-1.701	AVP_VIGRR	Pyrophosphate-energized vacuolar membrane proton pump (EC 3.6.1.1) (Pyrophosphate-energized inorganic pyrophosphatase) (H(+)-PPase) (Vacuolar H(+)-pyrophosphatase)		Arabidopsis thaliana (Mung bean) (Phaseolus aureus)	3D-structure; Direct protein sequencing; Disulfide bond; Hydrogen ion transport; Hydrolase; Ion transport; Magnesium; Membrane; Metal-binding; Transmembrane; Transmembrane helix; Transport; Vacuole
SRR646604_TR22799_c0_g1_i2_len=1024	SOC1_ARATH	Q:819-304;H:1-172	76.16%ID	E:1e-68	MADS-box protein SOC1	PF00319.15*SRF-TF*SRF-type transcription factor (DNA-binding and dimerisation domain)*10-57*E:5.1e-27 PF01486.14*K-box*K-box region*84-171*E:3.4e-28	0.319	-0.994	0.258	0.863	0.87	-0.22	0.559	0.309	0	-5.902	SOC1_ARATH	MADS-box protein SOC1 (Agamous-like MADS-box protein AGL20) (Protein SUPPRESSOR OF CONSTANS OVEREXPRESSION 1)	SOC1 AGL20 At2g45660 F17K2.19	Arabidopsis thaliana (Mouse-ear cress)	Activator; Complete proteome; Cytoplasm; DNA-binding; Developmental protein; Differentiation; Flowering; Nucleus; Reference proteome; Transcription; Transcription regulation
SRR646604_TR24194_c0_g1_i1_len=1753	FBK9_ARATH	Q:1434-388;H:15-378	40.55%ID	E:6e-65	F-box/kelch-repeat protein At1g23390	PF13964.3*Kelch_6*Kelch motif*138-182*E:2.9e-06	1	0	1	1.52	0	0	0	0	-3.881	FBK9_ARATH	F-box/kelch-repeat protein At1g23390	At1g23390 F26F24.26 F28C11.3	Arabidopsis thaliana (Mouse-ear cress)	Complete proteome; Kelch repeat; Reference proteome; Repeat
SRR646604_TR28211_c0_g1_i1_len=800	WAT1_ARATH	Q:50-391;H:275-389	77.12%ID	E:8e-48	Protein WALLS ARE THIN 1		0.461	0.298	0.001	1.542	0.02	1.451	1	-0.04	0	-4.104	WAT1_ARATH	Protein WALLS ARE THIN 1	WAT1 At1g75500 F10A5.28 F1B16.19	Arabidopsis thaliana (Mouse-ear cress)	Amino-acid biosynthesis; Aromatic amino acid biosynthesis; Auxin biosynthesis; Auxin signaling pathway; Cell wall biogenesis/degradation; Complete proteome; Membrane; Phosphoprotein; Plant defense; Reference proteome; Repeat; Transmembrane; Transmembrane helix; Tryptophan biosynthesis; Vacuole
SRR646604_TR29208_c0_g1_i2_len=1307	XTH2_SOYBN	Q:759-1307;H:97-282	79.03%ID	E:7e-105	Xyloglucan endotransglucosylase/hydrolase 2 (ECO:0000250)UniProtKB:Q38857)		1	0.855	1	1.684	1	0.238	1	-0.383	0	-2.602	XTH2_SOYBN	Xyloglucan endotransglucosylase/hydrolase 2 (EC 2.4.1.207) (Brassinosteroid-regulated protein BRU1)		Glycine max (Soybean) (Glycine hispida)	Apoplast; Cell wall; Complete proteome; Disulfide bond; Glycoprotein; Glycosidase; Hydrolase; Reference proteome; Secreted; Signal; Transferase
SRR646604_TR36156_c2_g1_i1_len=689	NA	NA	NA	NA	NA		1	-0.039	0.395	0.521	0.086	0.946	0.007	1.337	0	-7.378					
SRR646604_TR38081_c0_g3_i4_len=1533	ALFC2_ARATH	Q:141-1295;H:12-397	86.27%ID	E:0	Probable fructose-bisphosphate aldolase 2, chloroplastic	PF00274.16*Glycolytic*Fructose-bisphosphate aldolase class-I*79-423*E:6.2e-157	0.043	1.33	0.107	0.81	0.127	-0.327	0.049	-0.421	0	-1.303	ALFC2_ARATH	Probable fructose-bisphosphate aldolase 2, chloroplastic (EC 4.1.2.13)	FBA2 At4g38970 F19H22.70	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Carbohydrate degradation; glycolysis; D-glyceraldehyde 3-phosphate and glycerone phosphate from D-glucose: step 4/4.
SRR648705_TR683_c0_g8_i2_len=1382	PLAS_SOLLC	Q:724-248;H:1-170	77.16%ID	E:4e-67	Plastocyanin, chloroplastic	PF00127.17*Copper-bind*Copper binding proteins, plastocyanin/azurin family*108-205*E:3.4e-36	1	0.136	0.692	0.921	0.189	-1.501	0.356	-1.282	0	-1.189	PLAS_SOLLC	Plastocyanin, chloroplastic	PETE	Solanum lycopersicum (Tomato) (Lycopersicon esculentum)	Chloroplast; Complete proteome; Copper; Electron transport; Membrane; Metal-binding; Plastid; Reference proteome; Thylakoid; Transit peptide; Transport
SRR648705_TR980_c1_g1_i5_len=1345	VATL_VIGRR	Q:1097-606;H:1-164	97.56%ID	E:3e-67	Vacuolar proton ATPase 16 kDa proteolipid subunit	PF00137.18*ATP-synt_C*ATP synthase subunit C*16-75*E:6.2e-14 PF00137.18*ATP-synt_C*ATP synthase subunit C*96-154*E:6.6e-21	1	0.009	0.481	0.246	0.033	0.707	0.113	0.547	0	-7.136	VATL_VIGRR	Vacuolar proton ATPase 16 kDa proteolipid subunit (V-ATPase 16 kDa proteolipid subunit) (Vacuolar proton pump 16 kDa proteolipid subunit)	Vigna radiata var. radiata (Mung bean) (Phaseolus aureus)	Arabidopsis thaliana (Mung bean)	Transport; Vacuole
SRR648705_TR6991_c0_g2_i1_len=1391	RRP3_SPIOL	Q:348-652;H:77-178	80.95%ID	E:3e-53	30S ribosomal protein 3, chloroplastic	PF04539.10*PSRP-3_Ycf65*Plastid and cyanobacterial ribosomal protein (PSRP-3) (Ycf65)*165-211*E:9e-26	0.288	-0.544	1	-0.081	0.86	-0.15	1	-0.002	0	-1.431	RRP3_SPIOL	30S ribosomal protein 3, chloroplastic (Plastid-specific 30S ribosomal protein 3) (PSRP-3)	PSRP3	Spinacia oleracea (Spinach)	Chloroplast; Direct protein sequencing; Plastid; RNA-binding; Ribonucleoprotein; Ribosomal protein; Transit peptide; rRNA-binding
SRR648705_TR8497_c0_g2_i2_len=1839	FDFT_NICBE	Q:325-1554;H:1-410	81.71%ID	E:0	Squalene synthase	PF00494.16*SQS_PSY*Squalene/phytoene synthase*45-315*E:4.1e-45	1	-0.173	1	-0.337	1	0.045	0.86	-0.172	0.001	-1.003	FDFT_NICBE	Squalene synthase (SQS) (SS) (EC 2.5.1.21) (FPP:PPP farnesyltransferase) (Farnesyl-diphosphate farnesyltransferase)		Nicotiana benthamiana	PATHWAY: Terpene metabolism; lanosterol biosynthesis; lanosterol from farnesyl diphosphate: step 1/3.
SRR648705_TR9782_c0_g2_i1_len=772	RPC2_HUMAN	Q:160-435;H:1044-1129	67.39%ID	E:4e-37	DNA-directed RNA polymerase III subunit RPC2		1	0.419	0.316	-0.711	1	-3.473	0.629	1.278	0	-7.417	RPC2_HUMAN	DNA-directed RNA polymerase III subunit RPC2 (RNA polymerase III subunit C2) (EC 2.7.7.6) (C128) (DNA-directed RNA polymerase III 127.6 kDa polypeptide) (DNA-directed RNA polymerase III subunit B)	POLR3B	Homo sapiens (Human)	Alternative splicing; Antiviral defense; Complete proteome; DNA-directed RNA polymerase; Disease mutation; Immunity; Innate immunity; Leukodystrophy; Metal-binding; Nucleotidyltransferase; Nucleus; Polymorphism; Reference proteome; Transcription; Transferase; Zinc; Zinc-finger
SRR648705_TR12620_c0_g5_i2_len=1011	NA	NA	NA	NA	NA		1	0.006	1	0.331	1	1.48	1	0.077	0	-7.875					
SRR648705_TR12919_c1_g3_i4_len=1204	PLP3A_ARATH	Q:192-734;H:1-181	79.56%ID	E:7e-90	Thioredoxin domain-containing protein PLP3A	PF00085.17*Thioredoxin*Thioredoxin*89-173*E:8.7e-06	0.912	-0.051	1	-0.018	0.581	0.349	0.886	0.16	0	-3.778	PLP3A_ARATH	Thioredoxin domain-containing protein PLP3A (Phosducin-like protein 3A)	PLP3A At3g50960 F18B3.240	Arabidopsis thaliana (Mouse-ear cress)	Complete proteome; Cytoplasm; Microtubule; Nucleus; Reference proteome
SRR648705_TR13159_c0_g4_i7_len=1585	UBC2_WHEAT	Q:894-1202;H:50-152	95.15%ID	E:5e-64	Ubiquitin-conjugating enzyme E2 2	PF00179.23*UQ_con*Ubiquitin-conjugating enzyme*25-119*E:8.2e-39	0.763	0.213	0.34	-0.509	0.748	-0.266	0.748	-0.229	0.001	-2.307	UBC2_WHEAT	Ubiquitin-conjugating enzyme E2 2 (EC 2.3.2.23) (E2 ubiquitin-conjugating enzyme 2) (Ubiquitin carrier protein 2) (Ubiquitin-conjugating enzyme E2-16 kDa) (Ubiquitin-protein ligase)	UBC2 UBC1	Triticum aestivum (Wheat)	PATHWAY: Protein modification; protein ubiquitination. (ECO:0000255	PROSITE-ProRule:PRU00388).
SRR648705_TR14608_c0_g2_i3_len=2007	NA	NA	NA	NA	NA		1	-0.165	1	-1.067	1	-0.048	1	0.107	0.001	-2.716					
SRR648705_TR14618_c0_g1_i1_len=3012	4CLL7_ARATH	Q:360-2050;H:1-544	68.74%ID	E:0	4-coumarate--CoA ligase-like 7	PF00501.25*AMP-binding*AMP-binding enzyme*36-449*E:1.1e-101 PF13193.3*AMP-binding_C*AMP-binding enzyme C-terminal domain*458-533*E:1.2e-14	0.402	0.865	0.663	-0.365	0.524	0.639	0.312	0.85	0	-1.638	4CLL7_ARATH	4-coumarate--CoA ligase-like 7 (EC 6.2.1.-) (4-coumarate--CoA ligase isoform 6) (At4CL6)	4CLL7 At4g05160 C17L7.80	Arabidopsis thaliana (Mouse-ear cress)	ATP-binding; Complete proteome; Fatty acid biosynthesis; Fatty acid metabolism; Ligase; Lipid biosynthesis; Lipid metabolism; Nucleotide-binding; Oxylipin biosynthesis; Peroxisome; Reference proteome
SRR648705_TR14680_c0_g3_i1_len=3141	RPM1_ARATH	Q:182-285;H:1-889	33.04%ID	E:1e-119	Disease resistance protein RPM1	PF00931.19*NB-ARC*NB-ARC domain*177-466*E:1.1e-70	1	0.123	1	-1.257	1	-0.85	1	-1.832	0	-2.773	RPM1_ARATH	Disease resistance protein RPM1 (Resistance to Pseudomonas syringae protein 3)	RPM1 RPS3 At3g07040 F17A9.20	Arabidopsis thaliana (Mouse-ear cress)	ATP-binding; Complete proteome; Hypersensitive response; Leucine-rich repeat; Membrane; Nucleotide-binding; Plant defense; Reference proteome; Repeat
SRR648705_TR15869_c1_g6_i1_len=10680	TI214_COFAR	Q:4729-7005;H:995-1873	71.28%ID	E:0	Protein TIC 214 (ECO:0000250)UniProtKB:P56785)	PF05758.9*Ycf1*Ycf1*21-255*E:3.9e-160 PF05758.9*Ycf1*Ycf1*252-509*E:7.7e-82 PF05758.9*Ycf1*Ycf1*508-857*E:6.9e-173	0.34	-0.572	0.142	-0.858	0.874	-0.187	1	0.025	0	-1.011	TI214_COFAR	Protein TIC 214 (Translocon at the inner envelope membrane of chloroplasts 214) (AtTIC214)	TIC214 ycf1	Coffea arabica (Arabian coffee)	Chloroplast; Membrane; Plastid; Plastid inner membrane; Protein transport; Transmembrane; Transmembrane helix; Transport
SRR648705_TR16262_c1_g1_i1_len=2022	NA	NA	NA	NA	NA		0.77	-0.168	1	-0.061	1	0.1	1	-0.034	0	-5.386					
SRR648705_TR16824_c0_g1_i6_len=8036	PSAA_COFAR	Q:3926-6175;H:1-750	99.47%ID	E:0	Photosystem I P700 chlorophyll a apoprotein A1 (ECO:0000255	HAMAP-Rule:MF_00458)	PF00223.16*PsaA_PsaB*Photosystem I psaA/psaB protein*32-744*E:0	0.858	-0.104	0.655	-0.223	0.77	-0.211	1	0.002	0	-0.997	PSAA_COFAR	Photosystem I P700 chlorophyll a apoprotein A1 (EC 1.97.1.12) (PSI-A) (PsaA)	psaA	Coffea arabica (Arabian coffee)	4Fe-4S; Chlorophyll; Chloroplast; Chromophore; Electron transport; Iron; Iron-sulfur; Magnesium; Membrane; Metal-binding; Oxidoreductase; Photosynthesis; Photosystem I; Plastid; Thylakoid; Transmembrane; Transmembrane helix; Transport
SRR648705_TR17389_c0_g1_i3_len=1276	XTH2_SOYBN	Q:716-165;H:97-293	78.61%ID	E:4e-104	Xyloglucan endotransglucosylase/hydrolase 2 (ECO:0000250)UniProtKB:Q38857)		1	-0.265	0.129	-5.205	0.009	-5.306	0.118	-1.97	0	-3.137	XTH2_SOYBN	Xyloglucan endotransglucosylase/hydrolase 2 (EC 2.4.1.207) (Brassinosteroid-regulated protein BRU1)		Glycine max (Soybean) (Glycine hispida)	Apoplast; Cell wall; Complete proteome; Disulfide bond; Glycoprotein; Glycosidase; Hydrolase; Reference proteome; Secreted; Signal; Transferase
SRR648705_TR18952_c0_g1_i1_len=1186	NA	NA	NA	NA	NA		0.461	0.891	1	0.297	1	0.071	0.732	-0.773	0	-2.456					
SRR648705_TR21549_c0_g1_i5_len=975	SMD3_XENLA	Q:754-473;H:2-95	60.64%ID	E:2e-38	Small nuclear ribonucleoprotein Sm D3	PF01423.19*LSM*LSM domain*11-74*E:1.1e-16	0.822	-0.201	0.258	-0.884	0.692	1.044	0.692	0.884	0	-2.695	SMD3_XENLA	Small nuclear ribonucleoprotein Sm D3 (Sm-D3) (snRNP core protein D3)	snrpd3	Xenopus laevis (African clawed frog)	Cytoplasm; Methylation; Nucleus; RNA-binding; Repeat; Ribonucleoprotein; mRNA processing; mRNA splicing
SRR648705_TR21942_c2_g4_i3_len=582	NA	NA	NA	NA	NA		1	-0.316	1	0.455	1	-0.386	0.629	-0.914	0	-2.839					
SRR648705_TR23032_c0_g4_i6_len=2269	RH56_ARATH	Q:347-1513;H:39-427	95.63%ID	E:0	DEAD-box ATP-dependent RNA helicase 56	PF00270.26*DEAD*DEAD/DEAH box helicase*65-230*E:9.2e-38 PF04851.12*ResIII*Type III restriction enzyme, res subunit*81-227*E:2.1e-06 PF00271.28*Helicase_C*Helicase conserved C-terminal domain*271-377*E:2.2e-27	0.06	-0.765	0.915	0.08	0.395	0.649	0.395	0.597	0	-7.063	RH56_ARATH	DEAD-box ATP-dependent RNA helicase 56 (EC 3.6.4.13) (UAP56 homolog B)	RH56 UAP56B At5g11200 F2I11.90	Arabidopsis thaliana (Mouse-ear cress)	ATP-binding; Alternative splicing; Complete proteome; Helicase; Hydrolase; Nucleotide-binding; Nucleus; RNA-binding; Reference proteome; Transport; mRNA processing; mRNA splicing; mRNA transport
SRR648705_TR23308_c0_g3_i7_len=1826	SPDE_COFAR	Q:359-1411;H:1-750	79.89%ID	E:0	Spermidine synthase	PF01564.14*Spermine_synth*Spermine/spermidine synthase*60-305*E:5.7e-98	0.707	-0.39	0.381	0.744	0.059	-1.057	0.002	-1.985	0	-1.968	SPDE_COFAR	Spermidine synthase (SPDSY) (EC 2.5.1.16) (Putrescine aminopropyltransferase)		Coffea arabica (Arabian coffee)	PATHWAY: Amine and polyamine biosynthesis; spermidine biosynthesis; spermidine from putrescine: step 1/1.
SRR648705_TR23318_c0_g1_i4_len=1302	PSB33A_ARATH	Q:1027-416;H:1-204	92.16%ID	E:2e-137	Proteasome subunit beta type-3-A	PF00227.23*Proteasome*Proteasome subunit*7-189*E:1.2e-42	0.798	0.474	1	-0.064	0.076	2.087	0.132	1.968	0	-4.732	PSB33A_ARATH	Proteasome subunit beta type-3-A (EC 3.4.25.1) (20S proteasome beta subunit C-1) (Proteasome component T)	PBC1 PRCT At1g21720 F8K7.15	Arabidopsis thaliana (Mouse-ear cress)	Alternative splicing; Complete proteome; Cytoplasm; Hydrolase; Nucleus; Protease; Proteasome; Reference proteome; Threonine protease
SRR648705_TR23795_c0_g1_i3_len=888	YTHD1_MOUSE	Q:65-386;H:437-543	55.14%ID	E:1e-31	YTH domain-containing family protein 1 (ECO:0000305)	PF04146.12*YTH*YTS21-8-like domain*17-75*E:2e-12	0.412	0.599	0.721	0.121	0.002	1.842	0.195	0.926	0	-1.578	YTHD1_MOUSE	YTH domain-containing family protein 1 (Dermatomyositis associated with cancer putative autoantigen 1 homolog) (DACA-1 homolog)	Ythd1	Mus musculus (Mouse)	Acetylation; Complete proteome; Cytoplasm; Phosphoprotein; RNA-binding; Reference proteome
SRR648705_TR24010_c1_g1_i1_len=2247	Y1154_ARATH	Q:310-1782;H:1-464	64.71%ID	E:0	Probable serine/threonine-protein kinase At1g01540	PF00069.22*Pkinase*Protein kinase domain*186-453*E:7.5e-48 PF07714.14*Pkinase_Tyr*Protein tyrosine kinase*188-455*E:1.1e-45	1	0.029	1	0.058	1	1.004	1	0	0	-2.209	Y1154_ARATH	Probable serine/threonine-protein kinase At1g01540 (EC 2.7.11.1)	At1g01540 F22L4.8	Arabidopsis thaliana (Mouse-ear cress)	ATP-binding; Alternative splicing; Complete proteome; Kinase; Membrane; Nucleotide-binding; Phosphoprotein; Reference proteome; Serine/threonine-protein kinase; Transferase; Transmembrane; Transmembrane helix; Transport
SRR648705_TR24275_c0_g1_i1_len=682	SNAK2_SOLTU	Q:343-155;H:42-104	71.43%ID	E:6e-23	Snakin-2	PF02704.11*GASA*Gibberellin regulated protein*45-104*E:3.1e-19	0.502	3.842	1	2.865	0.254	4.592	0.502	3.927	0	-4.036	SNAK2_SOLTU	Snakin-2	SN2	Solanum tuberosum (Potato)	Antimicrobial; Cell wall; Complete proteome; Direct protein sequencing; Disulfide bond; Plant defense; Reference proteome; Secreted; Signal
SRR648705_TR26775_c0_g1_i1_len=2734	PAL1_TOBAC	Q:2460-337;H:1-715	88.48%ID	E:0	Phenylalanine ammonia-lyase	PF00221.16*Lyase_aromatic*Aromatic amino acid lyase*62-540*E:3.3e-154	0.25	0.42	0	2.554	0.026	0.491	0.003	0.644	0	-1.871	PAL1_TOBAC	Phenylalanine ammonia-lyase (EC 4.3.1.24)	TPA1 PALB	Nicotiana tabacum (Common tobacco)	PATHWAY: Phenylpropanoid metabolism; trans-cinnamate biosynthesis; trans-cinnamate from L-phenylalanine: step 1/1.
SRR648705_TR28375_c0_g1_i2_len=778	ARR9_ARATH	Q:564-109;H:1-158	76.1%ID	E:1e-79	Two-component response regulator ARR9	PF00072.21*Response_reg*Response regulator receiver domain*12-133*E:3.6e-21	0	0	1	0	1	0	1	0	0	-7.792	ARR9_ARATH	Two-component response regulator ARR9 (Response reactor 4)	ARR9 ATRR4 At3g57040 F24I3.120	Arabidopsis thaliana (Mouse-ear cress)	Complete proteome; Cytokinin signaling pathway; Nucleus; Phosphoprotein; Reference proteome; Transcription; Transcription regulation; Two-component regulatory system
SRR648705_TR29523_c0_g2_i1_len=1570	GOLS1_AJURE	Q:200-1216;H:1-333	83.78%ID	E:0	Galactinol synthase 1	PF01501.17*Glycos_transf_8*Glycosyl transferase family 8*33-274*E:3.6e-43	0.002	1.226	0	1.54	0.061	0.467	0.078	0.44	0.001	-0.763	GOLS1_AJURE	Galactinol synthase 1 (ArGolS1) (GolS-1) (EC 2.4.1.123)	GOLS1	Ajuga reptans (Bugle)	Carbohydrate metabolism; Cytoplasm; Galactose metabolism; Glycosyltransferase; Manganese; Metal-binding; Transferase
SRR648705_TR30731_c0_g3_i1_len=669	NA	NA	NA	NA	NA		0.129	-4.882	0.005	-4.728	1	2.644	1	1.78	0	-6.935					
SRR648705_TR33123_c0_g2_i1_len=2142	AROG_SOLTU	Q:304-782;H:30-510	84.79%ID	E:0	Phospho-2-dehydro-3-deoxyheptonate aldolase 2, chloroplastic	PF01474.13*DAHP_synth_2*Class-II DAHP synthetase family*2-384*E:1.3e-180	0.356	1.004	0.001	3.368	1	0.454	0.692	0.824	0	-1.824	AROG_SOLTU	Phospho-2-dehydro-3-deoxyheptonate aldolase 2, chloroplastic (EC 2.5.1.54) (3-deoxy-D-arabino-heptulosonate 7-phosphate synthase 2) (DAHP synthase 2) (Phospho-2-keto-3-deoxyheptonate aldolase 2)	SHKB ARO2	Solanum tuberosum (Potato)	PATHWAY: Metabolic intermediate biosynthesis; chorismate biosynthesis; chorismate from D-erythrose 4-phosphate and phosphoenolpyruvate: step 1/7.
SRR648705_TR34528_c0_g5_i1_len=1096	NA	NA	NA	NA	NA		0.502	-1.555	1	-1.432	1	0	1	0	0	-3.914					
SRR648705_TR36195_c0_g1_i1_len=569	NA	NA	NA	NA	NA		0.134	-0.493	0.051	-0.868	0.698	-0.251	0.34	-0.501	0	-1.68					
SRR648705_TR37405_c0_g1_i1_len=1033	Y5566_ARATH	Q:560-204;H:1-117	63.03%ID	E:2e-36	Uncharacterized protein At5g65660		1	0	1	0	1	0	1	0	0	-7.468	Y5566_ARATH	Uncharacterized protein At5g65660	At5g65660 K21L13.18	Arabidopsis thaliana (Mouse-ear cress)	Complete proteome; Membrane; Reference proteome; Transmembrane; Transmembrane helix
SRR648705_TR14240_c0_g2_i1_len=1205	VPS29_ARATH	Q:840-277;H:1-188	86.7%ID	E:2e-116	Vacuolar protein sorting-associated protein 29	PF12850.4*Metallophos_2*Calcineurin-like phosphoesterase superfamily domain*4-157*E:2.1e-19	0.626	0.141	0.539	0.209	0.002	0.991	0.003	0.956	0	-1.678	VPS29_ARATH	Vacuolar protein sorting-associated protein 29 (Protein MAIGO 1) (Vesicle protein sorting 29)	VPS29 MAG1 At3g47810 T23J7.140	Arabidopsis thaliana (Mouse-ear cress)	Complete proteome; Cytoplasm; Endosome; Golgi apparatus; Membrane; Protein transport; Reference proteome; Transport
SRR648705_TR14754_c0_g1_i1_len=539	NA	NA	NA	NA	NA		0.687	-0.107	0.012	0.602	1	0.909	0	1.044	0	-1.056					
SRR648705_TR14281_c0_g3_i1_len=1978	ILVS_ARATH	Q:1025-1708;H:358-589	92.21%ID	E:5e-146	Ketol-acid reductoisomerase, chloroplastic	PF01450.16*IlvC*Acetohydroxy acid isomeroreductase, catalytic domain*2-85*E:1.8e-08 PF01450.16*IlvC*Acetohydroxy acid isomeroreductase, catalytic domain*98-174*E:1.7e-08	0.781	0.493	0.312	-0.74	1	-0.362	1	-0.496	0	-2.127	ILVS_ARATH	Ketol-acid reductoisomerase, chloroplastic (EC 1.1.1.86) (Acetohydroxy-acid reductoisomerase) (Alpha,beta-dehydroxyacid reductoisomerase)	At3g58610 F14P22.200	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Amino-acid biosynthesis; L-isoleucine biosynthesis; L-isoleucine from 2-oxobutanoate: step 2/4.; PATHWAY: Amino-acid biosynthesis; L-valine biosynthesis; L-valine from pyruvate: step 2/4.
SRR648705_TR42562_c0_g1_i4_len=3061	XYL2_MEDSV	Q:225-2456;H:31-774	72.33%ID	E:0	Beta-xylosidase/alpha-L-arabinofuranosidase 2 (ECO:0000303)PubMed:17615411, (ECO:0000312)EMBL:AB425228.1)	PF00933.18*Glyco_hydro_3*Glycosyl hydrolase family 3 N terminal domain*125-366*E:1.1e-39 PF01915.19*Glyco_hydro_3_C*Glycosyl hydrolase family 3 C-terminal domain*413-642*E:4e-50 PF14310.3*Fn3-like*Fibronectin type III-like domain*702-769*E:8.6e-08	0.093	-0.788	0.006	-3.13	1	0.673	1	0.283	0	-2.126	XYL2_MEDSV	Beta-xylosidase/alpha-L-arabinofuranosidase 2 (Xylan 1,4-beta-xylosidase/Alpha-L-arabinofuranosidase 2) (MsXyl2) [Includes: Beta-xylosidase (EC 3.2.1.37) (1,4-beta-D-xylan xylohydrolase) (Xylan 1,4-beta-xylosidase); Alpha-L-arabinofuranosidase (Arabinosidase) (EC 3.2.1.55)]	Xyl2	Medicago sativa subsp. varia (Alfalfa) (Medicago varia)	Carbohydrate metabolism; Extracellular matrix; Glycoprotein; Glycosidase; Hydrolase; Multifunctional enzyme; Polysaccharide degradation; Secreted; Signal; Xylan degradation
SRR648705_TR43184_c0_g2_i4_len=880	H2B1_MEDTR	Q:249-564;H:57-148	98.91%ID	E:3e-57	Probable histone H2B.1	PF00125.21*Histone*Core histone H2A/H2B/H3/H4*41-164*E:2.5e-22	0.016	-1.138	0.069	-1.074	0.472	-0.761	0.195	-1.129	0	-0.943	H2B1_MEDTR	Probable histone H2B.1		Medicago truncatula (Barrel medic) (Medicago tribuloides)	Acetylation; Chromosome; DNA-binding; Isopeptide bond; Nucleosome core; Nucleus; Ubl conjugation
SRR648705_TR45115_c0_g2_i1_len=518	NA	NA	NA	NA	NA		1	-2.541	1	-1.631	1	0	1	0	0	-3.77.					
SRR648705_TR45324_c0_g1_i1_len=900	NA	NA	NA	NA	NA		1	-0.061	1	-2.523	0.254	-2.474	0.254	-2.572	0.001	-2.645.					
SRR648705_TR16635_c0_g1_i2_len=1385	TLC1_SOLTU	Q:145-987;H:348-631	85.56%ID	E:3e-158	Plastidic ATP/ADP-transporter	PF03219.11*TLC*TLC ATP/ADP transporter*6-232*E:7e-95	0	-0.276	0.076	0.148	0.004	-0.781	0.172	-0.364	0	-1.993	TLC1_SOLTU	Plastidic ATP/ADP-transporter		Solanum tuberosum (Potato)	
SRR648705_TR14751_c0_g1_i1_len=1458	MYB6_ARATH	Q:1262-1456;H:3-49	77.61%ID	E:1e-27	Transcription repressor MYB6	PF14547.3*Hypothetp_seed*Hypothetic seed protein*214-297*E:5.2e-24	0.132	-2.198	1	-1.09	1	0.407	1	-1.121	0	-2.021	MYB6_ARATH	Transcription repressor MYB6 (Myb-related protein 6) (AtMYB6)	MYB6 At4g09460 T15G18.120	Arabidopsis thaliana (Mouse-ear cress)	ATP-binding; Chloroplast; Complete proteome; Membrane; Nucleotide-binding; Plastid; Reference proteome; Transmembrane; Transmembrane helix; Transport
SRR648705_TR14776_c0_g2_i2_len=2300	AROG_SOLTU	Q:1956-478;H:30-510	84.79%ID	E:0	Phospho-2-dehydro-3-deoxyheptonate aldolase 2, chloroplastic	PF01474.13*DAHP_synth_2*Class-II DAHP synthetase family*2-384*E:1.3e-180	0	1.048	1	1.579	1	0.85	1	0.394	0	-6.934	AROG_SOLTU	Phospho-2-dehydro-3-deoxyheptonate aldolase 2, chloroplastic (EC 2.5.1.54) (3-deoxy-D-arabino-heptulosonate 7-phosphate synthase 2) (DAHP synthase 2) (Phospho-2-keto-3-deoxyheptonate aldolase 2)	SHKB ARO2	Solanum tuberosum (Potato)	PATHWAY: Metabolic intermediate biosynthesis; chorismate biosynthesis; chorismate from D-erythrose 4-phosphate and phosphoenolpyruvate: step 1/7.
SRR648705_TR14925_c0_g1_i2_len=2058	P2C30_ARATH	Q:949-1638;H:156-389	67.09%ID	E:1e-99	Probable protein phosphatase 2C 30	PF00481.18*PP2C*Protein phosphatase 2C*6-220*E:9.5e-56	0	6.029	0	8.845	0.002	5.327	0	5.822	0	-2.226	P2C30_ARATH	Probable protein phosphatase 2C 30 (AtPP2C30) (EC 3.1.3.16) (AtPP2C5)	PP2C5 At2g40180 T7M7.17	Arabidopsis thaliana (Mouse-ear cress)	
SRR648705_TR18141_c1_g2_i3_len=2582	SFGH_ARATH	Q:108-656;H:1-284	81.34%ID	E:3e-167	S-formylglutathione hydrolase	PF00756.17*Esterase*Putative esterase*25-275*E:2.7e-60 PF00326.18*Peptidase_S9*Prolyl oligopeptidase family*110-264*E:1.8e-08	1	-0.654	1	-0.302	1	0.452	1	0.899	0	-3.091	SFGH_ARATH	S-formylglutathione hydrolase (AtSFGH) (EC 3.1.2.12) (Esterase D)	SFGH At2g41530 T32G6.5	Arabidopsis thaliana (Mouse-ear cress)	Acetylation; Complete proteome; Hydrolase; Reference proteome; Serine esterase
SRR648705_TR19441_c0_g1_i1_len=2131	MYB44_ARATH	Q:1906-968;H:2-272	50%ID	E:5e-67	Transcription factor MYB44	PF00249.28*Myb_DNA-binding*Myb-like DNA-binding domain*14-89*E:9.5e-20 PF13921.3*Myb_DNA-bind_6*Myb-like DNA-binding domain*147-75*E:9.9e-18 PF00249.28*Myb_DNA-binding*Myb-like DNA-binding

SRR11446634_TR6469_c2_g1_i2_len=653	NA	NA	NA	NA	NA	NA		0	-7,496	0,377	-0,586	0,009	5,932	0,017	5,803	0,059	-1,022	.	.	.	.	.	.	.	.	.
SRR11446634_TR8715_c0_g2_i1_len=545	EF1A_TOBAC	Q:2427;H:295-436	97.89%ID	E:1e-94	Elongation factor 1-alpha	PF03143.14^GTP_EFTU_D3^Elongation factor Tu C-terminal domain^28-135^E:3.2e-39 PF00238.16^Ribosomal_L14^Ribosomal protein L14p/L23e^22-140^E:8.9e-36	0	-1,391	0,496	-0,262	0,431	0,35	0,419	-0,404	0,023	0,248	-1,391	.	.	.	.	Nicotiana tabacum (Common tobacco)				Cytoplasm; Elongation factor; GTP-binding; Nucleotide-binding; Phosphoprotein; Protein biosynthesis
SRR11446634_TR2278_c0_g1_i2_len=846	RL23_ARATH	Q:180-599;H:1-140	97.14%ID	E:4e-93	60S ribosomal protein L23	PF00298.16^Ribosomal_L14^Ribosomal protein L14p/L23e^22-140^E:8.9e-36	0	-0,96	0,155	-0,323	0,229	0,303	0,478	-0,195	0,211	-0,273	RL23_ARATH	60S ribosomal protein L23 (Protein EMBRYO DEFECTIVE 217!)	RPL23A At1g04480 F19P19.5; RPL23B At2g33370 F4P9.14; RPL23C EMB2171 At3g04460 T27C4.4	Arabidopsis thaliana (Mouse-ear cress)						Alternative splicing; Complete proteome; Reference proteome; Ribonucleoprotein; Ribosomal protein
SRR11446634_TR25396_c0_g1_i1_len=504	NRP2_ARATH	Q:144-485;H:1-107	70.18%ID	E:1e-44	NAP1-related protein 2	PF00956.15^NAP^Nucleosome assembly protein (NAP)^33-77^E:2.3e-07	0	-8,412	0	6,758	1	0	1	2,591	0	6,924	NRP2_ARATH	NAP1-related protein 2 (Nucleosome/chromatin assembly factor group A5) (Protein SET homolog 2)	NRP2 NFA5 At1g18800 F6A14.10	Arabidopsis thaliana (Mouse-ear cress)						Alternative splicing; Chaperone; Coiled coil; Complete proteome; Cytoplasm; Nucleus; Reference proteome
SRR11446634_TR31581_c0_g1_i1_len=930	RS33_ARATH	Q:69-734;H:1-222	89.64%ID	E:4e-145	40S ribosomal protein S3-3	PF00163.14^KH_4^KH domain^20-93^E:5.8e-12 PF00189.17^Ribosomal_S3_C^Ribosomal protein S3, C-terminal domain^106-188^E:4.4e-25	0	-0,85	0,175	0,306	0,285	0,257	0,713	0,092	1	-1,526	RS33_ARATH	40S ribosomal protein S3-3	RPS3C At5g35530 MOK9.14	Arabidopsis thaliana (Mouse-ear cress)						Complete proteome; Isopeptide bond; Phosphoprotein; RNA-binding; Reference proteome; Ribonucleoprotein; Ribosomal protein; Ubl conjugation
SRR11446634_TR32698_c0_g2_i1_len=703	RL34_TOBAC	Q:98-382;H:1-95	96.84%ID	E:4e-59	60S ribosomal protein L34	PF01199.15^Ribosomal_L34e^Ribosomal protein L34e^1-95^E:1e-38	0	-1,416	0,596	0,142	0,773	0,115	0,532	-0,218	0,202	-0,29	RL34_TOBAC	60S ribosomal protein L34	RPL34	Nicotiana tabacum (Common tobacco)						Ribonucleoprotein; Ribosomal protein
SRR122236_TR3141_c0_g1_i1_len=2618	NUCL2_ORYSJ	Q:1082-492;H:435-630	56.28%ID	E:3e-62	Nucleolin 2	PF00076.19^RRM_1^RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)^30-100^E:1e-19 PF13893.3^RRM_5^RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)^69-103^E:0.17^PF00076.19^RRM_1^RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)^133-203^E:2.7e-05 PF01777.15^Ribosomal_L27e^Ribosomal L27e protein family^52-135^E:6.9e-34	0	-3,8	0	2,321	1	0	1	0	1	0,314	NUCL2_ORYSJ	Nucleolin 2 (Protein NUCLEOLIN LIKE 2)	Os04g0620700 LOC_Os04g52960 OSJNBa0058K23.21	Oryza sativa subsp. japonica (Rice)						Complete proteome; Nucleus; RNA-binding; Reference proteome; Repeat; rRNA processing
SRR122237_TR4116_c0_g1_i1_len=720	RL273_ARATH	Q:607-203;H:1-135	80%ID	E:2e-62	60S ribosomal protein L27-3	PF00828.19^Ribosomal_L27^Ribosomal L27e protein family^52-135^E:6.9e-34	0	-0,942	0,343	-0,228	0,565	-0,153	0,145	-0,397	0,932	0,058	RL273_ARATH	60S ribosomal protein L27-3	RPL27C At4g15000 d13545w FCAALL.99	Arabidopsis thaliana (Mouse-ear cress)						Alternative splicing; Complete proteome; Reference proteome; Ribonucleoprotein; Ribosomal protein
SRR122237_TR6908_c0_g2_i1_len=554	RL9_PEA	Q:417-1;H:1-139	87.77%ID	E:2e-84	60S ribosomal protein L9	PF00347.20^Ribosomal_L6^Ribosomal protein L6^12-89^E:2.5e-12 PF08079.9^Ribosomal_L30_N^Ribosomal L30 N-terminal domain^36-10^E:5.7e-7 2^PF00327.13^Ribosomal_L30^Ribosomal protein L30p/L7e^112-162^E:5.8e-22	0	-1,033	0,012	0,737	0,4	-0,268	0,137	-0,451	1	-0,017	RL9_PEA	60S ribosomal protein L9 (Gibberellin-regulated protein GA)	RPL9	Pisum sativum (Garden pea)						Ribonucleoprotein; Ribosomal protein
SRR122237_TR9671_c0_g1_i1_len=1018	RL7A_ARATH	Q:946-209;H:1-244	82.93%ID	E:9e-138	60S ribosomal protein L7-4		0	-1,279	1	-0,02	0,229	0,519	0,407	0,376	0,542	0,212	RL7A_ARATH	60S ribosomal protein L7-4	RPL7D At3g13580 K20M4.2	Arabidopsis thaliana (Mouse-ear cress)						Complete proteome; Reference proteome; Ribonucleoprotein; Ribosomal protein
SRR122237_TR2783 6_c0_g1_i1_len=594	NA	NA	NA	NA	NA	NA	0	-1,589	0,38	0,222	0,451	0,302	1	-0,017	0,517	-1,063	.	.	.	.	.	.	.	.	.	.
SRR122238_TR4231_c0_g2_i1_len=703	NA	NA	NA	NA	NA		0	-1,184	0,341	0,427	0,108	-0,748	0,637	0,208	0,666	0,34	.	.	.	.	.	.	.	.	.	.
SRR122238_TR4631_c2_g1_i4_len=535	RL11_MEDSA	Q:465-1;H:1-155	96.13%ID	E:9e-98	60S ribosomal protein L11	PF00281.16^Ribosomal_L5^Ribosomal protein L5^32-85^E:5.7e-21 PF00673.16^Ribosomal_L5_C^ribosomal L5P family C-terminus^89-173^E:4.7e-20	0	-1,29	0,679	-0,101	0,38	0,245	0,802	-0,074	0,862	-0,062	RL11_MEDSA	60S ribosomal protein L11 (L5)	RPL11 RPL5	Medicago sativa (Alfalfa)						Cytoplasm; RNA-binding; Ribonucleoprotein; Ribosomal protein; rRNA-binding
SRR122238_TR11341_c0_g1_i6_len=619	RL35_EUPES	Q:516-148;H:1-123	95.12%ID	E:1e-73	60S ribosomal protein L35	PF00831.20^Ribosomal_L29^Ribosomal L29 protein^8-64^E:4.1e-18	0	-0,956	0,845	-0,047	0,381	0,214	0,651	0,113	0,567	-0,134	RL35_EUPES	60S ribosomal protein L35	RPL35	Euphorbia esula (Leafy spurge)						Ribonucleoprotein; Ribosomal protein
SRR122238_TR12177_c2_g1_i2_len=711	H32_WHEAT	Q:625-218;H:1-136	98.53%ID	E:1e-76	Histone H3.2	PF00125.21^Histone^Core histone H2A/H2B/H3/H4^29-160^E:5.2e-54	0	-7,577	0,254	-4,845	0,502	-3,752	0,502	-3,752	1	-2,742	H32_WHEAT	Histone H3.2		Triticum aestivum (Wheat)						Acetylation; Chromosome; Complete proteome; DNA-binding; Direct protein sequencing; Methylation; Nucleosome core; Nucleus; Phosphoprotein; Reference proteome
SRR122238_TR12828_c0_g2_i9_len=806	RL182_ARATH	Q:726-166;H:1-187	87.17%ID	E:7e-116	60S ribosomal protein L18-2	PF13135.1^Ribosomal_L18^Ribosomal protein 60S L18 and 50S L18e^28-213^E:6.1e-98 PF00828.18^Ribosomal_L27A^Ribosomal proteins 50S-L15, 50S-L18e, 60S-L27A^75-146^E:0.00012 PF00347.20^Ribosomal_L6^Ribosomal protein L6^12-89^E:5.8e-12 PF00347.20^Ribosomal_L6^Ribosomal protein L6^101-180^E:3.4e-12	0	-1,074	0,463	-0,165	0,36	0,227	0,957	-0,017	0,631	-0,125	RL182_ARATH	60S ribosomal protein L18-2	RPL18B At3g05590 F18C1.14	Arabidopsis thaliana (Mouse-ear cress)						Complete proteome; Cytoplasm; Reference proteome; Ribonucleoprotein; Ribosomal protein
SRR122238_TR13302_c0_g1_i1_len=972	RL9_PEA	Q:865-302;H:3-190	87.77%ID	E:2e-115	60S ribosomal protein L9		0	-1,225	0,045	-0,529	0,376	0,293	0,481	0,229	0,35	-0,559	RL9_PEA	60S ribosomal protein L9 (Gibberellin-regulated protein GA)	RPL9	Pisum sativum (Garden pea)						Ribonucleoprotein; Ribosomal protein
SRR122238_TR13960_c0_g1_i1_len=621	H2B_GOSHI	Q:132-386;H:63-147	96.47%ID	E:6e-53	Histone H2B		0	-3,44	0,002	-6,312	0,254	4,614	1	3,444	0,152	-0,884	H2B_GOSHI	Histone H2B	HIS2B	Gossypium hirsutum (Upland cotton) (Gossypium mexicanum)						Acetylation; Chromosome; DNA-binding; Isopeptide bond; Nucleosome core; Nucleus; Ubl conjugation
SRR122238_TR15196_c4_g2_i2_len=690	RL40_NICSY	Q:591-208;H:1-128	99.22%ID	E:3e-88	Ubiquitin-60S ribosomal protein L40	PF11976.5^Rad60-SLD^Ubiquitin-2 like Rad60 SUMO-like^1-71^E:1.5e-16 PF00240.20^ubiquitin^Ubiquitin family^3-74^E:2.2e-34 PF14560.3^Ubiquitin_2^Ubiquitin-like domain^12-69^E:0.00011 PF13881.3^Rad60-SLD_2^Ubiquitin-2 like Rad60 SUMO-like^12-72^E:0.017 PF01020.14^Ribosomal_L40e^Ribosomal L40e family^38-127^E:1e-31	0	-1,015	0,275	-0,237	0,068	0,416	0,368	0,209	0,836	0,073	RL40_NICSY	Ubiquitin-60S ribosomal protein L40 [Cleaved into: Ubiquitin; 60S ribosomal protein L40 (CEP52)]	UBICEP52-7 RPL40	Nicotiana sylvestris (Wood tobacco) (South American tobacco)						Cytoplasm; Isopeptide bond; Nucleus; Ribonucleoprotein; Ribosomal protein; Ubl conjugation
SRR122238_TR19572_c1_g1_i2_len=1090	PNAE_RAUSE	Q:183-935;H:12-262	45.74%ID	E:1e-63	Polyneuridine-aldehyde esterase	PF12146.5^Hydrolase_4^Serine aminopeptidase, S33^10-119^E:6e-07 PF00561.17^Abhydrolase_1^alpha/beta hydrolase fold^14-123^E:3.2e-09 PF12697.4^Abhydrolase_6^Alpha/beta hydrolase family^15-255^E:1.4e-14	0,001	-0,865	0,079	-0,463	0,27	0,296	0,89	-0,039	0,78	0,078	PNAE_RAUSE	Polyneuridine-aldehyde esterase (EC 3.1.1.78) (Polyneuridine aldehyde esterase)	PNAE	Rauvolfia serpentina (Serpentine wood) (Ophioxylon serpentinum)		PATHWAY: Alkaloid biosynthesis; ajmaline biosynthesis.				3D-structure; Alkaloid metabolism; Direct protein sequencing; Hydrolase; Serine esterase
SRR122238_TR23347_c0_g1_i1_len=988	SR45A_ARATH	Q:763-461;H:68-168	68.32%ID	E:3e-28	Serine/arginine-rich splicing factor SR45a	PF00076.19^RRM_1^RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)^85-154^E:9e-18 PF13893.3^RRM_5^RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)^124-161^E:0.026	0	-7,131	1	0	0,502	4,357	0,009	6,036	1	-0,02	SR45A_ARATH	Serine/arginine-rich splicing factor SR45a (At-SR45A) (AtSR45a) (Protein TRANSFORMER2-like) (atTra2)	SR45A TRA2 At1g07350 F22G5.31	Arabidopsis thaliana (Mouse-ear cress)						Alternative splicing; Complete proteome; Nucleus; Reference proteome; Ribonucleoprotein; Spliceosome; mRNA processing; mRNA splicing
SRR122238_TR29021_c0_g1_i3_len=925	NACA2_ARATH	Q:65-202;H:60-217	78.48%ID	E:1e-50	Nascent polypeptide-associated complex subunit alpha-like protein 2	PF01849.15^NAC^NAC domain^97-152^E:1.9e-23	0	-0,91	0,008	-0,645	0,867	0,055	0,897	-0,049	0,787	-0,085	NACA2_ARATH	Nascent polypeptide-associated complex subunit alpha-like protein 2 (NAC-alpha-like protein 2) (Alpha-NAC-like protein 2)	At3g49470 T9C5.70	Arabidopsis thaliana (Mouse-ear cress)						Complete proteome; Protein transport; Reference proteome; Transport
SRR122238_TR29833_c0_g1_i1_len=2383	RUBA_PEA	Q:215-479;H:25-587	87.63%ID	E:0	RuBisCO large subunit-binding protein subunit alpha, chloroplastic	PF01118.21^Cpn60_TCP1^TCP-1/cpn60 chaperonin family^75-574^E:4.8e-94	0	-1,018	0,176	-0,32	0,791	0,074	0,127	0,386	0,278	0,242	RUBA_PEA	RuBisCO large subunit-binding protein subunit alpha, chloroplastic (60 kDa chaperonin subunit alpha) (CPN-60 alpha)		Pisum sativum (Garden pea)						ATP-binding; Chaperone; Chloroplast; Direct protein sequencing; Nucleotide-binding; Plastid; Transit peptide
SRR122238_TR31182_c0_g1_i1_len=737	CH10_ARATH	Q:516-226;H:1-97	78.35%ID	E:7e-49	10 kDa chaperonin		0	-1,134	0,964	-0,027	0	2,643	0	0,964	0,692	-0,806	CH10_ARATH	10 kDa chaperonin (Chaperonin 10) (CPN10) (Protein groES)	CPN10 At1g14980 T15D22.2	Arabidopsis thaliana (Mouse-ear cress)						Chaperone; Complete proteome; Cytoplasm; Reference proteome
SRR122238_TR34938_c0_g1_i1_len=538	RS29_ARATH	Q:80-247;H:1-56	91.07%ID	E:6e-30	40S ribosomal protein S29		0	-3,751	0,008	-3,119	0,002	6,394	0,502	4,231	0,079	-0,542	RS29_ARATH	40S ribosomal protein S29	RPS29A At3g43980 T15B3.120; RPS29B At3g44010 T15B3.150; RPS29C At4g33865 F17I5.3	Arabidopsis thaliana (Mouse-ear cress)						Complete proteome; Metal-binding; Reference proteome; Ribonucleoprotein; Ribosomal protein; Zinc
SRR122238_TR36206_c0_g1_i3_len=718	RL211_ARATH	Q:595-104;H:1-164	81.11%ID	E:6e-99	60S ribosomal protein L21-1	PF01157.15^Ribosomal_L21e^Ribosomal protein L21e^5-98^E:1.6e-44	0	-1,074	0,491	-0,172	0,474	-0,196	0,155	-0,4	0,938	-0,03	RL211_ARATH	60S ribosomal protein L21-1	RPL21A At1g05590 F14J9.25; RPL21C At1g09690 F21M12.8	Arabidopsis thaliana (Mouse-ear cress)						Complete proteome; Reference proteome; Ribonucleoprotein; Ribosomal protein
SRR122238_TR38359_c0_g1_i3_len=1301	NA	NA	NA	NA	NA		0,001	-6,623	0,694	0,357	0,352	0,914	0,798	0,513	1	0	.	.	.	.	.	.	.	.	.	.
SRR122238_TR39862_c0_g1_i1_len=631	RL35_EUPES	Q:104-472;H:1-123	95.12%ID	E:5e-74	60S ribosomal protein L35	PF00831.20^Ribosomal_L29^Ribosomal L29 protein^8-64^E:7.8e-18	0,001	-0,886	0,047	-0,553	0,699	0,15	0,838	-0,097	0,093	-0,439	RL35_EUPES	60S ribosomal protein L35	RPL35	Euphorbia esula (Leafy spurge)						Ribonucleoprotein; Ribosomal protein
SRR122238_TR41920_c0_g1_i1_len=813	RS272_ARATH	Q:123-380;H:1-66	91.86%ID	E:3e-51	40S ribosomal protein S27-2		0	-1,058	0,9	0,039	0,066	0,55	0,76	0,096	0,191	-0,319	RS272_ARATH	40S ribosomal protein S27-2	RPS27B AR527A At3g61110 T20K12.10 T2T15_200	Arabidopsis thaliana (Mouse-ear cress)						Complete proteome; Metal-binding; Reference proteome; Ribonucleoprotein; Ribosomal protein; Zinc; Zinc-finger
SRR122238_TR43463_c0_g1_i1_len=607	RL371_ARATH	Q:127-384;H:10-85	88.37%ID	E:4e-47	60S ribosomal protein L37-1	PF00197.16^Ribosomal_L37e^Ribosomal protein L37e^36-86^E:2.1e-25	0	-1,068	0,003	-0,647	0,149	0,349	1	0,007	0,105	-0,344	RL371_ARATH	60S ribosomal protein L37-1	RPL37A At1g15250 F9L1.46	Arabidopsis thaliana (Mouse-ear cress)						Complete proteome; Metal-binding; RNA-binding; Reference proteome; Ribonucleoprotein; Ribosomal protein; Zinc; Zinc-finger; rRNA-binding
SRR122238_TR44471_c0_g1_i6_len=928	R13A4_ARATH	Q:819-202;H:1-206	89.32%ID	E:9e-135	60S ribosomal protein L13a-4	PF00572.15^Ribosomal_L13^Ribosomal protein L13^13-118^E:1.2e-09	0	-0,947	0,435	-0,183	0,519	0,165	0,516	-0,176	0,793	-0,163	R13A4_ARATH	60S ribosomal protein L13a-4	RPL13AD At5g48760 K24G6.9	Arabidopsis thaliana (Mouse-ear cress)						Complete proteome; Reference proteome; Ribonucleoprotein; Ribosomal protein
SRR122238_TR45425_c2_g1_i9_len=800	RS12_HORVU	Q:566-215;H:20-143	82.26%ID	E:2e-69	40S ribosomal protein S12	PF01248.23^Ribosomal_L7Ae^Ribosomal protein L7Ae/L30e/S12e/Gad045 family^27-120^E:4e-27	0,001	-6,576	0,009	6,043	1	0	1	0	1	-0,31	RS12_HORVU	40S ribosomal protein S12	RPS12	Hordeum vulgare (Barley)						Ribonucleoprotein; Ribosomal protein
SRR122238_TR48232_c1_g3_i6_len=1055	RS242_ARATH	Q:810-445;H:1-122	88.52%ID	E:4e-72	40S ribosomal protein S24-2	PF01282.16^Ribosomal_S24e^Ribosomal protein S24e^25-103^E:1.5e-36	0,001	-0,972	0,35	-0,288	0,283	0,441	1	0,024	0,721	-0,165	RS242_ARATH	40S ribosomal protein S24-2	RPS24B At5g28060 F15F15.130	Arabidopsis thaliana (Mouse-ear cress)						Complete proteome; Reference proteome; Ribonucleoprotein; Ribosomal protein
SRR122238_TR51732_c0_g1_i1_len=717	RL34_TOBAC	Q:622-338;H:1-95	96.84%ID	E:4e-59	60S ribosomal protein L34	PF01199.15^Ribosomal_L34e^Ribosomal protein L34e^32-127^E:2.1e-38	0	-1,07	0,188	-0,312	0,054	0,506	0,672	0,118	0,018	-0,624	RL34_TOBAC	60S ribosomal protein L34	RPL34	Nicotiana tabacum (Common tobacco)						Ribonucleoprotein; Ribosomal protein
SRR122238_TR57185_c0_g1_i2_len=866	RL18A_CASSA	Q:813-280;H:1-178	91.01%ID	E:5e-118	60S ribosomal protein L18a	PF01775.14^Ribosomal_L18A^Ribosomal proteins 50S-L18Ae/60S-L20/60S-L18A^24-145^E:2.4e-55	0	-0,895	0,418	-0,21	0,144	0,452	0,818	0,094	1	-0,115	RL18A_CASSA	60S ribosomal protein L18a	RPL18A	Castanea sativa (Sweet chestnut)						Ribonucleoprotein; Ribosomal protein
SRR122238_TR57280_c0_g1_i2_len=1089	RS27A_SOLTU	Q:85-552;H:1-156	96.79%ID	E:8e-85	Ubiquitin-40S ribosomal protein S27a	PF11976.5^Rad60-SLD^Ubiquitin-2 like Rad60 SUMO-like^29-99^E:3.7e-16 PF00240.20^ubiquitin^Ubiquitin family^31-102^E:5.4e-34 PF13881.3^Rad60-SLD_2^Ubiquitin-2 like Rad60 SUMO-like^38-118^E:0.0011 PF14560.3^Ubiquitin_2^Ubiquitin-like domain^59-97^E:0.00021 PF01599.16^Ribosomal_S27^Ribosomal protein S27a^130-175^E:3.8e-26	0	-1,062	1	-0,007	0,325	0,38	0,799	-0,098	0,098	-0,397	RS27A_SOLTU	Ubiquitin-40S ribosomal protein S27a [Cleaved into: Ubiquitin; 40S ribosomal protein S27a]	UBI3 RPS27A	Solanum tuberosum (Potato)						Complete proteome; Cytoplasm; Isopeptide bond; Metal-binding; Nucleus; Reference proteome; Ribonucleoprotein; Ribosomal protein; Ubl conjugation; Zinc; Zinc-finger
SRR122238_TR62934_c0_g1_i2_len=652	RPD6A_ARATH	Q:495-259;H:61-139	94.94%ID	E:1e-46	DNA-directed RNA polymerases II, IV and V subunit 6A	PF01192.19^RNA_pol_Rpb6^RNA polymerase Rpb6^53-104^E:8.3e-17	0	-2,234	0,014	-1,012	1	0	0	6,919	1	-1,817	RPD6A_ARATH	DNA-directed RNA polymerases II, IV and V subunit 6A (RNA polymerase Rpb6)	NRPB6A NRPD6A NRPE6A At5g51940 MSG15.2	Arabidopsis thaliana (Mouse-ear cress)						Complete proteome; DNA-directed RNA polymerase; Nucleus; Reference proteome; Transcription
SRR122238_TR63874_c0_g1_i6_len=712	RS13_SOYBN	Q:48-500;H:1-151	95.36%ID	E:1e-100	40S ribosomal protein S13	PF00416.19^Ribosomal_S13_N^Ribosomal S13/S15 N-terminal domain^16-75^E:3.2e-32 PF00312.19^Ribosomal_S15^Ribosomal protein S15^89-161^E:8e-18	0	-1,356	0,029	-0,601	0,942	0,044	0,821	-0,114	0,006	-0,742	RS13_SOYBN	40S ribosomal protein S13	RPS13	Glycine max (Soybean) (Glycine hispida)						Complete proteome; Reference proteome; Ribonucleoprotein; Ribosomal protein
SRR122238_TR66497_c1_g1_i1_len=1042	RL172_ARATH	Q:942-418;H:1-175	88%ID	E:2e-112	60S ribosomal protein L17-2	PF00237.16^Ribosomal_L22^Ribosomal protein L22p/L17e^19-151^E:2.9e-39	0	-0,889	0,385	-0,2	0,652	0,11	0,629	-0,127	0,641	-0,109	RL172_ARATH	60S ribosomal protein L17-2	RPL17B At1g67430 T1F15.11	Arabidopsis thaliana (Mouse-ear cress)						Alternative splicing; Complete proteome; Reference proteome; Ribonucleoprotein; Ribosomal protein
SRR122238_TR67156_c1_g1_i3_len=594	RS282_ARATH	Q:502-344;H:1-62	90.57%ID	E:6e-24	40S ribosomal protein S28-2		0	-1,141	0,227	-0,275	0,027	0,562	0,11	0,41	1	-0,19	RS282_ARATH	40S ribosomal protein S28-2	RPS28C At5g64140 MHJ24.12	Arabidopsis thaliana (Mouse-ear cress)						Complete proteome; Cytoplasm; Reference proteome; Ribonucleoprotein; Ribosomal protein
SRR122238_TR68648_c0_g1_i1_len=933	RL281_ARATH	Q:165-590;H:1-143	77.62%ID	E:1e-72	60S ribosomal protein L28-1	PF01778.14^Ribosomal_L28e^Ribosomal L28e protein family^8-122^E:1.7e-35	0	-0,908	0,335	-0,231	0,003	0,899	0,22	0,403	0,088	-0,409	RL281_ARATH	60S ribosomal protein L28-1	RPL28A At2g19730 F6F22.24	Arabidopsis thaliana (Mouse-ear cress)						Complete proteome; Reference proteome; Ribonucleoprotein; Ribosomal protein
SRR122238_TR71692_c0_g1_i3_len=505	NA	NA	NA	NA	NA		0	-3,372	1	-1,247	0,068	-1,007	0,1	-0,89	1	0	.	.	.	.	.	.	.	.	.	.
SRR122238_TR72925_c0_g1_i3_len=691	RS202_ARATH	Q:137-481;H:8-122	93.91%ID	E:1e-70	40S ribosomal protein S20-2	PF00338.19^Ribosomal_S10^Ribosomal protein S10p/S20e^25-119^E:3.7e-28	0	-0,989	0,913	0,027	0,38	0,214	0,806	-0,067	0,046	-0,448	RS202_ARATH	40S ribosomal protein S20-2	RPS20B At3g47370 T21L8.120	Arabidopsis thaliana (Mouse-ear cress)						Complete proteome; Reference proteome; Ribonucleoprotein; Ribosomal protein
SRR122238_TR73367_c0_g2_i2_len=732	NA	NA	NA	NA	NA	PF00428.16^Ribosomal_60s^60s Acidic ribosomal protein^18-112^E:2.8e-26 PF12868.4^DUF3824^Domain of unknown function (DUF3824)^72-103^E:0.3	0	-1,623	0,02	-0,608	0,784	-0,106	1	0,026	0,08	-0,39	.	.	.	.	.	.	.	.	.	.
SRR122238_TR73926_c0_g1_i4_len=654	RL321_ARATH	Q:65-463;H:1-133	86.47%ID	E:5e-74	60S ribosomal protein L32-1	PF01655.15^Ribosomal_L32e^Ribosomal protein L32^37-143^E:4.3e-50	0	-0,906	0,305	-0,237	0,067	0,456	0,297	0,266	0,204	-0,278	RL321_ARATH	60S ribosomal protein L32-1	RPL32A At4g18100 F15J5.70	Arabidopsis thaliana (Mouse-ear cress)						Complete proteome; Reference proteome; Ribonucleoprotein; Ribosomal protein
SRR122238_TR77044_c0_g1_i1_len=761	RL222_ARATH	Q:203-502;H:17-116	85%ID	E:1e-44	60S ribosomal protein L22-2	PF01778.14^Ribosomal_L28e^Ribosomal L28e protein family^65-173^E:1.3e-45	0	-0,936	0,067	-0,433	0,851	0,049	0,821	-0,072	0,303	-0,242	RL222_ARATH	60S ribosomal protein L22-2	RPL22B At3g05560 F18C11.17	Arabidopsis thaliana (Mouse-ear cress)						Complete proteome; Reference proteome; Ribonucleoprotein; Ribosomal protein
SRR122238_TR77058_c1_g1_i6_len=612	F16P1_SPIOL	Q:368-84;H:51-147	65.98%ID	E:9e-32	Fructose-1,6-bisphosphatase, chloroplastic	PF00316.17^FBPase^Fructose-1,6-bisphosphatase, N-terminal domain^117-176^E:2.7e-12	0,001	-6,56	1	0	0,034	5,65	0	6,729	1	1,191	F16P1_SPIOL	Fructose-1,6-bisphosphatase, chloroplastic (FBPase) (EC 3.1.3.11) (D-fructose-1,6-bisphosphate 1-phosphohydrolase)	Spinacia oleracea (Spinach)		PATHWAY: Carbohydrate biosynthesis; Calvin cycle.					3D-structure; Calvin cycle; Carbohydrate metabolism; Chloroplast; Direct protein sequencing; Disulfide bond; Hydrolase; Magnesium; Metal-binding; Plastid; Transit peptide
SRR122238_TR79922_c0_g1_i2_len=662	RS252_ARATH	Q:430-215;H:37-108	83.33%ID	E:7e-36	40S ribosomal protein S25-2	PF00297.12^Ribosomal_S25^S25 ribosomal protein^7-104^E:3e-42	0	-0,935	0,479	-0,157	0,436	0,189	0,181	-0,321	0,376	-0,25	RS252_ARATH	40S ribosomal protein S25-2	RPS25B Ap3g21580 F2G15.10	Arabidopsis thaliana (Mouse-ear cress)						Alternative splicing; Complete proteome; Reference proteome; Ribonucleoprotein; Ribosomal protein
SRR122238_TR83537_c0_g1_i1_len=1015	RS11_SOYBN	Q:217-693;H:1-159	91.19%ID	E:1e-90	40S ribosomal protein S11	PF16205.2^Ribosomal_S17_N^Ribosomal_S17 N-terminal^4-72^E:1.9e-32 PF00366.17^Ribosomal_S17^Ribosomal protein S17^74-142^E:7.6e-25	0	-0,931	0,781	-0,071	0,351	0,254	0,557	-0,172	0,264	-0,267	RS11_SOYBN	40S ribosomal protein S11	RPS11	Glycine max (Soybean) (Glycine hispida)						Complete proteome; RNA-binding; Reference proteome; Ribonucleoprotein; Ribosomal protein; rRNA-binding
SRR122238_TR87209_c0_g2_i3_len=578	R3SA1_ARATH	Q:549-214;H:1-112	91.07%ID	E:4e-70	60S ribosomal protein L35a-1	PF01247.15^Ribosomal_L35Ae^Ribosomal protein L35Ae^21-115^E:2.2e-46	0	-1,13	0,449	-0,187	0,88	0,055	0,154	-0,447	0,634	-0,237	R3SA1_ARATH	60S ribosomal protein L35a-1	RPL35AA At1g07070 F10K1.22	Arabidopsis thaliana (Mouse-ear cress)						Complete proteome; Reference proteome; Ribonucleoprotein; Ribosomal protein
SRR122238_TR87209_c0_g2_i4_len=748	R3SA3_ARATH	Q:700-365;H:1-112	91.96%ID	E:5e-69	60S ribosomal protein L35a-3	PF01247.15^Ribosomal_L35Ae^Ribosomal protein L35Ae^28-122^E:6.6e-46	0	-0,992	0,112	-0,394	0,023	0,662	0,425	0,248	0,066	-1,97	R3SA3_ARATH	60S ribosomal protein L35a-3	RPL35AC At1g74270 F1O17.6	Arabidopsis thaliana (Mouse-ear cress)						Complete proteome; Reference proteome; Ribonucleoprotein; Ribosomal protein
SRR12718577_TR6930_c0_g3_i3_len=1519	NA	NA	NA	NA	NA	PF00428.16^Ribosomal_60s^60s Acidic ribosomal protein^22-113^E:7.1e-25	0,001	-0,866	0,363	-0,224	0,416	0,221	0,71	-0,102	1	0,087	.	.	.	.	.	.	.	.	.	.
SRR12718577_TR8539_c0_g1_i4_len=535	H4_SOYBN	Q:125-370;H:22-103	100%ID	E:8e-60	Histone H4	PF15511.3^CENP-T_C^Centromere kinetochore component CENP-T histone fold^35-98^E:1.4e-08 PF02969.14^TAF^TATA box binding protein associated factor (TAF)^35-92^E:0.0018	0	-2,392	0,158	-1,802	1	0,157	0,629	-1,294	0,004	-0,853	H4_SOYBN	Histone H4		Glycine max (Soybean) (Glycine hispida)						Acetylation; Chromosome; Complete proteome; DNA-binding; Methylation; Nucleosome core; Nucleus; Reference proteome
SRR12718577_TR8825_c0_g1_i1_len=1077	NA	NA	NA	NA	NA		0,001	-2,136	1	0,635	0,076	-2,891	0,076	-2,331	0,

SRR342019_TR19026_c1_g1_i1_len=1517	RL32_ARATH	Q:1395-238,H:1-386	88.6%|D	E:0	60S ribosomal protein L3-2	PF00297.19*Ribosomal_L3*Ribosomal protein L3*1-370*E:2.4e-194	0,001	-1,17	0,755	-0,148	0,317	-0,499	0,153	-0,711	1	0,019	RL32_ARATH	60S ribosomal protein L3-2	ARP2 RPL3B At1g61580 T25B24.7	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Cytoplasm; Reference proteome; Ribonucleoprotein; Ribosomal protein
SRR342019_TR21392_c3_g2_i2_len=1130	RL7A_ORYSJ	Q:1052-276,H:1-258	87.26%|D	E:3e-150	60S ribosomal protein L7a	PF1248.23*Ribosomal_L7ae*Ribosomal protein L7Ae/L30e/S12e/Gad45 family*117-207*E:7.1e-25	0	-1	0,298	-0,284	0,203	0,442	0,807	0,104	0,264	-0,333	RL7A_ORYSJ	60S ribosomal protein L7a	RPL7A Os08g0326400 LOC_Os08g23710 OJ1136_A10.108 P0703C03.43	Oryza sativa subsp. japonica (Rice)		Complete proteome; Reference proteome; Ribonucleoprotein; Ribosomal protein
SRR342019_TR21392_c3_g2_i4_len=1327	RL7A_ORYSJ	Q:1217-672,H:1-181	84.62%|D	E:2e-112	60S ribosomal protein L7a	PF1248.23*Ribosomal_L7ae*Ribosomal protein L7Ae/L30e/S12e/Gad45 family*117-187*E:4.9e-21	0	-1,838	0,099	-0,808	0,461	1,4	1	-0,173	1	-0,711	RL7A_ORYSJ	60S ribosomal protein L7a	RPL7A Os08g0326400 LOC_Os08g23710 OJ1136_A10.108 P0703C03.43	Oryza sativa subsp. japonica (Rice)		Complete proteome; Reference proteome; Ribonucleoprotein; Ribosomal protein
SRR342019_TR22118_c4_g6_i2_len=1582	RS15_ELAOL	Q:563-318,H:72-153	86.59%|D	E:8e-44	40S ribosomal protein S15	PF00203.18*Ribosomal_S19*Ribosomal protein S19*50-115*E:2.6e-30	0	-0,945	0,739	-0,081	0,143	0,376	0,793	0,069	1	-0,058	RS15_ELAOL	40S ribosomal protein S15	RPS15	Elaeis oleifera (American oil palm) (Corozo oleifera)		Ribonucleoprotein; Ribosomal protein
SRR342019_TR22658_c1_g1_i1_len=798	NA	NA	NA	NA	NA	PF1474.12*HABPA_PAX-RIBP1*Hyaluronan / mRNA binding family*44-46*E:1.7e-07	0	-0,899	0,533	-0,151	0,769	0,084	0,353	-0,262	0,415	-0,295	.	.	.	.	.	.
SRR342019_TR23706_c2_g7_i8_len=2199	RS3A_CATRO	Q:972-274,H:28-261	99.15%|D	E:2e-152	40S ribosomal protein S3a (EC0:0000255)HAMAP-Rule:MF_03122)	PF10015.15*Ribosomal_S3Ae*Ribosomal S3Ae family*15-221*E:2.1e-99	0	-1,133	0,863	-0,053	0,758	0,107	0,458	-0,253	1	-0,05	RS3A_CATRO	40S ribosomal protein S3a (CYC07 protein)	RPS3A CYC07	Catharanthus roseus (Madagascar periwinkle) (Vinca rosea)		Cytoplasm; Ribonucleoprotein; Ribosomal protein
SRR342019_TR28947_c0_g1_i1_len=798	EF1B1_ARATH	Q:698-150,H:1-184	63.98%|D	E:5e-48	Elongation factor 1-beta 1	PF00736.16*EF1_GNE*EF-1 guanine nucleotide exchange domain*72-218*E:2e-11	0	-1,233	0,378	0,353	0,35	0,383	0,188	0,493	0,694	0,354	EF1B1_ARATH	Elongation factor 1-beta 1 (EF-1-beta 1) (Elongation factor 1-beta' 1) (EF-1-beta' 1) (Elongation factor 1B-alpha 1) (eEF1B alpha 1)	At5g12110 MXC9.7	Arabidopsis thaliana (Mouse-ear cress)		Acetylation; Cell membrane; Complete proteome; Elongation factor; Membrane; Protein biosynthesis; Reference proteome
SRR342019_TR34577_c2_g2_i1_len=634	RL132_BRANA	Q:108-626,H:1-173	86.13%|D	E:4e-110	60S ribosomal protein L13-2	PF01294.15*Ribosomal_L13e*Ribosomal protein L13e*7-175*E:7.3e-76	0	-1,203	0,654	0,122	0,575	0,187	0,736	-0,144	1	-0,008	RL132_BRANA	60S ribosomal protein L13-2 (Cold-induced protein C24B)		Brassica napus (Rape)		Ribonucleoprotein; Ribosomal protein
SRR342019_TR37006_c3_g1_i1_len=754	TBA4_ARATH	Q:510-1,H:1-170	98.82%|D	E:7e-104	Tubulin alpha-4 chain	PF00091.22*Tubulin*Tubulin/FtsZ family, GTPase domain*3-168*E:3.8e-52	0	-1,042	0	4,269	0,044	-0,759	0,206	-0,465	0,026	0,602	TBA4_ARATH	Tubulin alpha-4 chain	TUBA4 TUA4 At1g04820 F13M7.19	Arabidopsis thaliana (Mouse-ear cress)		Acetylation; Complete proteome; Cytoplasm; Cytoskeleton; GTP-binding; Microtubule; Nucleotide-binding; Phosphoprotein; Reference proteome
SRR342022_TR10275_c3_g3_i4_len=3102	NUCL2_ORYSJ	Q:1953-2543,H:435-630	56.28%|D	E:7e-62	Nucleolin 2	PF00076.19*RRM_1*RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)*412-482*E:3.8e-19 PF00076.19*RRM_1*RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)*515-585*E:9.9e-08	0,001	-1,074	0	1,678	0,381	2,056	1	1,035	0,619	0,134	NUCL2_ORYSJ	Nucleolin 2 (Protein NUCLEOLIN LIKE 2)	Os04g0620700 LOC_Os04g52960 OSJNBa0058K23.21	Oryza sativa subsp. japonica (Rice)		Complete proteome; Nucleus; RNA-binding; Reference proteome; Repeat; rRNA processing
SRR342022_TR11933_c0_g2_i1_len=521	RPBAL_ARATH	Q:120-326,H:1-69	91.3%|D	E:1e-40	DNA-directed RNA polymerase subunit 10-like protein (EC0:0000303)PubMed:19110459)		0	-1,465	1	0,02	0	1,34	0,003	1,032	0,559	-0,174	RPBAL_ARATH	DNA-directed RNA polymerase subunit 10-like protein (ABC10) (DNA-directed RNA polymerase III subunit L) (DNA-directed RNA polymerases I, II, and III subunit RPABC5) (RNA polymerases I, II, and III subunit ABC5) (RPB10 homolog)	NRPB10L At1g61700 T13M11.6	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; DNA-directed RNA polymerase; Metal-binding; Nucleus; Reference proteome; Transcription; Zinc
SRR342022_TR15406_c3_g5_i2_len=1692	RIR2_TOBAC	Q:131-1117,H:1-329	90.27%|D	E:0	Ribonucleoside-diphosphate reductase small chain	PF00268.18*Ribonuc_red_smr*Ribonucleotide reductase, small chain*59-325*E:3e-119	0,001	-1,25	0,014	-1,479	0,402	0,913	0,76	0,357	0,107	-0,68	RIR2_TOBAC	Ribonucleoside-diphosphate reductase small chain (EC 1.17.4.1) (Ribonucleoside-diphosphate reductase R2 subunit) (Ribonucleotide reductase small chain)		Nicotiana tabacum (Common tobacco)	PATHWAY: Genetic information processing; DNA replication.	Cytoplasm; DNA replication; Iron; Metal-binding; Oxidoreductase
SRR342022_TR17193_c0_g3_i3_len=607	RL29_ARATH	Q:95-277,H:1-61	81.97%|D	E:8e-27	60S ribosomal protein L29-1		0	-0,77	0,656	0,115	0	1,244	0	0,85	0,019	-0,604	RL29_ARATH	60S ribosomal protein L29-1	RPL29A At3g06700 F3E22.16 T8E24.8	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Phosphoprotein; Reference proteome; Ribonucleoprotein; Ribosomal protein
SRR342022_TR19763_c2_g2_i7_len=1802	PSBP_SPIOL	Q:2-805,H:5-267	74.91%|D	E:1e-135	Oxygen-evolving enhancer protein 2, chloroplastic	PF0178.9.13*PsbP*PsbP*78-267*E:6.2e-41	0	-1,056	0,215	-0,351	0,823	-0,112	0,262	-0,429	0,372	-0,247	PSBP_SPIOL	Oxygen-evolving enhancer protein 2, chloroplastic (OEE2) (23 kDa subunit of oxygen evolving system of photosystem II) (23 kDa thylakoid membrane protein) (OEC 23 kDa subunit)	PSBP	Spinacia oleracea (Spinach)		3D-structure; Chloroplast; Direct protein sequencing; Membrane; Photosynthesis; Photosystem II; Plastid; Thylakoid; Transit peptide
SRR342022_TR19776_c0_g2_i2_len=1806	EAAC_ARATH	Q:159-1310,H:1-379	71.36%|D	E:5e-173	Probable envelope ADP,ATP carrier protein, chloroplastic	PF00153.24*Mito_carr*Mitochondrial carrier protein*95-185*E:7.5e-24 PF00153.24*Mito_carr*Mitochondrial carrier protein*189-276*E:6.4e-21 PF00153.24*Mito_carr*Mitochondrial carrier protein*284-366*E:2.7e-20	0	-1,814	0,004	-1,724	1	0,898	1	-2,46	0,191	-0,402	EAAC_ARATH	Probable envelope ADP,ATP carrier protein, chloroplastic (Envelope ADP/ATP translocase)	EAAC At3g51870 ATEM1.12	Arabidopsis thaliana (Mouse-ear cress)		Chloroplast; Complete proteome; Membrane; Plastid; Reference proteome; Repeat; Transit peptide; Transmembrane; Transmembrane helix; Transport
SRR342022_TR26073_c3_g1_i13_len=567	NA	NA	NA	NA	NA	PF00226.26*DnaJ*DnaJ domain*12-77*E:1e-24	0	-1,521	0	1,794	1	-1,477	1	-1,477	1	1,187	.	.	.	.	.	.
SRR342023_TR5478_c1_g1_i2_len=2488	RFA1B_ARATH	Q:2278-458,H:1-588	67.54%|D	E:0	Replication protein A 70 kDa DNA-binding subunit B	PF00457.9*Rep-A_N*Replication factor-A protein 1, N-terminal domain*6-131*E:5e-22 PF10139.22*RNA_anti-codon*OB-fold nucleic acid binding domain*191-277*E:1.2e-10 PF16900.2*REPA_OB_2*Replication protein A OB domain*311-405*E:1e-22 PF08646.7*Rep_fac-A_C*Replication factor-A C terminal domain*468-612*E:6e-45	0,001	-1,433	0,025	-3,275	1	0,323	1	-0,665	0,203	-0,58	RFA1B_ARATH	Replication protein A 70 kDa DNA-binding subunit B (AtRPA70B) (AtRPA1-5) (Replication factor A protein 1B) (Replication protein A 1B) (AtRPA1B)	RPA1B RPA70B At5g08020 F13G24.220	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; DNA damage; DNA recombination; DNA repair; DNA replication; DNA-binding; Metal-binding; Nucleus; Reference proteome; Zinc; Zinc-finger
SRR342023_TR5478_c1_g1_i3_len=557	NHP2_ARATH	Q:378-4,H:1-124	76%|D	E:9e-56	H/ACA ribonucleoprotein complex subunit 2-like protein	PF1248.23*Ribosomal_L7ae*Ribosomal protein L7Ae/L30e/S12e/Gad45 family*41-122*E:2.6e-23	0	-1,067	0,24	0,349	0,132	0,746	1	-0,097	1	0,011	NHP2_ARATH	H/ACA ribonucleoprotein complex subunit 2-like protein (Nhp2-like protein)	At5g08180 T22D6.120	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Nucleus; RNA-binding; Reference proteome; Ribonucleoprotein; Ribosome biogenesis; rRNA processing
SRR342023_TR10865_c0_g3_i3_len=1344	FRI2_TOBAC	Q:1228-470,H:1-250	78.74%|D	E:2e-117	Ferritin-2, chloroplastic	PF00210.21*Ferritin*Ferritin-like domain*98-241*E:3.8e-34	0	-0,853	0,216	-0,297	0,359	0,281	1	0,022	0,035	-1,745	FRI2_TOBAC	Ferritin-2, chloroplastic (EC 1.16.3.1) (NtFer2)	FER2	Nicotiana tabacum (Common tobacco)		Chloroplast; Iron; Iron storage; Metal-binding; Oxidoreductase; Plastid; Transit peptide
SRR342023_TR13025_c0_g5_i2_len=1063	RS18_ARATH	Q:148-603,H:1-152	92.76%|D	E:7e-88	40S ribosomal protein S18	PF00416.19*Ribosomal_S13*Ribosomal protein S13/S18*14-142*E:3.8e-57	0	-1,002	0,804	0,057	0,335	0,23	0,755	-0,075	1	0,829	RS18_ARATH	40S ribosomal protein S18	RPS18A PFL At1g22780 T22J18.5; RPS18B At1g34030 F12G12.15 T15K4.9; RPS18C At4g09800 F17A8.150	Arabidopsis thaliana (Mouse-ear cress)		Acetylation; Complete proteome; Cytoplasm; Direct protein sequencing; RNA-binding; Reference proteome; Ribonucleoprotein; Ribosomal protein; rRNA-binding
SRR342023_TR16651_c0_g1_i1_len=1317	CYT5_ARATH	Q:634-359,H:22-114	59.14%|D	E:2e-31	Cysteine proteinase inhibitor 5	PF1068.15*Cystatin*Cystatin domain*34-119*E:4.4e-15 PF16845.2*SQAPI*Aspartic acid proteinase inhibitor*39-119*E:2.2e-37 PF07539.8*PPI1*Pollen filament protein PP1 cystatin-like domain*47-115*E:0.00013	0	-1,158	0,26	-0,355	0,065	0,709	0,555	0,271	0,192	0,442	CYT5_ARATH	Cysteine proteinase inhibitor 5 (AtCYS-5)	CYS5 At5g47550 MNJ7.14	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Glycoprotein; Plant defense; Protease inhibitor; Reference proteome; Secreted; Signal; Thiol protease inhibitor
SRR342023_TR17380_c0_g1_i1_len=886	RS141_MAIZE	Q:158-574,H:1-138	94.24%|D	E:2e-77	40S ribosomal protein S14	PF00411.16*Ribosomal_S11*Ribosomal protein S11*80-198*E:2.4e-47	0	-0,975	0,009	-0,6	0,753	-0,086	0,141	-0,393	0,016	-0,551	RS141_MAIZE	40S ribosomal protein S14 (Clone MCH1)		Zea mays (Maize)		Complete proteome; Reference proteome; Ribonucleoprotein; Ribosomal protein
SRR342023_TR20079_c6_g2_i2_len=579	H2A4_ORYSJ	Q:438-115,H:30-137	92.59%|D	E:6e-51	Probable histone H2A.4	PF00125.21*Histone*Core histone H2A/H2B/H3/H4*27-118*E:2e-13 PF16211.2*Histone_H2A_C*C-terminus of histone H2A*121-153*E:1.9e-18	0	-0,859	0,023	-0,617	0,002	0,999	0,018	0,791	0,211	-0,795	H2A4_ORYSJ	Probable histone H2A.4	Os05g0461400 LOC_Os05g38640 OJ1281_H05.14 OJ1525_A02.1 Osu_018061	Oryza sativa subsp. japonica (Rice)		Chromosome; Complete proteome; DNA-binding; Nucleosome core; Nucleus; Reference proteome
SRR342023_TR27937_c0_g3_i1_len=3061	RH3_ARATH	Q:192-2186,H:2-649	73.12%|D	E:0	DEAD-box ATP-dependent RNA helicase 3, chloroplastic	PF00270.29*DEAD*DEAD/DEAH box helicase*146-320*E:3.4e-47 PF04851.12*Res III*Type III restriction enzyme, res subunit*16-213*E:6.4e-07 PF00271.28*Helicase_C*Helicase conserved C-terminal domain*358-465*E:2.9e-30 PF08152.9*GUCT*GUCT (NUC152) domain*552-652*E:3.3e-19 PF00098.20*zf-CCHC*Zinc knuckle*742-757*E:1.2e-06 PF14392.3*zf-CCHC_4*Zinc knuckle*742-757*E:0.0061	0	-1,818	0,517	1,026	1	0,087	0,059	1,611	0,025	2,024	RH3_ARATH	DEAD-box ATP-dependent RNA helicase 3, chloroplastic (EC 3.6.4.13) (Protein EMBRYO DEFECTIVE 1138)	RH3 EMB1138 At5g26742 F21E10.1 T7I7.6	Arabidopsis thaliana (Mouse-ear cress)		ATP-binding; Alternative splicing; Chloroplast; Complete proteome; Helicase; Hydrolase; Metal-binding; Nucleotide-binding; Phosphoprotein; Plastid; RNA-binding; Reference proteome; Transit peptide; Zinc; Zinc-finger
SRR646572_TR4777_c0_g1_i1_len=1054	RS92_ARATH	Q:880-347,H:1-178	92.13%|D	E:2e-117	40S ribosomal protein S9-2	PF00163.16*Ribosomal_S4*Ribosomal protein S4/S9 N-terminal domain*8-64*E:2.2e-10 PF01479.22*S4*S4 domain*109-152*E:7.4e-19	0	-1,197	0,034	-0,477	0,786	-0,071	0,188	-0,338	0,009	-0,662	RS92_ARATH	40S ribosomal protein S9-2	RPS9C At5g39850 MYH19.1 MYH19.10	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; RNA-binding; Reference proteome; Ribonucleoprotein; Ribosomal protein; rRNA-binding
SRR646572_TR10126_c0_g2_i2_len=1290	CYSP3_SOLLC	Q:1585-809,H:44-302	78.38%|D	E:2e-150	Cysteine proteinase 3	PF00112.20*Peptidase_C1*Papain family cysteine protease*53-211*E:4.5e-51	0,001	-4,394	1	0	1	2,637	1	3,53	1	0	CYSP3_SOLLC	Cysteine proteinase 3 (EC 3.4.22.-)	CYP-3	Solanum lycopersicum (Tomato) (Lycopersicon esculum)		Complete proteome; Disulfide bond; Glycoprotein; Hydrolase; Protease; Reference proteome; Signal; Thiol protease; Vacuole; Zymogen
SRR646572_TR15250_c0_g1_i1_len=740	RL31_NICGU	Q:150-509,H:1-120	91.67%|D	E:2e-56	60S ribosomal protein L31	PF01198.16*Ribosomal_L31e*Ribosomal protein L31e*11-92*E:8.6e-44	0,001	-1,02	0,17	-0,443	0,057	0,749	0,113	0,632	0,038	-0,54	RL31_NICGU	60S ribosomal protein L31	RPL31	Nicotiana glutinosa (Tobacco)		Ribonucleoprotein; Ribosomal protein
SRR646572_TR24379_c0_g1_i1_len=1162	RL24_PRUAV	Q:80-382,H:1-101	97.03%|D	E:3e-55	60S ribosomal protein L24	PF01246.17*Ribosomal_L24e*Ribosomal protein L24e*3-67*E:6e-30	0	-1,521	0,416	-0,235	0,165	0,506	0,799	0,134	0,804	0,102	RL24_PRUAV	60S ribosomal protein L24	RPL24	Prunus avium (Cherry) (Cerasus avium)		Ribonucleoprotein; Ribosomal protein
SRR646596_TR2772_c0_g1_i1_len=1453	RS6_ASPOF	Q:1304-601,H:1-243	85.07%|D	E:1e-127	40S ribosomal protein S6		0	-1,148	0,355	0,348	0,431	0,316	0,684	0,19	0,538	0,219	RS6_ASPOF	40S ribosomal protein S6	rps6	Asparagus officinalis (Garden asparagus)		Phosphoprotein; Ribonucleoprotein; Ribosomal protein
SRR646596_TR16528_c1_g2_i1_len=803	RS27A_SOLTU	Q:673-206,H:1-156	96.79%|D	E:3e-86	Ubiquitin-40S ribosomal protein S27a	PF11976.5*Rad60-SLD*Ubiquitin-2 like Rad60 SUMO-like*1-71*E:2.5e-16 PF00240.20*ubiquitin*Ubiquitin family*3-74*E:3.7e-34 PF14560.3*Ubiquitin_2*Ubiquitin-like domain*12-69*E:0.00017 PF13881.3*Rad60-SLD_2*Ubiquitin-2 like Rad60 SUMO-like*13-90*E:0.00085 PF01599.16*Ribosomal_S27*Ribosomal protein S27a*102-147*E:2.8e-26	0	-0,978	0,397	-0,229	0,397	0,27	0,68	-0,138	0,472	-0,731	RS27A_SOLTU	Ubiquitin-40S ribosomal protein S27a (Cleaved into: Ubiquitin; 40S ribosomal protein S27a)	UBI3 RPS27A	Solanum tuberosum (Potato)		Complete proteome; Cytoplasm; Isopeptide bond; Metal-binding; Nucleus; Reference proteome; Ribonucleoprotein; Ribosomal protein; Ubl conjugation; Zinc; Zinc-finger
SRR646596_TR21334_c0_g1_i1_len=850	RS23_FRAAN	Q:154-579,H:1-142	98.59%|D	E:4e-95	40S ribosomal protein S23	PF00164.22*Ribosom_S12_S23*Ribosomal protein S12/S23*9-141*E:6e-63	0	-1,164	0,538	-0,172	0,536	0,23	0,894	-0,052	0,502	-4,26	RS23_FRAAN	40S ribosomal protein S23 (S12)	RPS23	Fragaria ananassa (Strawberry)		Hydroxylation; Ribonucleoprotein; Ribosomal protein
SRR646596_TR21991_c0_g1_i1_len=2286	CH62_CUCMA	Q:2180-486,H:1-565	90.97%|D	E:0	Chaperonin CPN60-2, mitochondrial	PF00118.21*Cpn60_TCP1*TCP-1/cpn60 chaperonin family*54-555*E:8.4e-66	0,001	-1,157	0,038	0,703	0,153	0,769	1	0,098	0,854	-0,111	CH62_CUCMA	Chaperonin CPN60-2, mitochondrial (HSP60-2)	CPN60-2	Cucurbita maxima (Pumpkin) (Winter squash)		ATP-binding; Chaperone; Direct protein sequencing; Mitochondrion; Nucleotide-binding; Stress response; Transit peptide
SRR646596_TR29729_c0_g1_i1_len=884	ACP1_CASGL	Q:197-607,H:1-136	67.88%|D	E:2e-49	Acyl carrier protein 1, chloroplastic	PF00550.22*PP-binding*Phosphopantetheine attachment site*61-128*E:6.3e-10	0	-1,504	0,813	0,076	0,289	0,359	0,097	0,562	0,463	0,622	ACP1_CASGL	Acyl carrier protein 1, chloroplastic (ACP 1)	ACP1	Casuarina glauca (Swamp oak)	PATHWAY: Lipid metabolism; fatty acid biosynthesis.	Chloroplast; Fatty acid biosynthesis; Fatty acid metabolism; Lipid biosynthesis; Lipid metabolism; Phosphopantetheine; Phosphoprotein; Plastid; Transit peptide
SRR646596_TR31372_c0_g1_i1_len=1519	RL3_ORYSJ	Q:1427-261,H:1-389	88.17%|D	E:0	60S ribosomal protein L3	PF00297.19*Ribosomal_L3*Ribosomal protein L3*31-400*E:8.4e-195	0	-1,279	0,007	1,143	0,655	-0,275	0,232	-0,602	0,436	0,258	RL3_ORYSJ	60S ribosomal protein L3	RPL3 Os12g0167900 LOC_Os12g07010	Oryza sativa subsp. japonica (Rice)		Complete proteome; Cytoplasm; Reference proteome; Ribonucleoprotein; Ribosomal protein
SRR646604_TR14082_c0_g2_i1_len=1901	UBP1_NICPL	Q:1597-437,H:21-406	88.92%|D	E:0	Oligouridylate-binding protein 1	PF00076.19*RRM_1*RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)*50-116*E:1.1e-13 PF13893.3*RRM_5*RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)*67-118*E:0.2 PF00076.19*RRM_1*RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)*135-205*E:3.4e-19 PF00076.19*RRM_1*RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)*256-322*E:1.1e-12	0	-3,363	1	-0,46	0,005	4,958	0,034	4,236	1	0,18	UBP1_NICPL	Oligouridylate-binding protein 1 (NpUBP1) (Polyuridylate-binding protein UBP1) (PolyU)-binding protein UBP1)	UBP1	Nicotiana plumbaginifolia (Leafworticleaved tobacco) (TexMex tobacco)		Nucleus; RNA-binding; Repeat; mRNA processing
SRR646604_TR19240_c0_g1_i4_len=2511	BAM9_ARATH	Q:721-2187,H:67-521	53.67%|D	E:7e-161	Inactive beta-amylase 9	PF0139.13*Glyco_hydro_14*Glycosyl hydrolase family 14*13-210*E:1.6e-34	0	-6,036	0,756	0,25	1	-0,941	1	-0,687	1	0,326	BAM9_ARATH	Inactive beta-amylase 9 (1,4-alpha-D-glucan maltohydrolase) (Inactive beta-amylase 3)	BAM9 BMY3 At5g18670 T1A4.50	Arabidopsis thaliana (Mouse-ear cress)		Carbohydrate metabolism; Complete proteome; Cytoplasm; Phosphoprotein; Polysaccharide degradation; Reference proteome
SRR646604_TR30453_c0_g1_i1_len=589	H32_WHEAT	Q:488-81,H:1-136	99.26%|D	E:7e-78	Histone H3.2	PF00125.21*Histone*Core histone H2A/H2B/H3/H4*34-165*E:1.8e-54	0	-7,367	1	-2,289	1	0	1	0	1	0	H32_WHEAT	Histone H3.2		Triticum aestivum (Wheat)		Acetylation; Chromosome; Complete proteome; DNA-binding; Direct protein sequencing; Methylation; Nucleosome core; Nucleus; Phosphoprotein; Reference proteome
SRR646604_TR31202_c0_g1_i1_len=679	RL273_ARATH	Q:113-517,H:1-135	80%|D	E:1e-62	60S ribosomal protein L27-3	PF01777.15*Ribosomal_L27e*Ribosomal L27e protein family*52-135*E:6.9e-34	0	-8,111	0,452	-0,588	1	-0,061	0,103	-1,495	0,732	-0,108	RL273_ARATH	60S ribosomal protein L27-3	RPL27C At4g15000 dl3545w FCAALL.99	Arabidopsis thaliana (Mouse-ear cress)		Alternative splicing; Complete proteome; Reference proteome; Ribonucleoprotein; Ribosomal protein
SRR648705_TR1373_c0_g2_i1_len=999	RS7_ARUMI	Q:136-705,H:1-190	83.16%|D	E:2e-114	40S ribosomal protein S7	PF01251.15*Ribosomal_S7e*Ribosomal protein S7e*7-187*E:2e-78	0	-1,195	0,349	-0,238	0,878	-0,056	0,047	0,724	0,275	-0,268	RS7_AVIMR	40S ribosomal protein S7	RPS7	Avicennia marina (Grey mangrove) (Sceura marina)		Ribonucleoprotein; Ribosomal protein
SRR648705_TR3981_c0_g1_i3_len=2589	CH62_CUCMA	Q:198-1892,H:1-565	89.38%|D	E:0	Chaperonin CPN60-2, mitochondrial	PF00118.21*Cpn60_TCP1*TCP-1/cpn60 chaperonin family*54-555*E:4.7e-64	0	-1,425	1	0,018	0,014	3,56	0,381	2,233	0,648	-0,197	CH62_CUCMA	Chaperonin CPN60-2, mitochondrial (HSP60-2)	CPN60-2	Cucurbita maxima (Pumpkin) (Winter squash)		ATP-binding; Chaperone; Direct protein sequencing; Mitochondrion; Nucleotide-binding; Stress response; Transit peptide
SRR648705_TR5819_c1_g1_i1_len=409	NA	NA	NA	NA	NA		0,001	-6,657	0,283	0,63	0,001	2,969	0,066	2,09	0,692	-1,004	.	.	.	.	.	.
SRR648705_TR7638_c1_g1_i2_len=1108	RL111_ARATH	Q:224-76,H:2-180	95.53%|D	E:3e-112	60S ribosomal protein L11-1	PF00281.16*Ribosomal_L5*Ribosomal protein L5*1-52*E:2.4e-19 PF00673.16*Ribosomal_L5_C*ribosomal L5P family C-terminal domain*56-154*E:5.5e-21	0,001	-1,797	1	0,076	1	0,123	0,643	-0,445	0,062	-0,465	RL111_ARATH	60S ribosomal protein L11-1 (L16A)	RPL11A RPL16A At2g42740 F7D19.26	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Cytoplasm; RNA-binding; Reference proteome; Ribonucleoprotein; Ribosomal protein; rRNA-binding
SRR648705_TR8541_c2_g1_i3_len=1354	RSSA_DAUCA	Q:163-978,H:1-269	76.92%|D	E:2e-138	40S ribosomal protein SA (EC0:0000255)HAMAP-Rule:MF_03015)	PF00318.17*Ribosomal_S2*Ribosomal protein S2*18-112*E:1.4e-12 PF00318.17*Ribosomal_S2*Ribosomal protein S2*117-182*E:1.9e-12	0,001	-1,173	0	10,892	1	0	1	0	0,353	-0,229	RSSA_DAUCA	40S ribosomal protein SA (p40)	179B	Daucus carota (Wild carrot)		Cytoplasm; Ribonucleoprotein; Ribosomal protein
SRR648705_TR13379_c0_g1_i1_len=1139	RS212_ARATH	Q:627-669,H:1-81	81.48%|D	E:4e-42	40S ribosomal protein S21-2		0,001	-3,379	1	-0,046	1	2,862	1	0	0,066	1,735	RS212_ARATH	40S ribosomal protein S21-2	RPS21C At5g27700 T1G16.30	Arabidopsis thaliana (Mouse-ear cress)		Acetylation; Complete proteome; Reference proteome; Ribonucleoprotein; Ribosomal protein
SRR648705_TR13379_c0_g1_i3_len=692	RS212_ARATH	Q:180-422,H:1-81	81.48%|D	E:3e-44	40S ribosomal protein S21-2		0	-7,167	0,282	-0,271	1	0,174	1	0,232	0	4,454	RS212_ARATH	40S ribosomal protein S21-2	RPS21C At5g27700 T1G16.30	Arabidopsis thaliana (Mouse-ear cress)		Acetylation; Complete proteome; Reference proteome; Ribonucleoprotein; Ribosomal protein
SRR648705_TR13569_c0_g2_i2_len=2079	EF1A_TOBAC	Q:1791-484,H:1-436	97.94%|D	E:0	Elongation factor 1-alpha	PF00009.24*GTP_EFTU*Elongation factor Tu GTP binding domain*6-221*E:1e-52 PF03144.22*GTP_EFTU_D2*Elongation factor Tu domain 2*248-313*E:7.3e-15 PF03143.14*GTP_EFTU_D3*Elongation factor Tu C-terminal domain*322-429*E:3.9e-38	0	-0,948	0,287	0,281	0,005	-0,724	0,007	-0,697	0,904	-0,057	EF1A_TOBAC	Elongation factor 1-alpha (EF-1-alpha) (Vitronectin-like adhesion protein 1) (PVN1)		Nicotiana tabacum (Common tobacco)		Cytoplasm; Elongation factor; GTP-binding; Nucleotide-binding; Phosphoprotein; Protein biosynthesis
SRR648705_TR13636_c0_g1_i1_len=2030	RL7A_ORYSJ	Q:205-981,H:1-258	87.64%|D	E:1e-146	60S ribosomal protein L7a	PF1248.23*Ribosomal_L7ae*Ribosomal protein L7Ae/L30e/S12e/Gad45 family*117-206*E:9.9e-25	0	-1,173	0,162	-0,454	0,407	0,474	0,57	0,351	0,219	-0,408	RL7A_ORYSJ	60S ribosomal protein L7a	RPL7A Os08g0326400 LOC_Os08g23710 OJ1136_A10.108 P0703C03.43	Oryza sativa subsp. japonica (Rice)		Complete proteome; Reference proteome; Ribonucleoprotein; Ribosomal protein
SRR648705_TR15837_c0_g1_i1_len=885	R15A1_ARATH	Q:171-560,H:1-130	97.69%|D	E:2e-87	40S ribosomal protein S15a-1	PF00410.16*Ribosomal_S8*Ribosomal protein S8*7-130*E:5e-22	0	-0,962	0,236	-0,264	0,015	0,601	0,224	0,308	0,469	-0,161	R15A1_ARATH	40S ribosomal protein S15a-1	RPS15AA At1g07770 F24B9.12; RPS15AF At5g59850 MNB10.16 MMN10.8	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Cytoplasm; Reference proteome; Ribonucleoprotein; Ribosomal protein
SRR648705_TR16695_c0_g1_i3_len=578	NA	NA	NA	NA	NA		0	-1,03	0,002	-0,744	0,195	0,351	0,684	0,124	0,014	-0,554	.	.	.	.	.	.
SRR648705_TR19195_c0_g2_i1_len=3341	MCM2_ORYSI	Q:3068-267,H:6-960	79.33%|D	E:0	DNA replication licensing factor MCM2	PF12619.5*MCM2_N*Minichromosome maintenance protein 2*62-218*E:1.7e-22 PF14551.3*MCM_N*Mcm4 N-ter

SRR924147_TR16878_c0_g1_i1_len=1173	SODC_IPOBA	Q:961-506;H:1-152	88.16%ID	E:2e-88	Superoxide dismutase [Cu-Zn]	P:Hypoxia;P:dismutase activity;C:cytosol;F:superoxide dismutase (SODC);P:response to stimulus;F:superoxide dismutase (SODC);P:oxidation-reduction process;F:copper ion binding;F:superoxide dismutase (SODC);P:cellular response to oxidative stress;F:superoxide dismutase (SODC);P:cellular response to hypoxia;F:superoxide dismutase (SODC);P:cellular response to copper ion;F:superoxide dismutase (SODC);P:cellular response to stimulus;F:superoxide dismutase (SODC);P:cellular response to oxygen-containing compound;F:superoxide dismutase (SODC);P:response to oxygen-containing compound;F:superoxide dismutase (SODC);P:response to stimulus;F:superoxide dismutase (SODC);P:response to hypoxia;F:superoxide dismutase (SODC);P:response to copper ion;F:superoxide dismutase (SODC);P:response to oxidative stress;F:superoxide dismutase (SODC);P:response to oxygen-containing compound;F:superoxide dismutase (SODC);P:response to reactive oxygen species;F:superoxide dismutase (SODC);P:response to copper ion

SRR122238_TR63692_c1_g1_i4_len=1181	TLPH_ARATH	Q:283-957;H:17-241	77.33%ID	E:2e-124	Thaumatin-like protein	PF00314.14*Thaumatin*Thaumatin family*35-247*E:7.3e-83	0,139	-0,598	0	-4,612	0,044	-1,992	0,319	-0,959	0,275	-0,269 TLPH_ARATH	Thaumatin-like protein	At1g18250 T10O22.21	Arabidopsis thaliana (Mouse-ear cress)	-	Alternative splicing; Complete proteome; Disulfide bond; Reference proteome; Signal
SRR122238_TR64653_c0_g1_i1_len=657	NUD26_ARATH	Q:71-487;H:78-216	71.22%ID	E:6e-69	Nudix hydrolase 26, chloroplastic	PF00293.25*NUDIX*NUDIX domain*1-155*E:3.2e-19	0,44	0,933	0	-7,541	1	0,344	0,017	-5,739	0,193	-0,739 NUD26_ARATH	Nudix hydrolase 26, chloroplastic (AtNUDT26) (EC 3.6.1.-) (Bis(5'-nucleosyl)-tetraphosphatase (asymmetrical))	NUDT26 NUDX26 At3g10620 F13M14.9 F18K10.24	Arabidopsis thaliana (Mouse-ear cress)	-	Chloroplast; Complete proteome; Hydrolase; Magnesium; Manganese; Metal-binding; Plastid; Reference proteome; Transit peptide
SRR122238_TR64963_c0_g1_i1_len=1061	NA	NA	NA	NA	NA	-	1	-0,1	0,001	-2,312	0,258	-1,086	0,258	-0,965	0,729	0,155	-	-	-	-	-
SRR122238_TR67122_c0_g1_i2_len=1057	NA	NA	NA	NA	NA	PF03745.11*DUF3097*Domain of unknown function (DUF3097)*84-140*E:3.1e-20	1	-0,484	0	-1,346	0,014	-1,427	0,121	-0,827	0,692	1,454	-	-	-	-	-
SRR122238_TR70112_c0_g3_i3_len=1778	PIN1C_ORYSJ	Q:997-70;7;H:492-588	91.75%ID	E:3e-47	Probable auxin efflux carrier component 1c	-	0,407	0,617	0	-2,683	0,316	-0,727	0,021	-1,647	0,832	-0,4 PIN1C_ORYSJ	Probable auxin efflux carrier component 1c (OsPIN1c)	PIN1C Os06g0232300 LOC_Os06g12610 P0479H10.14	Oryza sativa subsp. japonica (Rice)	-	Auxin signaling pathway; Complete proteome; Glycoprotein; Membrane; Reference proteome; Transmembrane; Transmembrane helix; Transport
SRR122238_TR71350_c2_g1_i5_len=545	FD6E1_SOYBN	Q:11-304;H:288-387	85%ID	E:2e-56	Omega-6 fatty acid desaturase, endoplasmic reticulum isozyme 1	PF00487.21*FA_desaturase*Fatty acid desaturase*13-65*E:6.8e-09	0,211	-0,74	0	-2,515	0,231	-0,565	0,684	-0,202	0,098	-0,479 FD6E1_SOYBN	Omega-6 fatty acid desaturase, endoplasmic reticulum isozyme 1 (EC 1.14.19.-)	FAD2-1	Glycine max (Soybean) (Glycine hispida)	PATHWAY: Lipid metabolism; polyunsaturated fatty acid biosynthesis.	Complete proteome; Membrane; Metal-binding; Reference proteome; Transmembrane; Transmembrane helix
SRR122238_TR71611_c0_g1_i1_len=1244	NA	NA	NA	NA	NA	-	0,298	0,686	0	-7,121	0,472	0,694	0,472	0,744	1	-0,004	-	-	-	-	-
SRR122238_TR72948_c0_g1_i10_len=2409	RK13_ARATH	Q:223-846;H:30-241	77.36%ID	E:3e-110	50S ribosomal protein L13, chloroplastic	PF00572.15*Ribosomal_L13*Ribosomal protein L13*103-225*E:2e-50	0,031	-0,555	0	-1,45	0,334	-0,281	0,409	-0,249	0,518	-0,159 RK13_ARATH	50S ribosomal protein L13, chloroplastic (CL13) (Protein EMBRYO DEFECTIVE 1473)	RPL13 EMB1473 At1g78630 T30F21.4	Arabidopsis thaliana (Mouse-ear cress)	-	Chloroplast; Complete proteome; Plastid; Reference proteome; Ribonucleoprotein; Ribosomal protein; Transit peptide
SRR122238_TR74069_c0_g1_i2_len=844	NA	NA	NA	NA	NA	PF05499.8*RALF*Rapid Alkalinization Factor (RALF)*72-131*E:7.4e-09	0,78	0,143	0	-1,742	0,43	0,589	0,543	0,43	0,589	0,543	-	-	-	-	-
SRR122238_TR75102_c0_g1_i12_len=680	NA	NA	NA	NA	NA	PF01530.20*HIT*HIT domain*16-87*E:1.9e-17	0,454	-0,325	0	-1,837	0,443	-0,273	0,07	-0,637	0,258	-0,819	-	-	-	-	-
SRR122238_TR76038_c1_g2_i1_len=757	NA	NA	NA	NA	NA	-	0,124	-0,371	0	-1,268	0,195	-0,322	0,215	-0,311	0,18	-0,31	-	-	-	-	-
SRR122238_TR78180_c1_g1_i5_len=527	NA	NA	NA	NA	NA	-	0,017	-0,566	0	-1,789	0,002	0,864	0,025	0,635	0,003	0,665	-	-	-	-	-
SRR122238_TR78653_c0_g1_i8_len=1068	ASPG2_ARATH	Q:1018-188;H:13-470	32.39%ID	E:2e-22	Protein ASPARTIC PROTEASE IN GUARD CELL 2	PF14543.3*TAXI_N*Xylanase inhibitor N-terminal*9-105*E:5.8e-18 PF00026.20*Asp*Eukaryotic aspartyl protease*13-277*E:2.1e-11 PF14543.3*TAXI_C*Xylanase inhibitor C-terminal*128-274*E:1.5e-33	0,781	-0,136	0	-1,763	0,381	1,428	1	0,647	0,402	-1,097 ASPG2_ARATH	Protein ASPARTIC PROTEASE IN GUARD CELL 2 (AtASPG2) (EC 3.4.23.-)	ASPG2 At3g20015 MZE19.7	Arabidopsis thaliana (Mouse-ear cress)	-	Aspartyl protease; Complete proteome; Membrane; Reference proteome; Signal
SRR122238_TR78693_c0_g1_i2_len=1407	CH62_CUCMA	Q:1019-372;H:350-565	92.13%ID	E:2e-131	Chaperonin CPN60-2, mitochondrial	PF00118.21*Cpn60_TCP1*TCP-1/cpn60 chaperonin family*2-209*E:8.4e-37	1	1,518	0	-2,844	1	0	0,01	0,1	0,781	-1,85 CH62_CUCMA	Chaperonin CPN60-2, mitochondrial (HSP60-2)	CPN60-2	Cucurbita maxima (Pumpkin) (Winter squash)	-	ATP-binding; Chaperone; Direct protein sequencing; Mitochondrion; Nucleotide-binding; Stress response; Transit peptide
SRR122238_TR79570_c0_g1_i1_len=966	HBL2_SOLLC	Q:216-641;H:1-142	77.46%ID	E:3e-78	Non-symbiotic hemoglobin 2	PF00042.19*Globin*Globin*8-116*E:2.2e-19	0,175	-0,335	0	-1,531	0,006	-0,654	0,004	-0,689	0,102	-0,434 HBL2_SOLLC	Non-symbiotic hemoglobin 2 (Hb2) (SOLly GLB2)	HB2 GLB2	Solanum lycopersicum (Tomato) (Lycopersicon esculentum)	-	Complete proteome; Heme; Iron; Metal-binding; Reference proteome
SRR122238_TR79722_c0_g1_i2_len=436	Y1523_ARATH	Q:2-196;H:490-548	72.31%ID	E:4e-23	C-type lectin receptor-like tyrosine-protein kinase At1g52310	-	0,002	-1,466	0	-2,304	0,679	0,404	0,811	-0,242	0,211	-0,652 Y1523_ARATH	C-type lectin receptor-like tyrosine-protein kinase At1g52310 (EC 2.7.10.1)	At1g52310 F19K6.8	Arabidopsis thaliana (Mouse-ear cress)	-	ATP-binding; Cell membrane; Complete proteome; Disulfide bond; Glycoprotein; Kinase; Lectin; Membrane; Nucleotide-binding; Receptor; Reference proteome; Signal; Transferase; Transmembrane; Transmembrane helix; Tyrosine-protein kinase
SRR122238_TR82347_c1_g1_i1_len=787	NA	NA	NA	NA	NA	-	0,56	0,194	0	-4,015	0,588	-0,213	0,231	0,425	0,91	0,042	-	-	-	-	-
SRR122238_TR83592_c0_g2_i8_len=961	NA	NA	NA	NA	NA	-	0,455	0,206	0	-0,922	0,849	0,047	0,343	0,221	0,22	-0,301	-	-	-	-	-
SRR122238_TR83629_c0_g5_i2_len=731	PSAH1_ARATH	Q:610-242;H:1-123	81.3%ID	E:6e-51	Photosystem I reaction center subunit VI-1, chloroplastic	PF03244.11*PSI_PsaH*Photosystem I reaction centre subunit VI*7-145*E:1.9e-71	0,174	-0,31	0,001	-0,815	0,001	-0,724	0,203	-0,277	0,132	0,688 PSAH1_ARATH	Photosystem I reaction center subunit VI-1, chloroplastic (PSI-H1)	PSAH1 At3g16140 MSL1.18	Arabidopsis thaliana (Mouse-ear cress)	-	Chloroplast; Complete proteome; Membrane; Photosynthesis; Photosystem I; Plastid; Reference proteome; Thylakoid; Transit peptide; Transmembrane; Transmembrane helix; Transport
SRR122238_TR84806_c0_g1_i2_len=909	RR9_SPIOL	Q:104-67;H:9-197	73.06%ID	E:2e-90	30S ribosomal protein S9, chloroplastic	PF00380.16*Ribosomal_S9*Ribosomal protein S9/S16*102-223*E:2e-41	0,066	-0,428	0	-1,12	0,024	-0,565	0,085	-0,425	0,05	-0,439 RR9_SPIOL	30S ribosomal protein S9, chloroplastic (Fragment)	PRP59	Spinacia oleracea (Spinach)	-	3D-structure; Acetylation; Chloroplast; Direct protein sequencing; Plastid; RNA-binding; Ribonucleoprotein; Ribosomal protein; Transit peptide; rRNA-binding
SRR122238_TR86788_c0_g1_i2_len=1186	RK18_ARATH	Q:1065-613;H:11-170	73.75%ID	E:2e-74	50S ribosomal protein L18, chloroplastic	PF02900.15*LigB*Catalytic LigB subunit of aromatic ring-opening dioxygenase*59-164*E:9e-05 PF00861.19*Ribosomal_L18p*Ribosomal L18 of archaea, bacteria, mitoch. and chloroplast*72-191*E:4.4e-47	0,057	-0,468	0	-1,464	0,046	-0,569	0,272	-0,312	0,18	0,832 RK18_ARATH	50S ribosomal protein L18, chloroplastic (CL18)	RPL18 At1g48350 F11A17.10	Arabidopsis thaliana (Mouse-ear cress)	-	Chloroplast; Complete proteome; Plastid; RNA-binding; Reference proteome; Ribonucleoprotein; Ribosomal protein; Transit peptide; rRNA-binding
SRR122238_TR86802_c0_g1_i7_len=1051	STR9_ARATH	Q:40-263;H:39-230	76.56%ID	E:2e-105	Rhodanese-like domain-containing protein 9, chloroplastic	-	0,34	-0,222	0,001	-0,81	0,002	-0,699	0,001	-0,733	0,254	0,278 STR9_ARATH	Rhodanese-like domain-containing protein 9, chloroplastic (Sulfurtransferase 9) (AtStr9)	STR9 At2g42220 T24P15.13	Arabidopsis thaliana (Mouse-ear cress)	-	Chloroplast; Complete proteome; Membrane; Plastid; Reference proteome; Transit peptide; Transmembrane; Transmembrane helix
SRR122238_TR87466_c1_g4_i5_len=5277	PHOT2_ARATH	Q:4710-3247;H:64-533	70.28%ID	E:0	Phototropin-2	PF13426.4*PAS_9*PAS domain*176-272*E:2.2e-19 PF00989.22*PAS*PAS fold*182-267*E:7.8e-09 PF08447.9*PAS_3*PAS fold*183-266*E:4.3e-08 PF13426.4*PAS_9*PAS domain*446-538*E:1e-19 PF00989.22*PAS*PAS fold*449-538*E:1.2e-06 PF08447.9*PAS_3*PAS fold*450-535*E:1.1e-05	0,878	-0,162	0,001	-2,348	0,002	-1,071	0,002	-2,108	1	0,007 PHOT2_ARATH	Phototropin-2 (EC 2.7.11.1) (Defective in chloroplast avoidance protein 1) (Non-phototropic hypocotyl 1-like protein 1) (AtNPL1) (NPH1-like protein 1)	PHOT2 CAV1 KIN7 NPL1 At5g58140 K21L19.6	Arabidopsis thaliana (Mouse-ear cress)	-	Chloroplast; Complete proteome; DNA-binding; Nucleus; Reference proteome; Repeat; Transcription; Transcription regulation
SRR122238_TR89076_c0_g1_i4_len=1628	IOJAC_ARATH	Q:848-546;H:138-238	80.2%ID	E:5e-51	Protein Iojap, chloroplastic	-	0,129	-0,446	0	-1,19	1	0,237	0,811	0,459	0,816	-0,183 IOJAC_ARATH	Protein Iojap, chloroplastic	IJ At3g12930 MGH6.5	Arabidopsis thaliana (Mouse-ear cress)	-	Chloroplast; Complete proteome; Plastid; Reference proteome; Transit peptide
SRR122238_TR90209_c0_g3_i1_len=550	PSBW_ARATH	Q:480-169;H:19-119	62.86%ID	E:1e-22	Photosystem II reaction center W protein, chloroplastic	PF07123.9*PsbW*Photosystem II reaction centre W protein (PsbW)*7-141*E:4e-56	0,46	0,154	0	-1,116	0,024	-0,469	0,066	-0,379	0,931	-0,033 PSBW_ARATH	Photosystem II reaction center W protein, chloroplastic (PSII 6.1 kDa protein)	PSBW At2g30570 T6B20.8	Arabidopsis thaliana (Mouse-ear cress)	-	Chloroplast; Complete proteome; Membrane; Photosynthesis; Photosystem II; Plastid; Reference proteome; Thylakoid; Transit peptide; Transmembrane; Transmembrane helix
SRR1271857_TR3589_c0_g2_i10_len=2929	EGY2_ARATH	Q:1623-1020;H:206-479	79.85%ID	E:7e-123	Probable zinc metalloprotease EGY2, chloroplastic	-	0,811	-0,395	0	-2,839	1	2,217	1	1,816	1	-0,085 EGY2_ARATH	Probable zinc metalloprotease EGY2, chloroplastic (EC 3.4.24.-) (Protein ETHYLENE-DEPENDENT GRAVITROPISM-DEFICIENT AND YELLOW-GREEN 2)	EGY2 At5g05740 MJJ3.15	Arabidopsis thaliana (Mouse-ear cress)	-	Alternative splicing; Chloroplast; Complete proteome; Hydrolase; Membrane; Metalloprotease; Plastid; Protease; Reference proteome; Transit peptide; Transmembrane; Transmembrane helix
SRR1271857_TR3622_c0_g1_i1_len=1385	NA	NA	NA	NA	NA	-	0,064	-0,745	0	-2,529	0,226	-1,741	0,226	-1,999	0,392	0,363	-	-	-	-	-
SRR1271857_TR4997_c0_g2_i1_len=814	NA	NA	NA	NA	NA	-	0,448	-0,288	0	-1,482	0,938	0,044	0,758	0,134	0,385	-0,285	-	-	-	-	-
SRR1271857_TR5837_c0_g3_i6_len=709	NA	NA	NA	NA	NA	PF03473.14*MOSC*MOSC domain*60-162*E:6.6e-18	0,357	-0,712	0	-2,221	1	0,54	0,629	1,043	1	-0,299	-	-	-	-	-
SRR1271857_TR7192_c0_g1_i2_len=859	GTL2_ARATH	Q:656-63;H:296-475	39.22%ID	E:2e-22	Trihelix transcription factor GTL2	-	0,066	0,501	0	-1,312	0,534	0,466	1	-0,081	0,081	-0,457 GTL2_ARATH	Trihelix transcription factor GTL2 (GT2-LIKE protein 2) (AtGTL2) (Trihelix DNA-binding protein GTL2)	At5g28300 T8M17.70	Arabidopsis thaliana (Mouse-ear cress)	-	Coiled coil; Complete proteome; DNA-binding; Nucleus; Reference proteome; Repeat; Transcription; Transcription regulation
SRR1271857_TR7523_c1_g1_i1_len=633	NA	NA	NA	NA	NA	-	0,502	3,894	0	-7,492	1	2,698	1	0	1	-1,951	-	-	-	-	-
SRR1271857_TR9204_c0_g1_i6_len=4613	NA	NA	NA	NA	NA	-	0,111	-0,83	0	-3,264	0,068	-1,302	0,01	-1,911	0,76	0,363	-	-	-	-	-
SRR1271857_TR11267_c0_g3_i1_len=1912	CHLM_ARATH	Q:1659-823;H:44-311	75.63%ID	E:7e-140	Magnesium protoporphyrin IX methyltransferase, chloroplastic	PF13489.3*Methyltransf_23*Methyltransferase domain*189-343*E:3.9e-08 PF13847.3*Methyltransf_31*Methyltransferase domain*189-276*E:1.2e-06 PF13649.3*Methyltransf_25*Methyltransferase domain*193-289*E:1.3e-11 PF08242.9*Methyltransf_12*Methyltransferase domain*195-288*E:1.3e-07 PF08241.9*Methyltransf_11*Methyltransferase domain*195-275*E:5.6e-06 PF07109.8*Mg-por_mtran_C*Magnesium-protoporphyrin IX methyltransferase C-terminus*267-362*E:5.7e-35	0,077	-0,525	0	-1,266	0,018	-0,864	0,654	-0,654	0,261	0,309 CHLM_ARATH	Magnesium protoporphyrin IX methyltransferase, chloroplastic (EC 2.1.1.11)	CHLM At4g25080 F13M23.220	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Porphyrin-containing compound metabolism; chlorophyll biosynthesis.	Alternative splicing; Chlorophyll biosynthesis; Chloroplast; Complete proteome; Membrane; Methyltransferase; Plastid; Reference proteome; S-adenosyl-L-methionine; Thylakoid; Transferase; Transit peptide
SRR1271857_TR14295_c0_g1_i3_len=2009	RK4_TOBAC	Q:713-1411;H:25-253	79.83%ID	E:3e-124	50S ribosomal protein L4, chloroplastic	PF00573.19*Ribosomal_L4*Ribosomal protein L4/L1 family*60-260*E:4.1e-52	0,046	-0,499	0	-1,315	0,008	-0,756	0,052	-0,536	0,046	-0,488 RK4_TOBAC	50S ribosomal protein L4, chloroplastic (CL4) (R-protein L4)	RPL4	Nicotiana tabacum (Common tobacco)	-	Chloroplast; Plastid; RNA-binding; Ribonucleoprotein; Ribosomal protein; Transit peptide; rRNA-binding
SRR1271857_TR15387_c0_g3_i1_len=2124	PHYLO_ARATH	Q:1612-305;H:1277-1712	50.57%ID	E:1e-138	Protein PHYLLO, chloroplastic	PF02230.13*Abhydrolase_2*Phospholipase/Carboxylesterase*123-238*E:3.1e-07 PF12146.5*Hydrolase_4*Serine aminopeptidase, S33*130-379*E:1.8e-12 PF00561.17*Abhydrolase_1*alpha/beta hydrolase fold*131-247*E:2.5e-18 PF12697.4*Abhydrolase_6*Alpha/beta hydrolase family*133-385*E:5.1e-22 PF03096.11*Ndr*Ndr family*150-392*E:2.6e-08 PF07859.10*Abhydrolase_3*alpha/beta hydrolase fold*182-305*E:3.2e-05 PF08840.8*BAAT_C*Acyl-CoA thioester hydrolase C terminal*200-376*E:4.3e-05	0,439	-0,349	0	-1,84	0,452	-0,519	0,719	-0,374	0,461	-0,88 PHYLO_ARATH	Protein PHYLLO, chloroplastic (Includes: Inactive isochorismate synthase (MENF); 2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylate synthase (EC 2.2.1.9) (MEND); o-succinylbenzoate synthase (EC 4.2.1.113) (MENC); 2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase (EC 4.2.99.20) (MENH))	PHYLLO At1g68890/At1g68900 T6L1.7/T6L1.8	Arabidopsis thaliana (Mouse-ear cress)	-	Alternative splicing; Chloroplast; Complete proteome; Lyase; Magnesium; Manganese; Membrane; Metal-binding; Multifunctional enzyme; Plastid; Reference proteome; Thiamine pyrophosphate; Transferase; Transit peptide; Transmembrane; Transmembrane helix
SRR1271857_TR17006_c0_g1_i1_len=646	ATL66_ARATH	Q:79-522;H:9-156	50%ID	E:3e-36	RING-H2 finger protein ATL66	PF12861.4*zf-ANAPC11*Anaphase-promoting complex subunit 11 RING-H2 finger*100-149*E:5.5e-05 PF13639.3*zf-RING_2*Ring finger domain*101-144*E:1.4e-14 PF17123.2*zf-RING_11*RING-like zinc finger*101-130*E:3.1e-09 PF13923.3*zf-C3HC4_2*Zinc finger, C3HC4 type (RING finger)*101-143*E:8.4e-08 PF13445.3*zf-RING_UBOX*RING-type zinc-finger*102-141*E:2.9e-05 PF00097.22*zf-C3HC4*Zinc finger, C3HC4 type (RING finger)*102-143*E:3.3e-05 PF12678.4*zf-rbx1*RING-H2 zinc finger domain*109-144*E:2.9e-08	0,593	-0,673	0	-3,602	1	0,903	1	0,849	0,123	0,715 ATL66_ARATH	RING-H2 finger protein ATL66	ATL66 At3g11110 F11B9.7 F9F8.8	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Protein modification; protein ubiquitination.	Complete proteome; Membrane; Metal-binding; Reference proteome; Transmembrane; Transmembrane helix; Ubl conjugation pathway; Zinc; Zinc-finger
SRR1271857_TR17959_c0_g1_i6_len=2474	NA	NA	NA	NA	NA	-	0,609	-0,286	0	-1,778	0,564	-0,427	0,43	-0,699	1	-0,065	-	-	-	-	-
SRR1271857_TR18439_c1_g1_i7_len=2302	NA	NA	NA	NA	NA	PF14215.3*bHLH-MYC_N*bHLH-MYC and R2R3-MYB transcription factors N-terminal*13-136*E:2.7e-14	0,524	-0,561	0,001	-3,427	0,025	-3,884	0,005	-4,609	0,066	5,337	-	-	-	-	-
SRR1271857_TR18456_c0_g1_i1_len=1216	RK3_TOBAC	Q:242-997;H:8-259	82.42%ID	E:2e-122	50S ribosomal protein L3, chloroplastic	PF00297.19*Ribosomal_L3*Ribosomal protein L3*158-245*E:1.9e-17	0,202	-0,29	0	-1,302	0,067	-0,432	0,27	-0,258	0,937	-0,024 RK3_TOBAC	50S ribosomal protein L3, chloroplastic (Fragment)	RPL3	Nicotiana tabacum (Common tobacco)	-	Chloroplast; Plastid; RNA-binding; Ribonucleoprotein; Ribosomal protein; Transit peptide; rRNA-binding
SRR1271857_TR20290_c2_g7_i1_len=1820	NA	NA	NA	NA	NA	-	1	-0,074	0	-1,969	0,111	-0,87	0,077	-1,014	0,446	-0,311	-	-	-	-	-
SRR1271857_TR21102_c0_g2_i1_len=1671	NA	NA	NA	NA	NA	PF01738.15*DLH*Dienelactone hydrolase family*5-150*E:8e-22 PF08386.7*Abhydrolase_4*TAP-like protein*78-128*E:6.5e-08	1	-0,069	0	-2,5	1	2,164	1	0	0,798	0,153	-	-	-	-	-
SRR1271857_TR21977_c0_g1_i2_len=808	NA	NA	NA	NA	NA	-	0,732	-0,83	0	-2,639	1	-0,725	1	-1,056	0,258	-1,046	-	-	-	-	-
SRR1271857_TR23215_c0_g1_i7_len=1850	RR1_SPIOL	Q:505-107;H:165-335	30.16%ID	E:2e-22	30S ribosomal protein S1, chloroplastic	PF00575.20*S1*S1 RNA binding domain*193-269*E:1.2e-16	1	-0,095	0,001	-1,928	0,262	-0,54	0,673	-0,252	0,472	-0,356 RR1_SPIOL	30S ribosomal protein S1, chloroplastic (CS1)	RPS1	Spinacia oleracea (Spinach)	-	Chloroplast; Direct protein sequencing; Plastid; RNA-binding; Repeat; Ribonucleoprotein; Ribosomal protein; Transit peptide
SRR1271857_TR24843_c0_g1_i2_len=971	SYGM1_ARATH	Q:884-177;H:489-724	78.39%ID	E:5e-117	Glycine--tRNA ligase, mitochondrial 1 (EC0000305)	PF03129.17*HGTP_anticodon*Anticodon binding domain*107-194*E:4.4e-21	0,903	0,047	0	-1,111	0,381	0,662	1	0,067	0,732	-0,625 SYGM1_ARATH	Glycine--tRNA ligase, mitochondrial 1 (EC 6.1.1.14) (Diadenosine tetraphosphate synthetase) (AP-4-A synthetase) (Glycyl-tRNA synthetase 1) (GlyRS-1)	At1g29880 F1N18.8	Arabidopsis thaliana (Mouse-ear cress)	-	Alternative splicing; Chloroplast; Complete proteome; Direct protein sequencing; Plastid; Reference proteome; Transit peptide
SRR1271857_TR25567_c0_g2_i6_len=1798	SGAT_ARATH	Q:383-1582;H:1-400	89%ID	E:0	Serine--glyoxylate aminotransferase	PF00266.16*Aminotran_5*Aminotransferase class-V*12-325*E:7.5e-33	0,342	-0,313	0	-1,324	0,637	-0,109	0,797	0,058	0,522	1,44 SGAT_ARATH	Serine--glyoxylate aminotransferase (EC 2.6.1.45) (Alanine--glyoxylate aminotransferase) (AGT) (EC 2.6.1.44) (Asparagine aminotransferase) (EC 2.6.1.-) (Serine--pyruvate aminotransferase) (EC 2.6.1.51)	AGT1 At2g13360 F14O4.7	Arabidopsis thaliana (Mouse-ear cress)	-	ATP-binding; Allosteric enzyme; Chloroplast; Complete proteome; Nucleotide-binding; Nucleotidyltransferase; Phosphoprotein; Plastid; Reference proteome; Starch biosynthesis; Transferase; Transit peptide
SRR1271857_TR26789_c0_g2_i2_len=1685	XTH32_ARATH	Q:120-908;H:37-299	82.89%ID	E:2e-163	Probable xyloglucan endotransglucosylase/hydrolase protein 32	PF00722.18*Glyco_hydro_16*Glycosyl hydrolases family 16*48-229*E:2e-53 PF06955.9*XET_C*Xyloglucan endo-transglycosylase (XET) C-terminus*276-331*E:1.8e-17	0,763	-0,206	0	-2,297	1	0,187	1	-1,328	0,001	1,647 XTH32_ARATH	Probable xyloglucan endotransglucosylase/hydrolase protein 32 (At5-XTH32) (XTH-32) (EC 2.4.1.207)	XTH32 At2g36870 T1J8.5	Arabidopsis thaliana (Mouse-ear cress)	-	Alternative splicing; Apoplast; Cell wall; Cell wall biogenesis/degradation; Complete proteome; Disulfide bond; Glycosidase; Hydrolase; Reference proteome; Secreted; Signal; Transferase
SRR1271857_TR28513_c0_g1_i1_len=951	NA	NA	NA	NA	NA	-	0,115	-0,769	0	-2,86	0,132	1,295	0,132	1,281	0,079	-0,452	-	-	-	-	-
SRR1271857_TR31850_c0_g2_i11_len=2063	NA	NA	NA	NA	NA	PF13540.3*RCC1_2*Regulator of chromosome condensation (RCC1) repeat*36-65*E:4.4e-09 PF00415.15*RCC1*Regulator of chromosome condensation (RCC1) repeat*163-209*E:1.9e-10	0,564	-0,288	0,001	-2,055	0,156	-0,584	0,226	-0,472	0,385	-0,342	-	-	-	-	-
SRR1271857_TR32133_c0_g1_i1_len=991	FTRV_MAIZE	Q:573-331;H:17-96	58.02%ID	E:3e-25	Ferredoxin-thioredoxin reductase, variable chain	PF02941.12*FeThRed_A*Ferredoxin thioredoxin reductase variable alpha chain*142-215*E:9.9e-24	0,186	-0,327	0	-1,104	0,357	-0,245	1	0	0,211	0,61 FTRV_MAIZE	Ferredoxin-thioredoxin reductase, variable chain (FTR-V) (Ferredoxin-thioredoxin reductase subunit A) (FTR-A)	Zea mays (Maize)	-	Chloroplast; Complete proteome; Direct protein sequencing; Oxidoreductase; Plastid; Reference proteome	-
SRR1271857_TR32830_c0_g8_i6_len=580	ROC1_NICPL	Q:31-264;H:201-279	86.08%ID	E:1e-37	30 kDa ribonucleoprotein, chloroplastic	PF00230.17*MIP*Major intrinsic protein*65-294*E:7.6e-85	0,227	-0,346	0,001	-1,007	0,377	0,571	0,079	1,01	1	0,592 ROC1_NICPL	30 kDa ribonucleoprotein, chloroplastic (CP-RBP30)	Nicotiana plumbaginifolia (Leadwortleaved tobacco) (Tex-Mex tobacco)	Chloroplast; Plastid; RNA-binding; Repeat; Ribonucleoprotein; Transit peptide; mRNA processing	-	-
SRR1271857_TR33180_c0_g1_i2_len=1085	RR10_MESCR	Q:478-837;H:78-197	87.5%ID	E:1e-71	30S ribosomal protein S10, chloroplastic	-	0,046	-0,478	0	-1,197	0,124	-0,391	0,467	-0,188	0	7,485 RR10_MESCR	30S ribosomal protein S10, chloroplastic	RPS10	Mesembryanthemum crystallinum (Common ice plant) (Cryophytum crystallinum)	-	Chloroplast; Plastid; Ribonucleoprotein; Ribosomal protein; Transit peptide
SRR1271857_TR33534_c0_g1_i5_len=3589	NA	NA	NA	NA	NA	-	1	0,02	0	-4,543	0,028	1,458	0,112	1,071	0,076	2,629	-	-	-	-	-
SRR1271857_TR33753_c1_g1_i5_len=2124	SYS_HELAN	Q:370-1665;H:1-432	86.81%ID	E:0	Serine--tRNA ligase	PF02403.19*Seryl_tRNA_N*Seryl-tRNA synthetase N-terminal domain*1-112*E:1.1e-26 PF00587.22*tRNA-synt_2b*tRNA synthetase class II core domain (G, H, P, S and T)*221-407*E:1.6e-35	0,132	-0,69	0	-7,212	0,066	-5,389	1	-5,389	0,066	-0,583	1	-0,022 SYS_HELAN	Serine--tRNA ligase (EC 6.1.1.11) (Seryl-tRNA synthetase) (SerRS) (Seryl-tRNA(Ser/Sec) synthetase)	Helianthus annuus (Common sunflower)	PATHWAY: Aminoacyl-tRNA biosynthesis; selenocysteine-tRNA(Sec) biosynthesis; Liver-tRNA(Sec) from L-serine and tRNA(Sec): step 1/1.	-	ATP-binding; Aminoacyl-tRNA synthetase; Ligase; Nucleotide-binding; Protein biosynthesis
SRR1271857_TR34511_c0_g1_i9_len=2146	ALGC_PSEEM	Q:552-1670;H:53-395	28.88%ID	E:8e-36	Phosphomannomutase/phosphoglucomutase	PF02878.13*PGM_PMM_I*Phosphoglucomutase/phosphomannomutase, alpha/beta/alpha domain I*77-228*E:4.4e-28 PF02878.13*PGM_PMM_II*Phosphoglucomutase/phosphomannomutase, alpha/beta/alpha domain II*251-359*E:6.8e-21 PF02880.13*PGM_PMM_III*Phosphoglucomutase/phosphomannomutase, alpha/beta/alpha domain III*363-463*E:1.1e-12	0,856	0,101	0	-1,213	1	-0,071	1	-0,079	0,33	-0,369 ALGC_PSEEM	Phosphomannomutase/phosphoglucomutase (PMM / PGM) (EC 5.4.2.2) (EC 5.4.2.8)	algC PSPTO_0083	Pseudomonas syringae pv. tomato (strain DC3000)	PATHWAY: Nucleotide-sugar biosynthesis; GDP-alpha-D-mannose biosynthesis; alpha-D-mannose 1-phosphate from D-fructose 6-phosphate: step 2/2.; PATHWAY: Bacterial outer membrane biogenesis; lipopolysaccharide biosynthesis.	Alginate biosynthesis; Complete proteome; Isomerase; Lipopolysaccharide biosynthesis; Magnesium; Metal-binding; Multifunctional enzyme; Phosphoprotein; Reference proteome	-
SRR1271857_TR34790_c0_g2_i2_len=1279	NA	NA	NA	NA	NA	-	0,663	-0,511	0	-2,387	0,073	2,228	0,118	2,115	1	-0,327	-	-	-	-	-
SRR1271857_TR35199_c3_g5_i6_len=2487	NA	NA	NA	NA	NA	PF03168.10*LEA_2*Late embryogenesis abundant protein*97-197*E:2.1e-05	0,832	-0,246	0	-3,434	1	0,58	1	0,898	0,021	-1,281	-	-	-	-	-
SRR1271857_TR36568_c0_g1_i2_len=1176	PIP27_ARATH	Q:107-209;H:1-280	87.28%ID	E:2e-176	Aquaporin PIP2-7	PF00230.13*MIP*Major intrinsic protein*71-300*E:1.1e-82	0,056	-0,407	0	-2,111	0,031	-0,463	0,19	-0,28	0,379	-0,209 PIP27_ARATH	Aquaporin PIP2-7 (Plasma membrane intrinsic protein 2-7) (AtPIP2;7) (Plasma membrane intrinsic protein 3) (Salt stress-induced major intrinsic protein) [Cleaved into: Aquaporin PIP2.7, N-terminally processed]	PIP2-7 PIP

SRR342017_TR4629_c0_g1_i2_len=1340	PPD5_ARATH	Q:1052-291,H:35-297	68.94%ID	E:2e-122	PsbP domain-containing protein 5, chloroplastic	PF01789.13*PsbP*PsbP*1175-278*E:8.7e-12	0.204	-0.431	0	-1.307	0.086	-0.98	0.086	-1.006	0.446	0.335	PPD5_ARATH	PsbP domain-containing protein 5, chloroplastic (OEC23-like protein 6) (PsbP-related thylakoid lumenal protein 4) (Thylakoid lumenal 35.8 kDa protein)	PPD5 At5g11450 F15N18.40	Arabidopsis thaliana (Mouse-ear cress)		Chloroplast; Complete proteome; Direct protein sequencing; Plastid; Reference proteome; Thylakoid; Transit peptide
SRR342017_TR5172_c0_g1_i3_len=1021	NA	NA	NA	NA	NA	NA	0.339	-0.295	0	-1.81	0.509	0.313	0.318	-0.468	0.057	0.602	.	.	.	.	.	.	.
SRR342017_TR6674_c1_g1_i1_len=743	EPL9_ARATH	Q:468-238,H:25-102	64.56%ID	E:8e-27	EPIDERMAL PATTERNING FACTOR-like protein 9 (ECO:0000303|PubMed:19435754)	PF16851.2*Stomagen*Stomagen*70-118*E:3.8e-31	0.276	-0.326	0	-1.594	0.297	-0.323	1	-0.01	0.403	-0.261	EPL9_ARATH	EPIDERMAL PATTERNING FACTOR-like protein 9 (EPF-like protein 9) [Cleaved into: Stomagen]	EPFL9 STOMAGEN At4g12970 F25G13.60	Arabidopsis thaliana (Mouse-ear cress)		3D-structure; Apoplast; Complete proteome; Developmental protein; Direct protein sequencing; Disulfide bond; Reference proteome; Secreted; Signal
SRR342017_TR7022_c0_g3_i3_len=521	NA	NA	NA	NA	NA	.	0.026	1.877	0	-7.86	1	0	1	2.843	0.212	-0.601	.	.	.	.	.	.	.
SRR342017_TR7988_c6_g1_i2_len=562	IF2C_ARATH	Q:192-518,H:907-1015	71.56%ID	E:2e-41	Translation initiation factor IF-2, chloroplastic	.	0.132	-0.839	0	-2.213	0.014	-0.943	0.003	-1.169	0.134	-0.503	IF2C_ARATH	Translation initiation factor IF-2, chloroplastic	At1g17220 F20D23.8	Arabidopsis thaliana (Mouse-ear cress)		Chloroplast; Complete proteome; GTP-binding; Initiation factor; Nucleotide-binding; Plastid; Protein biosynthesis; Reference proteome; Transit peptide
SRR342017_TR8359_c0_g3_i1_len=764	NA	NA	NA	NA	NA	.	0.62	-0.654	0.001	-2.699	0.44	-0.927	0.282	-1.08	0.472	-0.813	.	.	.	.	.	.	.
SRR342017_TR9948_c0_g9_i2_len=547	UCRIB_TOBAC	Q:2-226,H:156-228	92%ID	E:4e-42	Cytochrome b6-f complex iron-sulfur subunit 2, chloroplastic	.	0.187	0.606	0.001	-1.054	0.849	0.088	0.368	0.293	0.018	-0.549	UCRIB_TOBAC	Cytochrome b6-f complex iron-sulfur subunit 2, chloroplastic (EC 1.10.9.1) (Plastohydroquinone plastocyanin oxidoreductase iron-sulfur protein 2) (Rieske iron-sulfur protein 2) (ISP 2) (RISP 2)	pet C2	Nicotiana tabacum (Common tobacco)		2Fe-2S; Chloroplast; Disulfide bond; Electron transport; Iron; Iron-sulfur; Membrane; Metal-binding; Oxidoreductase; Plastid; Thylakoid; Transit peptide; Transmembrane; Transmembrane helix; Transport
SRR342017_TR10207_c0_g1_i1_len=1783	CCD32_ARATH	Q:757-1662,H:71-367	50.48%ID	E:2e-96	Cyclin-D3-2	PF00134.20*Cyclin_N*Cyclin_N-terminal domain*96-201*E:2.2e-27PF02984.16*Cyclin_C*Cyclin_C-terminal domain*203-312*E:5.2e-23	0.003	-0.962	0	-3.582	0.138	-0.89	0.035	-1.397	0.438	-0.275	CCD32_ARATH	Cyclin-D3-2 (G1/S-specific cyclin-D3-2) (CycD3;2)	CYCD3-2 At5g67260 K3G17.2	Arabidopsis thaliana (Mouse-ear cress)		Cell cycle; Cell division; Complete proteome; Cyclin; Reference proteome
SRR342017_TR10435_c0_g3_i2_len=1330	Y1816_ARATH	Q:1-1330,H:1-1330	36.97%ID	E:4e-31	Uncharacterized protein At1g08160	PF03168.10*LEA_2*Late embryogenesis abundant protein*105-203*E:5.3e-15	0.618	-0.307	0	-2.14	0.023	-0.724	0.004	-2.57	1	-0.064	Y1816_ARATH	Uncharacterized protein At1g08160	At1g08160 T23G18.2 T6D22.24	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Membrane; Reference proteome; Transmembrane; Transmembrane helix
SRR342017_TR10755_c0_g5_i2_len=874	NA	NA	NA	NA	NA	.	0.654	0.162	0.001	-1.141	0.18	0.765	0.086	0.927	1	-0.024	.	.	.	.	.	.	.
SRR342017_TR11246_c0_g1_i1_len=1688	TBB8_ARATH	Q:3-1199,H:28-426	99.5%ID	E:0	Tubulin beta-8 chain	PF00091.22*Tubulin*Tubulin/FtsZ family, GTPase domain*2-184*E:1.4e-55PF03953.14*Tubulin_C*Tubulin C-terminal domain*234-354*E:6.4e-41	0.268	-0.417	0	-1.324	0.849	0.117	0.642	0.234	0.028	-0.721	TBB8_ARATH	Tubulin beta-8 chain (Beta-8-tubulin)	TUBB8 TUB8 At5g23860 MRO11.10	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Cytoplasm; Cytoskeleton; GTP-binding; Microtubule; Nucleotide-binding; Reference proteome
SRR342017_TR11303_c0_g1_i2_len=1532	NA	NA	NA	NA	NA	.	0.497	-0.159	0	-1.558	0.157	-0.353	0.853	-0.05	0.057	-0.609	.	.	.	.	.	.	.
SRR342017_TR11456_c1_g2_i1_len=376	NA	NA	NA	NA	NA	.	0.108	-0.697	0	-2.018	0.356	1.069	0.042	1.827	0.02	-1.15	.	.	.	.	.	.	.
SRR342017_TR11486_c0_g1_i1_len=2734	ICE1_ARATH	Q:969-1862,H:212-462	60.4%ID	E:3e-86	Transcription factor ICE1	PF00010.23*HLH*Helix-loop-helix DNA-binding domain*392-435*E:3.4e-09	0.116	-0.514	0.001	-1.546	0.428	-0.398	0.745	-0.187	0.9	-0.063	ICE1_ARATH	Transcription factor ICE1 (Basic helix-loop-helix protein 116) (AtbHLH116) (bHLH 116) (Inducer of CBF expression 1) (Transcription factor EN 45) (Transcription factor SCREAM) (bHLH transcription factor bHLH116)	SCRM BHLH116 EN45 ICE1 At3g26744 MDJ14.1 MLJ15.14	Arabidopsis thaliana (Mouse-ear cress)		Activator; Alternative splicing; Coiled coil; Complete proteome; DNA-binding; Developmental protein; Isopeptide bond; Nucleus; Reference proteome; Stress response; Transcription; Transcription regulation; Ubl conjugation
SRR342017_TR12047_c0_g1_i1_len=2075	APR1_ARATH	Q:1809-496,H:29-465	75.74%ID	E:0	5'-adenylylsulfate reductase 1, chloroplastic	PF01507.16*PAPS_reduct*Phosphoadenosine phosphosulfate reductase family*115-295*E:6.8e-43PF00355.17*Thioredoxin*Thioredoxin*369-461*E:1.5e-11	0.101	-0.55	0	-2.464	0.002	-0.718	0.089	-0.396	0.563	0.151	APR1_ARATH	5'-adenylylsulfate reductase 1, chloroplastic (EC 1.8.4.9) (3'-phosphoadenosine-5'-phosphosulfate reductase homolog 19) (Prh-19) (Adenosine 5'-phosphosulfate 5'-adenylylsulfate sulfotransferase 1) (APS sulfotransferase 1) (Thioredoxin-independent APS reductase 1)	APR1 PRH19 At4g04610 F4H6.13	Arabidopsis thaliana (Mouse-ear cress)		Activator; Alternative splicing; Coiled coil; Complete proteome; DNA-binding; Developmental protein; Isopeptide bond; Nucleus; Reference proteome; Stress response; Transcription; Transcription regulation; Ubl conjugation
SRR342017_TR12197_c1_g2_i1_len=969	NA	NA	NA	NA	NA	.	0.308	-0.45	0	-1.786	0.84	-0.191	1	0.182	0.341	0.401	.	.	.	.	.	.	.
SRR342017_TR12606_c0_g1_i2_len=1005	NA	NA	NA	NA	NA	.	0.068	-1.245	0	-6.624	0.076	-3.323	0.017	-3.752	0.874	0.205	.	.	.	.	.	.	.
SRR342017_TR13028_c0_g2_i1_len=2002	XTH_TOBAC	Q:1150-260,H:1-295	75.76%ID	E:3e-169	Probable xyloglucan endotransglucosylase/hydrolase protein	PF00722.18*Glyco_hydro_16*Glycosyl hydrolases family 16*35-215*E:2.6e-60PF06955.9*XET_C*Xyloglucan endo-transglycosylase (XET) C-terminus*244-291*E:8.9e-17	0.095	-0.709	0.001	-2.169	0.299	1.444	1	0.558	0.777	-0.124	XTH_TOBAC	Probable xyloglucan endotransglucosylase/hydrolase protein (EC 2.4.1.207)	XTH EXGT	Nicotiana tabacum (Common tobacco)		Apoplast; Cell wall; Cell wall biogenesis/degradation; Disulfide bond; Glycoprotein; Glycosidase; Hydrolase; Secreted; Signal; Transferase
SRR342017_TR13461_c0_g2_i1_len=1207	NA	NA	NA	NA	NA	.	0.002	-0.78	0	-1.598	0.736	-0.148	0.752	0.146	0.17	-0.347	.	.	.	.	.	.	.
SRR342017_TR14859_c2_g2_i1_len=1916	STP9_SPIOL	Q:1811-645,H:1-387	81.63%ID	E:0	Sedoheptulose-1,7-bisphosphatase, chloroplastic	PF00316.17*FBPase*Fructose-1-6-bisphosphatase, N-terminal domain*104-280*E:8.3e-58	0.915	-0.032	0.002	-0.798	0.002	-0.677	0.037	-0.442	0.611	0.115	STP9_SPIOL	Sedoheptulose-1,7-bisphosphatase, chloroplastic (EC 3.1.3.37) (SED(1,7)P2ase) (Sedoheptulose bisphosphatase) (SBPase)	Spinacia oleracea (Spinach)	PATHWAY: Carbohydrate biosynthesis; Calvin cycle.		Calvin cycle; Carbohydrate metabolism; Chloroplast; Disulfide bond; Hydrolase; Magnesium; Metal-binding; Plastid; Transit peptide
SRR342017_TR15341_c2_g8_i5_len=1275	C72A1_CATRO	Q:1274-843,H:380-523	99.31%ID	E:1e-94	Secologanin synthase	PF00067.19*p450*Cytochrome P450*1-118*E:2.9e-39	1	0.221	0	-3.798	1	0	1	0	1	-1.15	0.802	0.126	C72A1_CATRO	Secologanin synthase (SLS) (EC 1.3.3.9) (CYPLXXI) (Cytochrome P450 *21A1)	CYP72A1 CYP72 P450CR3	Catharanthus roseus (Madagascar periwinkle) (Vinca rosea)	PATHWAY: Alkaloid biosynthesis; secologanin biosynthesis.	Alkaloid metabolism; Heme; Iron; Membrane; Metal-binding; Monooxygenase; NADP; Oxidoreductase; Transmembrane; Transmembrane helix; Vacuole
SRR342017_TR16388_c0_g1_i2_len=847	PSAG_ARATH	Q:191-613,H:27-160	72.34%ID	E:7e-67	Photosystem I reaction center subunit V, chloroplastic	PF10241.15*PSI_PSAK*Photosystem I psaG / psaK*53-144*E:2.5e-26	0.288	0.251	0	-1.58	0.04	-0.453	0.232	-0.261	0	1.027	PSAG_ARATH	Photosystem I reaction center subunit V, chloroplastic (PSI-G)	PSAG At1g55670 F20N2.21 F20N2.33 F20N2_3	Arabidopsis thaliana (Mouse-ear cress)		Chloroplast; Complete proteome; Membrane; Photosynthesis; Photosystem I; Plastid; Reference proteome; Thylakoid; Transit peptide; Transmembrane; Transmembrane helix
SRR342017_TR17640_c0_g2_i1_len=718	NA	NA	NA	NA	NA	.	0.142	-0.851	0	-6.69	0.629	-1.321	1	-0.978	0.452	-0.587	.	.	.	.	.	.	.
SRR342017_TR18200_c0_g1_i1_len=1852	CB22_TOBAC	Q:1079-285,H:1-265	93.96%ID	E:1e-179	Chlorophyll a/b binding protein 21, chloroplastic	PF00504.18*Chloroa_b-bind*Chlorophyll A/B binding protein*65-231*E:1.6e-50	0.034	-0.771	0	-2.14	0.255	-0.443	0.003	-1.238	0.369	0.349	CB22_TOBAC	Chlorophyll a/b binding protein 21, chloroplastic (LHCII type I CAB-21) (LHCP)	CAB21	Nicotiana tabacum (Common tobacco)		Acetylation; Chlorophyll; Chloroplast; Chromophore; Magnesium; Membrane; Metal-binding; Phosphoprotein; Photosynthesis; Photosystem I; Photosystem II; Plastid; Thylakoid; Transit peptide; Transmembrane; Transmembrane helix
SRR342017_TR18577_c0_g2_i20_len=1972	FKB65_ARATH	Q:140-1762,H:40-558	49.37%ID	E:9e-176	Peptidyl-prolyl cis-trans isomerase FKBP65	PF00254.25*FKBP_C*FKBP-type peptidyl-prolyl cis-trans isomerase*68-157*E:1.7e-31	0.318	-0.456	0	-2.938	1	0.15	1	-0.063	0.93	-0.057	FKB65_ARATH	Peptidyl-prolyl cis-trans isomerase FKBP65 (PPIase FKBP65) (EC 5.2.1.8) (70 kDa peptidyl-prolyl isomerase) (PK506-binding protein 65) (AtKBP65) (Immunophilin FKBP65) (Peptidyl-prolyl isomerase ROF2) (Protein ROTAMASE FKBP 2) (Rotamase)	FKBP65 ROF2 At5g48570 K15N18.12	Arabidopsis thaliana (Mouse-ear cress)		Acetylation; Calmodulin-binding; Chaperone; Complete proteome; Cytoplasm; Isomerase; Nucleus; Reference proteome; Repeat; TPR repeat
SRR342017_TR18632_c0_g4_i1_len=539	MAN5_ARATH	Q:455-165,H:337-431	55.67%ID	E:9e-30	Mannan endo-1,4-beta-mannosidase 5	.	1	0	0	-7.414	1	0	1	0	1	0	MAN5_ARATH	Mannan endo-1,4-beta-mannosidase 5 (EC 3.2.1.78) (Beta-mannanase 5) (Endo-beta-1,4-mannanase 5) (AtMAN5)	MAN5 At4g28320 F26K10.200	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Glycoprotein; Glycosidase; Hydrolase; Reference proteome; Secreted; Signal
SRR342017_TR19031_c4_g5_i1_len=963	NA	NA	NA	NA	NA	.	0.326	-0.53	0	-1.762	1	0.043	0.763	0.216	1	-0.167	.	.	.	.	.	.	.
SRR342017_TR19163_c0_g3_i2_len=1129	APA1_ARATH	Q:1126-50,H:121-481	65.1%ID	E:2e-175	Aspartic proteinase A1	PF00026.20*Asp*Eukaryotic aspartyl protease*3-356*E:8.9e-90PF03489.14*SapB_2*Saposin-like type B, region 2*197-229*E:8.4e-13PF05184.12*SapB_1*Saposin-like type B, region 1*259-295*E:1.5e-12	0.36	0.302	0	-1.475	0.11	0.586	0.279	-0.262	1	0.6	APA1_ARATH	Aspartic proteinase A1 (EC 3.4.23.-)	APA1 PRA1 At1g11910 F12F1.24	Arabidopsis thaliana (Mouse-ear cress)		Aspartyl protease; Complete proteome; Disulfide bond; Glycoprotein; Hydrolase; Protease; Reference proteome; Repeat; Signal; Vacuole; Zymogen
SRR342017_TR19173_c0_g1_i1_len=1674	ROC4_NICSY	Q:240-1253,H:1-312	59.82%ID	E:6e-96	31 kDa ribonucleoprotein, chloroplastic	PF00076.19*RRM_1*RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)*162-231*E:1.3e-20PF00076.19*RRM_1*RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)*256-326*E:3.3e-22	0.032	-0.478	0	-0.784	0.755	-0.083	0.292	0.262	0.94	-0.019	ROC4_NICSY	31 kDa ribonucleoprotein, chloroplastic	Nicotiana sylvestris (Wood tobacco) (South American tobacco)	Arabidopsis thaliana (Mouse-ear cress)		Chloroplast; Direct protein sequencing; Plastid; RNA-binding; Repeat; Ribonucleoprotein; Transit peptide; mRNA processing
SRR342017_TR19201_c0_g1_i1_len=1082	ATPX_SPIOL	Q:725-288,H:77-222	80.82%ID	E:2e-63	ATP synthase subunit b', chloroplastic	PF00430.15*ATP-synt_B*ATP synthase B/B' CF(0)*92-220*E:1.7e-14PF01402.15*Apolipoprotein*Apolipoprotein A1/A4/E domain*125-164*E:20PF01402.15*Apolipoprotein*Apolipoprotein A1/A4/E domain*129-218*E:0.13	1	0	0	-2.431	0.252	-0.535	0.438	-0.365	1	0	ATPX_SPIOL	ATP synthase subunit b', chloroplastic (ATP synthase F(0) sector subunit b') (ATPase subunit II)	ATPG	Spinacia oleracea (Spinach)		ATP-binding; CF(0); Chloroplast; Direct protein sequencing; Hydrogen ion transport; Ion transport; Membrane; Nucleotide-binding; Plastid; Thylakoid; Transit peptide; Transmembrane; Transmembrane helix; Transport
SRR342017_TR19621_c2_g1_i3_len=1883	AMI1_ARATH	Q:218-1546,H:1-421	60.94%ID	E:2e-162	Amidase 1	PF01425.18*Amidase*Amidase*9-462*E:1.2e-19PF01425.18*Amidase*Amidase*210-296*E:1.2e-05	0.628	-0.637	0.017	-5.787	0.419	-0.377	AMI1_ARATH	Amidase 1 (AMAM1) (EC 3.5.1.4) (Translocon at the outer membrane of chloroplasts 64-I) (ATOC64-I)	AMI1 TOC64-I At1g08980 F7G19.15	Arabidopsis thaliana (Mouse-ear cress)		Acetylation; Auxin biosynthesis; Complete proteome; Cytoplasm; Hydrolase; Reference proteome
SRR342017_TR19664_c0_g1_i1_len=2119	CXE17_ARATH	Q:1698-766,H:28-339	35.19%ID	E:6e-57	Probable carboxylesterase 17	PF10340.6*DUF2424*Protein of unknown function (DUF2424)*31-200*E:1.8e-07PF00135.25*Coesterase*Carboxylesterase family*58-165*E:1.5e-06PF07859.10*Abhydrolase_3*alpha/beta hydrolase fold*71-289*E:3.4e-48	0.558	-0.224	0.001	-1.184	1	0.409	1	0.563	0.918	-0.093	CXE17_ARATH	Probable carboxylesterase 17 (AtCXE17) (EC 3.1.1.1)	CXE17 At5g16080 F1N13.220	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Hydrolase; Reference proteome; Serine esterase
SRR342017_TR20102_c2_g4_i1_len=752	PER42_ARATH	Q:7-330,H:223-330	87.04%ID	E:7e-60	Peroxidase 42	PF00141.20*peroxidase*Peroxidase*18-71*E:1.4e-09	0.261	0.391	0	-4.343	0.086	0.965	0.564	-0.522	0.099	0.363	PER42_ARATH	Peroxidase 42 (Atperox P42) (EC 1.11.1.7) (ATP1a/ATP1b) (PRXR1)	PER42 P42 At4g21960 F1N20.3 T8O5.170	Arabidopsis thaliana (Mouse-ear cress)		Biological rhythms; Calcium; Complete proteome; Disulfide bond; Glycoprotein; Heme; Hydrogen peroxide; Iron; Metal-binding; Oxidoreductase; Peroxidase; Reference proteome; Secreted; Signal
SRR342017_TR20586_c0_g4_i1_len=1413	PMA1_NICPL	Q:1031-291,H:71-457	92.31%ID	E:4e-128	Plasma membrane ATPase 1	PF14225.3*Rhetorican_gag_2*gag-polypeptide of LTR copia-type*59-187*E:7e-34PF00098.20*zf-CCHC*Zinc knuckle*227-242*E:0.00234PF13976.3*gag_pre-integrase*GAG pre-integrase domain*397-464*E:1.3e-14PF08665.23*rve*Integrase core domain*480-594*E:2.5e-26	0.747	-0.104	0	-1.346	0.651	-0.17	0.126	-0.507	0.034	-0.582	PMA1_NICPL	Plasma membrane ATPase 1 (EC 3.6.3.6) (Proton pump 1)	PMA1	Nicotiana plumbaginifolia (Leadworts-leved tobacco) (Tex-Mex tobacco)		ATP-binding; Cell membrane; Hydrogen ion transport; Hydrolase; Ion transport; Magnesium; Membrane; Metal-binding; Nucleotide-binding; Phosphoprotein; Transmembrane; Transmembrane helix; Transport
SRR342017_TR20775_c0_g1_i1_len=588	TLP14_ORYSJ	Q:538-293,H:365-445	79.27%ID	E:1e-33	Tubby-like F-box protein 14	.	1	0	0	-8.161	0.034	-5.565	0.034	-5.565	1	0	TLP14_ORYSJ	Tubby-like F-box protein 14 (OsTLP14) (Tubby-like F-box protein 4) (OsTLP4)	TULP14 TULP4 Os12g0163400 LOC_Os12g08630 Osj_033954	Oryza sativa subsp. japonica (Rice)		Complete proteome; Reference proteome
SRR342017_TR21338_c0_g1_i1_len=550	NA	NA	NA	NA	NA	.	0.951	-0.034	0	-1.398	0.793	-0.098	0.64	-0.182	0.027	-0.665	.	.	.	.	.	.	.
SRR342017_TR21756_c0_g1_i5_len=1453	NA	NA	NA	NA	NA	.	0.587	-0.268	0	-1.675	0.079	-1.073	0.004	-1.966	0.708	-0.182	.	.	.	.	.	.	.
SRR342017_TR22056_c0_g1_i3_len=484	NA	NA	NA	NA	NA	.	0.253	-0.367	0	-1.479	0.627	-0.166	0.954	0.046	0.311	-0.396	.	.	.	.	.	.	.
SRR342017_TR25020_c2_g3_i1_len=763	NA	NA	NA	NA	NA	.	0.126	-0.375	0	-1.923	0.239	-1.273	0.239	-1.45	0.3	0.238	.	.	.	.	.	.	.
SRR342017_TR25222_c0_g2_i1_len=1299	NA	NA	NA	NA	NA	.	0.548	0.227	0	-1.474	0.635	0.354	0.87	0.258	0	1.031	.	.	.	.	.	.	.
SRR342017_TR25892_c2_g4_i6_len=4889	POLX_TOBAC	Q:4888-3482,H:858-1323	55.65%ID	E:1e-150	Retrovirus-related Pol polyprotein from transposon TNT 1-94	PF04949.10*Transcrip_act*Transcriptional activator*23-170*E:1.6e-74	0	-4.536	0	-1.503	0	1.941	0	1.869	0	3.153	POLX_TOBAC	Retrovirus-related Pol polyprotein from transposon TNT 1-94 [Includes: Protease (EC 3.4.23.-); Reverse transcriptase (EC 2.7.7.49); Endonuclease]	Nicotiana tabacum (Common tobacco)			Endonuclease; Hydrolase; Metal-binding; Nuclease; Nucleotidyltransferase; Protease; RNA-directed DNA polymerase; Transferase; Transposable element; Zinc; Zinc-finger
SRR342017_TR26233_c2_g8_i2_len=1347	GTOMC_ORYSJ	Q:169-1017,H:75-357	44.01%ID	E:6e-83	Probable tocopherol O-methyltransferase, chloroplastic	PF13489.3*Methyltransf_23*Methyltransferase domain*49-173*E:2.1e-14PF01209.15*Ubie_methyltran*ubiE/COQ5 methyltransferase family*64-178*E:1.9e-10PF13847.3*Methyltransf_31*Methyltransferase domain*68-174*E:1.6e-11PF13649.3*Methyltransf_25*Methyltransferase domain*70-165*E:5.2e-10PF08242.9*Methyltransf_12*Methyltransferase domain*72-166*E:1.2e-12PF00702.23*Hydrolase*haloacid dehalogenase-like hydrolase*69-267*E:1.4e-15PF13419.3*HAD_2*Haloacid dehalogenase-like hydrolase*91-274*E:5.9e-28PF13242.3*Hydrolase_like*HAD-hydrolase-like*231-295*E:2.5e-05PF10436.18*NHL*NHL repeat*625-652*E:4.2e-07PF00665.24*Sulfotransfer_1*Sulfotransferase domain*3-69*E:2.2e-08	0.029	0.473	0	-0.964	1	-0.006	0.002	-0.742	0.043	0.438	GTOMC_ORYSJ	Probable tocopherol O-methyltransferase, chloroplastic (EC 2.1.1.95) (Gamma-tocopherol methyltransferase) (Vitamin E pathway gene 4 protein)	VTE4 G-TMT TMT Os02g0701600 LOC_Os02g47310 OJ1111_E07.25	Oryza sativa subsp. japonica (Rice)	PATHWAY: Cofactor biosynthesis; tocopherol biosynthesis.	Chloroplast; Complete proteome; Membrane; Photosynthesis; Photosystem I; Plastid; Reference proteome; Thylakoid; Transit peptide; Transmembrane; Transmembrane helix; Transport
SRR342017_TR26436_c1_g4_i10_len=3559	NHLC2_BOVIN	Q:1359-3203,H:32-708	35.79%ID	E:3e-112	NHL repeat-containing protein 2	PF01185.16*CR51_Yhb1*CR51 / Yhb1 (CRM) domain*131-211*E:7.6e-16	0.18	-0.816	0.001	-1.799	1	-0.264	0.822	0.238	0.472	-0.311	NHLC2_BOVIN	NHL repeat-containing protein 2	NHLRC2	Bos taurus (Bovine)		Complete proteome; Reference proteome; Repeat
SRR342017_TR27170_c0_g1_i1_len=709	NA	NA	NA	NA	NA	.	0.544	-0.205	0	-2.399	0.03	-1.136	0.001	-1.241	0.395	-0.595	.	.	.	.	.	.	.
SRR342017_TR27230_c0_g1_i1_len=711	NA	NA	NA	NA	NA	.	0.159	-0.45	0	-4.132	0.163	-0.659	0.007	-1.504	0.76	-0.098	.	.	.	.	.	.	.
SRR342017_TR27610_c0_g1_i1_len=1163	MDHG_CITLA	Q:1118-129,H:28-355	72.37%ID	E:2e-162	Malate dehydrogenase, glyoxysomal	PF00056.20*Ldh_1_N*lactate/malate dehydrogenase, NAD binding domain*1-126*E:3.1e-28PF02866.15*Ldh_1_C*lactate/malate dehydrogenase, alpha/beta C-terminal domain*128-295*E:2.7e-41PF01370.18*Epimerase*NAD dependent epimerase/dehydratase family*17-287*E:1.2e-59PF03435.15*Sacchrop_dh_NAD*Saccharopine dehydrogenase NAD* binding domain*17-94*E:9.3e-07PF01073.16*3Beta_HSD*3-beta hydroxysteroid dehydrogenase/isomerase family*19-142*E:8.6e-07PF16363.2*GDP_Man_Dehyd*GDP-mannose 4,6 dehydratase*21-362*E:1.4e-30	0.249	-0.49	0	-2.237	0.517	0.815	1	0.452	1	0	MDHG_CITLA	Malate dehydrogenase, glyoxysomal (EC 1.1.1.37)	Citrullus lanatus (Watermelon) (Citrullus vulgaris)	Arabidopsis thaliana (Mouse-ear cress)		3D-structure; Direct protein sequencing; Glyoxylate bypass; Glyoxysome; NAD; Oxidoreductase; Peroxisome; Transit peptide; Tricarboxylic acid cycle
SRR342017_TR28770_c2_g3_i3_len=2469	AXS2_ARATH	Q:1477-323,H:5-389	90.13%ID	E:0	UDP-D-apiose/UDP-D-xylose synthase 2	.	1	1.628	0	-6.984	0.524	0.582	1	0.194	0.502	-4.349	AXS2_ARATH	UDP-D-apiose/UDP-D-xylose synthase 2	AXS2 At1g08200 T23G18.6	Arabidopsis thaliana (Mouse-ear cress)		Cell wall biogenesis/degradation; Complete proteome; Cytoplasm; NAD; Reference proteome
SRR342017_TR29077_c0_g1_i2_len=569	PIP28_ARATH	Q:549-301,H:196-278	93.98%ID	E:2e-46	Probable aquaporin PIP2-8	.	0.552	0.229	0	-4.658	0.826	-0.135	0.917	0.099	0.02	-0.636	PIP28_ARATH	Probable aquaporin PIP2-8 (Plasma membrane intrinsic protein 2-8) (AtPIP2;8) (Plasma membrane intrinsic protein 3b) (PIP3b)	PIP2-8 PIP3B At2g16850 F12A24.3	Arabidopsis thaliana (Mouse-ear cress)		Cell membrane; Complete proteome; Membrane; Phosphoprotein; Reference proteome; Repeat; Transmembrane; Transmembrane helix; Transport
SRR342017_TR30559_c0_g5_i1_len=820	RLF33_ARATH	Q:649-317,H:1-115	54.05%ID	E:4e-29	Protein RALF-like 33	PF05498.8*RALF*Rapid ALkalinization Factor (RALF)*106-168*E:4.1e-29	0.161	-0.385	0	-1.572	0.055	-0.527	0.017	-0.663	0.461	-1.367	RLF33_ARATH	Protein RALF-like 33	RALFL33 At4g15800 dl3940c FCAALL.206	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Disulfide bond; Glycoprotein; Hormone; Reference proteome; Secreted; Signal
SRR342017_TR31242_c0_g1_i1_len=720	NA	NA	NA	NA	NA	.	0.407	-0.466	0.001	-1.721	0.505	0.447	0.729	0.263	0.041	-0.91	.	.	.	.	.	.	.
SRR342017_TR31253_c0_g2_i1_len=1608	ALIS5_ARATH	Q:288-1331,H:21-345	56.9%ID	E:5e-133	ALA-interacting subunit 5	.	0.87	-0.225	0	-2.628	0.798	-0.539	0.402	-0.888	0.874	-0.204	ALIS5_ARATH	ALA-interacting subunit 5 (AtALIS5)	ALIS5 At1g79450 T8K14.13	Arabidopsis thaliana (Mouse-ear cress)		Acetylation; Alternative splicing; Complete proteome; Endoplasmic reticulum; Golgi apparatus; Membrane; Reference proteome; Transmembrane; Transmembrane helix
SRR342017_TR31736_c3_g3_i1_len=819	DADIS_PANGI	Q:492-307,H:699-760	91.94%ID	E:1e-30	Dammarenediol II synthase	.	0.889	0.086	0	-1.955	0.025	-1.436	0.013	-1.617	0.803	-0.165	DADIS_PANGI	Dammarenediol II synthase (EC 4.2.1.125)	PNA DDS	Panax ginseng (Korean ginseng)		Isomerase; Lyase; Membrane; Repeat; Transmembrane; Transmembrane helix
SRR342019_TR1230_c0_g2_i2_len=2630	EF3P_SYNP2	Q:300-848,H:2-184	59.56%ID	E:2e-69	Elongation factor P (EC0:0000255|HAMAP-Rule:MF_00141)	PF17177.1*PPR_long*Pentacotripeptide-repeat region of PROPR*132-243*E:6.2e-10PF13041.3*PPR_2*PPR repeat family*142-191*E:4.8e-13PF01535.17*PPR*PPR repeat*145-175*E:0.00064PF13812.3*PPR_3*Pentatricopeptide repeat domain*166-222*E:4.6e-16PF12854.4*PPR_1*PPR repeat*194-209*E:1.1e-13PF13041.3*PPR_2*PPR repeat family*177-225*E:4.8e-19PF01535.17*PPR*PPR repeat*181-210*E:2.1e-08PF12854.4*PPR_1*PPR repeat*209-238*E:8.9e-10PF13041.3*PPR_2*PPR repeat family*223-271*E:2.5e-16PF01535.17*PPR*PPR repeat*216-242*E:0.0047PF13812.3*PPR_3*Pentatricopeptide repeat domain*236-294*E:4.1e-08PF12854.4*PPR_1*PPR repeat*246-274*E:2.6e-10PF13041.3*PPR_2*PPR repeat family*247-296*E:1.9e-14PF01535.17*PPR*PPR repeat*250-280*E:1.1e-07PF12854.4*PPR_1*PPR repeat*278-311*E:7.2e-07PF13041.3*PPR_2*PPR repeat family*282-331*E:3e-15PF01535.17*PPR*PPR repeat*285-315*E:3.1e-07PF13812.3*PPR_3*Pentatricopeptide repeat domain*306-349*E:0.00024PF13041.3*PPR_2*PPR repeat family*317-366*E:5.2e-10PF01535.17*PPR*PPR repeat*320-350*E:0.0015	0.034	-1.185	0	-2.218	0.593	-0.63	0.402	-0.984	0.736	-0.145	EF3P_SYNP2	Elongation factor P (EF-P)	e	p SYNPCC7002_A0053	Synechococcus sp. (strain ATCC 27264 / PCC 7002 / PR-6) (Agmenellum quadruplicatum)	PATHWAY: Protein biosynthesis; polypeptide chain elongation. (ECO:0000255|HAMAP-Rule:MF_00141).	Complete proteome; Cytoplasm; Elongation factor; Protein bi

SRR342029_TR35308_c7_g9_i6_len=3747	LHTL8_ARATH	Q:1944-3509,H:1-517	89.87%ID	E:0	Lysine histidine transporter-like 8	PF00332.15*Glyco_hydro_17*Glycosyl hydrolases family 17*59-378*E:2.2e-78*PF07883.10*X8*X8 domain*396-467*E:2.2e-21	0.275	-0.386	0	-2.114	0.282	1.174	0.692	-0.96	1	0 LHTL8_ARATH	Lysine histidine transporter-like 8 (Amino acid transporter-like protein 1)	AATL1 At1g47670 F16N3.4	Arabidopsis thaliana (Mouse-ear cress)	Amino-acid transport; Cell membrane; Complete proteome; Membrane; Reference proteome; Transmembrane; Transmembrane helix; Transport
SRR342029_TR35455_c0_g1_i2_len=670	NA	NA	NA	NA	NA	-	0.151	-0.372	0	-2.004	0.926	-0.032	0.685	-0.104	1	1.672 -	-	-	-	-
SRR342029_TR36508_c0_g3_i1_len=975	DNAJ8_ARATH	Q:516-767,H:55-137	64.71%ID	E:6e-29	Chaperone protein dnaJ 8, chloroplastic	PF00226.28*DnaJ*DnaJ domain*43-96*E:2.1e-15	1	-0.806	0	-5.83	0	2.313	0	1.3	1	1.373 DNAJ8_ARATH	Chaperone protein dnaJ 8, chloroplastic (AtDjC8) (AJ8)	ATJ8 C8 J8 At1g80920 F23A5.28	Arabidopsis thaliana (Mouse-ear cress)	Chaperone; Chloroplast; Complete proteome; Plastid; Reference proteome; Transit peptide
SRR342029_TR36688_c0_g2_i4_len=734	RS12_HORVU	Q:215-586,H:20-143	83.06%ID	E:2e-61	40S ribosomal protein S12	PF01248.23*Ribosomal_L7Ae*Ribosomal protein L7Ae/L30e/S12e/Gad045 family*27-120*E:1.9e-26	1	0	0	-7.844	0.86	0.27	0.545	-0.544	1	0 RS12_HORVU	40S ribosomal protein S12	RPS12	Hordeum vulgare (Barley)	Ribonucleoprotein; Ribosomal protein
SRR342029_TR37672_c0_g1_i1_len=973	NA	NA	NA	NA	NA	-	0.28	-0.313	0	-1.504	1	0.034	0.233	0.444	0.005	-0.632 -	-	-	-	-
SRR342029_TR39291_c0_g1_i9_len=2822	AMSH2_ARATH	Q:639-187,H:1-223	64.24%ID	E:8e-64	AMSH-like ubiquitin thioesterase 2	-	1	0.023	0	-1.889	0.147	-0.93	0.214	-0.809	1	1.405 AMSH2_ARATH	AMSH-like ubiquitin thioesterase 2 (EC 3.4.19.-) (Deubiquitinating enzyme AMSH2)	AMSH2 At1g10600 F20B24.2 T10O24.25	Arabidopsis thaliana (Mouse-ear cress)	-
SRR342029_TR1145_c0_g3_i5_len=1370	HACD2_BOVIN	Q:1246-749,H:37-201	36.14%ID	E:9e-26	Very long-chain (3R)-3-hydroxyacyl-CoA dehydratase 2 (ECO:0000305)	PF04387.11*PTPLA*Protein tyrosine phosphatase-like protein, PTPLA*52-210*E:2.4e-43	0.004	-0.962	0	-1.841	0.142	-0.817	0.326	-0.523	0.16	-0.524 HACD2_BOVIN	Very long-chain (3R)-3-hydroxyacyl-CoA dehydratase 2 (EC 4.2.1.134) (3-hydroxyacyl-CoA dehydratase 2) (HACD2) (Protein-tyrosine phosphatase-like member B)	HACD2 PTPLB	Bos taurus (Bovine)	PATHWAY: Lipid metabolism; fatty acid biosynthesis. (ECO:0000250)UniProtKB:Q6Y1H2).
SRR342029_TR1495_c0_g1_i1_len=1000	CB23_SOLLC	Q:307-819,H:95-265	95.32%ID	E:4e-113	Chlorophyll a-b binding protein 13, chloroplastic	PF00504.18*Chloroa_b-bind*Chlorophyll A-B binding protein*1-128*E:9.8e-30	0.503	-0.208	0	-1.111	0.002	-0.784	0.065	-0.451	0.181	0.282 CB23_SOLLC	Chlorophyll a-b binding protein 13, chloroplastic (LHCII type III CAB-13)	CAB13 LHBC1	Solanum lycopersicum (Tomato) (Lycopersicon esculentum)	Chlorophyll; Chloroplast; Chromophore; Complete proteome; Direct protein sequencing; Magnesium; Membrane; Metal-binding; Phosphoprotein; Photosynthesis; Photosystem I; Photosystem II; Plastid; Reference proteome; Thylakoid; Transit peptide; Transmembrane; Transmembrane helix
SRR342029_TR351_c0_g1_i1_len=1274	NA	NA	NA	NA	NA	-	0.76	-0.682	0	-2.824	1	-0.079	1	-1.22	1	0.774 -	-	-	-	-
SRR342029_TR895_c1_g4_i1_len=1434	TOC34_PEA	Q:177-1070,H:6-302	72.82%ID	E:2e-154	Translocase of chloroplast 34	PF03189.13*DUF258*Protein of unknown function, DUF258*24-97*E:1.9e-08 PF04548.13*AIG1*AIG1 family*38-228*E:2.4e-20 PF03193.13*DUF261*Plant and archaea inner membrane protein with unknown function*8-139*E:2.1e-21 PF01926.20*MMR_HSR1*50S ribosome-binding GTPase*40-142*E:2.1e-12	0.004	-0.873	0	-1.413	0.832	-0.26	1	0.087	0.207	-0.378 TOC34_PEA	Translocase of chloroplast 34 (EC 3.6.5.-) (34 kDa chloroplast outer envelope protein) (GTP-binding protein IAP34) (GTP-binding protein OEP34)	TOC34 IAP34 OEP34	Pisum sativum (Garden pea)	3D-structure; Chloroplast; Complete proteome; Direct protein sequencing; GTP-binding; Hydrolase; Membrane; Nucleotide-binding; Plastid; Plastid outer membrane; Protein transport; Transmembrane; Transmembrane helix; Transport
SRR342029_TR985_c7_g1_i1_len=651	RCA_MALDO	Q:599-366,H:359-436	76.92%ID	E:4e-35	Ribulose bisphosphate carboxylase/oxygenase activase, chloroplastic	-	0.059	-0.615	0	-2.092	0.121	0.329	0.945	0.016	0.012	-0.61 RCA_MALDO	Ribulose bisphosphate carboxylase/oxygenase activase, chloroplastic (RA) (RuBisCO activase)	RCA	Malus domestica (Apple) (Pyrus malus)	ATP-binding; Chloroplast; Nucleotide-binding; Plastid; Transit peptide
SRR342029_TR1215_c4_g12_i1_len=2882	AVP_VIGRR	Q:156-2462,H:1-766	90.9%ID	E:0	Pyrophosphate-energized vacuolar membrane proton pump	PF03030.13*H_PPase*Inorganic H+ pyrophosphatase*21-754*E:8.5e-260	1	0.059	0	-1.414	0.89	0.074	0.89	0.081	0.228	0.98 AVP_VIGRR	Pyrophosphate-energized vacuolar membrane proton pump (EC 3.6.1.1) (Pyrophosphate-energized inorganic pyrophosphatase) (Vacuolar H+-pyrophosphatase)	VIGRR AVP1	Vigna radiata var. radiata (Mung bean) (Phaseolus aureus)	3D-structure; Direct protein sequencing; Disulfide bond; Hydrogen ion transport; Hydrolase; Ion transport; Magnesium; Membrane; Metal-binding; Transmembrane; Transmembrane helix; Transport; Vacuole
SRR342029_TR1398_c0_g1_i1_len=2667	MFP1_TOBAC	Q:237-2252,H:1-690	52.88%ID	E:0	MAR-binding filamentlike protein 1-1	-	0.216	-0.387	0	-1.385	0.095	-0.614	0.436	-0.298	0.176	0.439 MFP1_TOBAC	MAR-binding filamentlike protein 1-1	MFP1-1	Nicotiana tabacum (Common tobacco)	Coiled coil; DNA-binding; Nucleus
SRR342029_TR1434_c0_g1_i1_len=1884	NA	NA	NA	NA	NA	-	0.35	-0.61	0	-3.346	0.004	-2.421	0.004	-2.477	0.712	-0.135 -	-	-	-	-
SRR342029_TR1885_c0_g1_i3_len=522	MCCB_ARATH	Q:471-232,H:508-587	68.75%ID	E:3e-29	Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial	-	1	0	0.001	-1.904	1	0	1	0	1	0 MCCB_ARATH	Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial (MCCase subunit beta) (EC 6.4.1.4) (3-methylcrotonoyl-CoA carboxylase 2) (3-methylcrotonoyl-CoA:carbon dioxide ligase subunit beta)	MCCB At4g34030 F17I5.220 F28A23.210	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Amino-acid degradation; L-leucine degradation; (S)-3-hydroxy-3-methylglutaryl-CoA from 3-isovaleryl-CoA; step 2/3.
SRR342029_TR2238_c7_g1_i10_len=2909	FPG_ARATH	Q:138-1016,H:1-294	79.25%ID	E:5e-148	Formamidopyrimidine-DNA glycosylase	PF01149.21*Fapy_DNA_glyco*Formamidopyrimidine-DNA glycosylase N-terminal domain*1-131*E:2.2e-28 PF06831.11*H2TH*Formamidopyrimidine-DNA glycosylase H2TH domain*146-235*E:3.5e-29	1	-1.49	0	-6.199	0.216	-2.629	0.016	-2.287	1	0 FPG_ARATH	Formamidopyrimidine-DNA glycosylase (Fapy-DNA glycosylase) (EC 3.2.2.23) (EC 4.2.99.18) (DNA-(apurinic or apyrimidinic site) lyase FPG1) (Formamidopyrimidine-DNA glycosylase 1) (AtFPG-1) (Formamidopyrimidine-DNA glycosylase 2) (AtFPG-2) (Protein MutM homolog 1) (AtMMH-1) (Protein MutM homolog 2) (AtMMH-2)	FPG1 FPG2 At1g52500 F6D8.28	Arabidopsis thaliana (Mouse-ear cress)	3D-structure; Alternative splicing; Complete proteome; DNA damage; DNA repair; DNA-binding; Glycosidase; Hydrolase; Lyase; Multifunctional enzyme; Nucleus; Reference proteome
SRR342029_TR2436_c1_g9_i7_len=1121	EXPA4_ARATH	Q:1120-563,H:72-257	89.25%ID	E:6e-121	Expansin-A4	PF03330.15*DPBB_1*Lytic transglycolase*1-82*E:1.4e-19 PF01357.18*Pollen_allerg_1*Pollen allergen*93-170*E:9.3e-25	0.796	-0.082	0	-2.513	1	0.061	0.169	-0.62	1	-0.016 EXPA4_ARATH	Expansin-A4 (AtEXPA4) (Alpha-expansin-4) (Alt-EXP4) (AtEx4) (Alth-Exp Alpha-1.6)	EXPA4 EXP4 At2g39700 F17A14.7	Arabidopsis thaliana (Mouse-ear cress)	Cell wall; Cell wall biogenesis/degradation; Complete proteome; Direct protein sequencing; Disulfide bond; Membrane; Reference proteome; Secreted; Signal
SRR342029_TR2829_c1_g3_i17_len=3033	Y3471_ARATH	Q:2332-1588,H:347-588	48.57%ID	E:2e-67	Putative receptor-like protein kinase At3g47110	PF00560.30*LRR_1*Leucine Rich Repeat*47-69*E:1.1 PF13855.3*LRR_8*Leucine rich repeat*71-131*E:1.7e-09 PF00560.30*LRR_1*Leucine Rich Repeat*75-93*E:0.089 PF13855.3*LRR_8*Leucine rich repeat*93-108*E:0.34 PF00560.30*LRR_1*Leucine Rich Repeat*95-113*E:0.024 PF13855.3*LRR_8*Leucine rich repeat*122-177*E:2.6e-06 PF00560.30*LRR_1*Leucine Rich Repeat*168-189*E:0.18 PF00560.30*LRR_1*Leucine Rich Repeat*194-214*E:0.41	0.763	-0.225	0	-2.762	0.001	-1.016	0.001	-1.025	0.173	-0.674 Y3471_ARATH	Putative receptor-like protein kinase At3g47110 (EC 2.7.11.1)	At3g47110 F13I12.160	Arabidopsis thaliana (Mouse-ear cress)	-
SRR342029_TR2901_c4_g1_i6_len=897	NA	NA	NA	NA	NA	-	1	0	0.001	-1.653	0.679	0.48	1	-0.184	1	0 -	-	-	-	-
SRR342029_TR3295_c2_g6_i3_len=825	NA	NA	NA	NA	NA	-	0.114	-0.421	0	-1.009	0.05	-0.582	0.146	-0.423	0.527	0.152 -	-	-	-	-
SRR342029_TR4532_c1_g6_i1_len=922	RK35_SPIOL	Q:259-549,H:6-158	73.74%ID	E:7e-29	50 ribosomal protein L35, chloroplastic	PF01632.16*Ribosomal_L35p*Ribosomal protein L35*83-139*E:4.3e-20	0.018	-0.544	0	-0.873	0.007	-0.618	0.114	-0.357	0.056	-0.428 RK35_SPIOL	50S ribosomal protein L35, chloroplastic (CL35)	RPL35	Spinacia oleracea (Spinach)	3D-structure; Chloroplast; Direct protein sequencing; Plastid; Ribonucleoprotein; Ribosomal protein; Transit peptide
SRR342029_TR4639_c0_g1_i16_len=3762	PHOT1_ARATH	Q:428-3502,H:3-996	69.84%ID	E:0	Phototropin-1	PF13426.4*PAS_9*PAS domain*215-311*E:1.5e-20 PF00989.22*PAS*PAS fold*221-306*E:1.7e-08 PF08447.9*PAS_3*PAS fold*222-305*E:1.5e-08 PF13426.4*PAS_9*PAS domain*510-602*E:3.5e-20 PF00989.22*PAS*PAS fold*513-602*E:1.1e-06 PF08447.9*PAS_3*PAS fold*514-599*E:4.2e-07 PF00989.22*Kinase*Protein kinase domain*690-975*E:1.3e-62 PF07714.14*Pkinase_Tyr*Protein tyrosine kinase*691-950*E:1.4e-26	0.438	-0.325	0	-2.257	0.174	-0.583	0.586	-0.245	0.568	-0.248 PHOT1_ARATH	Phototropin-1 (EC 2.7.11.1) (Non-phototropic hypocotyl protein 1) (Root phototropism protein 1)	PHOT1 JK224 NPH1 RPT1 At3g45780 T6D9_110	Arabidopsis thaliana (Mouse-ear cress)	-
SRR342029_TR4728_c1_g1_i5_len=1841	PTR6_ARATH	Q:170-724,H:106-594	59.1%ID	E:0	Protein NRT1/ PTR FAMILY 1.2	PF00854.18*PTR2*POT family*3-410*E:2.6e-73	0.096	-0.679	0	-8.539	0.228	1.223	0.461	-1.455	1	0.71 PTR6_ARATH	Protein NRT1/ PTR FAMILY 1.2 (AtNPF1.2) (Nitrate transporter 1.11)	NPF1.2 NRT1.11 At1g52190 F9I5.4	Arabidopsis thaliana (Mouse-ear cress)	-
SRR342029_TR5134_c0_g1_i2_len=2001	LCYE_ARATH	Q:179-1762,H:1-524	75.83%ID	E:0	Lycopene epsilon cyclase, chloroplastic	PF05834.9*Lycopene_cyclase*Lycopene cyclase protein*113-505*E:2.3e-152	1	-0.02	0	-1.318	0.02	-0.782	0.073	-0.586	0.091	0.537 LCYE_ARATH	Lycopene epsilon cyclase, chloroplastic (EC 5.5.1.18) (Protein LUTEIN DEFICIENT 2)	LUT2 At5g57030 MHM17.16	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Carotenoid biosynthesis; alpha-zeacarotene biosynthesis.; PATHWAY: Carotenoid biosynthesis; delta-carotene biosynthesis.
SRR342029_TR5277_c0_g1_i1_len=655	NA	NA	NA	NA	NA	-	1	-0.297	0	-7.73	0.515	0.211	0.91	0.047	1	0 -	-	-	-	-
SRR342029_TR5356_c1_g2_i1_len=1588	LPA3_ARATH	Q:260-1258,H:26-358	76.58%ID	E:0	Protein LOW PSII ACCUMULATION 3, chloroplastic	PF09353.7*DUF1995*Domain of unknown function (DUF1995)*113-375*E:5.2e-50	0.754	-0.405	0	-5.591	0.007	-0.859	0.021	-0.784	0.822	-0.307 LPA3_ARATH	Protein LOW PSII ACCUMULATION 3, chloroplastic	LPA3 At1g73060 F3N23.26	Arabidopsis thaliana (Mouse-ear cress)	Acetylation; Chloroplast; Complete proteome; Membrane; Plastid; Reference proteome; Thylakoid; Transit peptide
SRR342029_TR5371_c0_g3_i1_len=1044	RK12_TOBAC	Q:118-684,H:1-186	81.58%ID	E:9e-80	50S ribosomal protein L12, chloroplastic	PF16320.2*Ribosomal_L12_N*Ribosomal protein L7/L12 dimerisation domain*62-109*E:1.5e-13 PF00542.16*Ribosomal_L12*Ribosomal protein L7/L12 C-terminal domain*122-188*E:1.2e-23	0.048	-0.437	0	-1.282	0.056	-0.442	0.244	-0.27	0.196	-0.279 RK12_TOBAC	50S ribosomal protein L12, chloroplastic (CL12)	RPL12	Nicotiana tabacum (Common tobacco)	Chloroplast; Direct protein sequencing; Plastid; Ribonucleoprotein; Ribosomal protein; Transit peptide
SRR342029_TR6523_c1_g1_i1_len=1070	TL17_ARATH	Q:897-301,H:36-236	68.6%ID	E:2e-99	Thylakoid lumenal 17.4 kDa protein, chloroplastic (ECO:0000303)(PubMed:9654141)	PF03957.8*PsbQ*Oxygen evolving enhancer protein 3 (PsbQ)*73-186*E:8.7e-19 PF00015.19*Pentapeptide*Pentapeptide repeats (8 copies)*156-186*E:1.9e-07 PF13599.3*Pentapeptide_4*Pentapeptide repeats (9 copies)*157-216*E:3.9e-09 PF00015.19*Pentapeptide*Pentapeptide repeats (8 copies)*187-205*E:5.8e-08	0.839	-0.115	0	-1.721	1	0.087	1	0.04	0.076	-2.62 TL17_ARATH	Thylakoid lumenal 17.4 kDa protein, chloroplastic (P17.4)	TL17 At5g53490 MNC6.3	Arabidopsis thaliana (Mouse-ear cress)	Alternative splicing; Chloroplast; Complete proteome; Direct protein sequencing; Plastid; Reference proteome; Repeat; Thylakoid; Transit peptide
SRR342029_TR6614_c3_g2_i2_len=1398	RRP2_SPIOL	Q:405-947,H:80-260	75.69%ID	E:8e-79	30S ribosomal protein 2, chloroplastic	PF00076.19*RRM_1*RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)*81-151*E:1.2e-21 PF13893.3*RRM_5*RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)*87-155*E:0.008 PF00076.19*RRM_1*RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)*181-251*E:2.6e-17 PF13893.3*RRM_5*RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)*220-252*E:0.2	0.184	-0.312	0	-0.889	0.058	-0.478	0.449	-0.193	0.495	-0.161 RRP2_SPIOL	30S ribosomal protein 2, chloroplastic (Plastid-specific 30S ribosomal protein 2) (PSRP-2)	PSRP2	Spinacia oleracea (Spinach)	Chloroplast; Direct protein sequencing; Plastid; RNA-binding; Repeat; Ribonucleoprotein; Ribosomal protein; Transit peptide; rRNA-binding
SRR342029_TR6664_c0_g7_i1_len=616	NA	NA	NA	NA	NA	-	0.161	-0.352	0	-1.685	0.001	-0.751	0.004	-0.677	0.226	-2.074 -	-	-	-	-
SRR342029_TR7233_c0_g3_i1_len=1851	DNAJ_CYAP4	Q:532-1569,H:2-343	54.31%ID	E:6e-114	Chaperone protein DnaJ (ECO:0000255)HAMAP-Rule:MF_01152)	PF00226.28*DnaJ*DnaJ domain*74-135*E:1.5e-26 PF01556.15*DnaJ_C*DnaJ C terminal domain*194-411*E:3.9e-32 PF00684.16*DnaJ_CXXCXXCXXCG*DnaJ central domain*220-284*E:2.5e-12	1	0.684	0	-7.206	0.941	0.062	0.438	0.28	1	0 DNAJ_CYAP4	Chaperone protein DnaJ	dnaJ Cyan7425_4692	Cyanothece sp. (strain PCC 7425 / ATCC 29141)	Chaperone; Complete proteome; Cytoplasm; DNA replication; Metal-binding; Reference proteome; Repeat; Stress response; Zinc; Zinc-finger
SRR342029_TR7506_c0_g1_i1_len=1191	RR6_ARATH	Q:199-756,H:17-206	73.16%ID	E:1e-73	30S ribosomal protein S6 alpha, chloroplastic	PF01250.14*Ribosomal_S6*Ribosomal protein S6*96-194*E:7.2e-19	0.031	-0.516	0	-1.195	0.346	-0.255	0.773	-0.076	0	6.374 RR6_ARATH	30S ribosomal protein S6 alpha, chloroplastic	RPS6 At1g64510 F1N19.8	Arabidopsis thaliana (Mouse-ear cress)	Chloroplast; Complete proteome; Plastid; RNA-binding; Reference proteome; Ribonucleoprotein; Ribosomal protein; Transit peptide; rRNA-binding
SRR342029_TR7764_c0_g1_i1_len=1561	UGPI7_ARATH	Q:333-1165,H:21-278	73.82%ID	E:1e-121	Uncharacterized GPI-anchored protein At4g28100	-	0.502	-0.254	0	-2.201	0.094	-1.157	0.007	-2.088	1	0.005 UGPI7_ARATH	Uncharacterized GPI-anchored protein At4g28100	At4g28100 T13J8.210	Arabidopsis thaliana (Mouse-ear cress)	Cell membrane; Complete proteome; GPI-anchor; Glycoprotein; Lipoprotein; Membrane; Reference proteome; Signal
SRR342029_TR7920_c1_g1_i1_len=1955	LAX3_MEDTR	Q:1698-283,H:1-465	56.23%ID	E:0	Auxin transporter-like protein 3	PF01490.15*Aa_trans*Transmembrane amino acid transporter protein*44-434*E:3e-73	0.43	-0.312	0	-2.024	0.257	-0.799	0.175	-1.024	0.844	0.114 LAX3_MEDTR	Auxin transporter-like protein 3 (AUX1-like protein 3) (MILAX3)	LAX3	Medicago truncatula (Barrel medic) (Medicago tribuloides)	Amino-acid transport; Auxin-efflux carrier pathway; Cell membrane; Membrane; Symport; Transmembrane; Transmembrane helix; Transport
SRR342029_TR8568_c2_g10_i2_len=596	RS12_HORVU	Q:416-45,H:20-143	83.06%ID	E:3e-62	40S ribosomal protein S12	PF01248.23*Ribosomal_L7Ae*Ribosomal protein L7Ae/L30e/S12e/Gad045 family*27-120*E:1.9e-26	1	1.156	0	-8.422	0.794	0.072	0.395	-0.233	1	-0.038 RS12_HORVU	40S ribosomal protein S12	RPS12	Hordeum vulgare (Barley)	Ribonucleoprotein; Ribosomal protein
SRR342029_TR8866_c3_g12_i2_len=2962	P2C71_ORYSJ	Q:965-99,H:162-463	50.99%ID	E:1e-93	Probable protein phosphatase 2C 71	PF07628.9*SpoIIE*Stage II sporulation protein E (SpoIIE)*337-501*E:9.1e-07 PF12174.7*PP2C_2*Protein phosphatase 2C*352-453*E:9.9e-08 PF00481.18*PP2C*Protein phosphatase 2C*419-469*E:4e-06	1	0.947	0.001	-6.653	1	-3.659	1	-3.659	0.461	-1.197 P2C71_ORYSJ	Probable protein phosphatase 2C 71 (OsPP2C71) (EC 3.1.3.16)	Os10g0370000 LOC_Os10g22460 OJ1003C07.6 OsJ_030057	Oryza sativa subsp. japonica (Rice)	Complete proteome; Hydrolase; Magnesium; Manganese; Metal-binding; Protein phosphatase; Reference proteome
SRR342029_TR9396_c5_g9_i2_len=1050	NA	NA	NA	NA	NA	-	1	0.003	0.001	-1.032	0.838	0.057	0.374	0.224	1	0.962 -	-	-	-	-
SRR342029_TR9794_c0_g7_i1_len=3160	C82A2_SOYBN	Q:1999-2550,H:336-620	54.59%ID	E:1e-57	Cytochrome P450 82A2	PF00067.19*p450*Cytochrome P450*35-288*E:5.5e-30	0.702	0.155	0	-2.556	0.381	-2.437	0.129	-3.164	1	0 C82A2_SOYBN	Cytochrome P450 82A2 (EC 1.14.-.-) (Cytochrome P450 CP4)	CYP82A2	Glycine max (Soybean) (Glycine hispida)	Complete proteome; Heme; Iron; Membrane; Metal-binding; Monooxygenase; Oxidoreductase; Reference proteome
SRR342029_TR9794_c0_g7_i2_len=2242	C82A3_SOYBN	Q:187-1632,H:39-525	47.26%ID	E:4e-130	Cytochrome P450 82A3	PF00067.19*p450*Cytochrome P450*35-492*E:2.3e-92	0.715	0.139	0	-2.727	0.692	-0.937	0.381	-1.615	1	-0.218 C82A3_SOYBN	Cytochrome P450 82A3 (EC 1.14.-.-) (Cytochrome P450 CP6)	CYP82A3	Glycine max (Soybean) (Glycine hispida)	Complete proteome; Heme; Iron; Membrane; Metal-binding; Monooxygenase; Oxidoreductase; Reference proteome
SRR342029_TR10047_c1_g3_i1_len=838	HEXO1_ARATH	Q:47-484,H:396-541	67.81%ID	E:3e-61	Beta-hexosaminidase 1	PF00728.19*Glyco_hydro_20*Glycosyl hydrolase family 20, catalytic domain*12-93*E:2.2e-14	1	0	0	-7.427	1	-3.066	1	-3.066	0.16	-1.143 HEXO1_ARATH	Beta-hexosaminidase 1 (EC 3.2.1.52) (Beta-GlcNAcase 1) (Beta-N-acetylhexosaminidase 1) (Beta-hexosaminidase 2) (AtHEX2) (N-acetyl-beta-glucosaminidase 1)	HEXO1 HEX2 At3g55260 T26I12.140	Arabidopsis thaliana (Mouse-ear cress)	Complete proteome; Disulfide bond; Glycoprotein; Glycosidase; Hydrolase; Reference proteome; Signal; Vacuole
SRR342029_TR10137_c0_g1_i2_len=1546	NA	NA	NA	NA	NA	-	1	0.32	0	-7.891	0.917	0.112	0.548	0.294	1	0 -	-	-	-	-
SRR342029_TR10210_c2_g8_i16_len=2005	Y3589_ARATH	Q:755-1786,H:1-350	64.74%ID	E:4e-151	PTI1-like tyrosine-protein kinase At3g15890	PF03188.13*Cytochrom_B561*Eukaryotic cytochrome b561*57-188*E:3.3e-37	0.76	-0.552	0	-3.754	0.074	0.875	0.241	0.646	1	-0.11 Y3589_ARATH	PTI1-like tyrosine-protein kinase At3g15890 (EC 2.7.10.2)	At3g15890 MVC8.1	Arabidopsis thaliana (Mouse-ear cress)	ATP-binding; Complete proteome; Kinase; Nucleotide-binding; Reference proteome; Transferase; Tyrosine-protein kinase
SRR342029_TR11257_c0_g2_i1_len=1049	ACFR3_ARATH	Q:123-767,H:2-217	56.02%ID	E:3e-59	Probable transmembrane ascorbate ferrireductase 3	-	0.158	1.548	0	-6.953	0.066	-5.376	0.066	-5.376	0.025	-3.179 ACFR3_ARATH	Probable transmembrane ascorbate ferrireductase 3 (EC 1.16.5.1) (Arb:561-3) (Protein b561A,tha14)	CYB561C At1g14730 F10B6.13	Arabidopsis thaliana (Mouse-ear cress)	Complete proteome; Electron transport; Heme; Iron; Membrane; Metal-binding; Oxidoreductase; Reference proteome; Transmembrane; Transmembrane helix; Transport
SRR342029_TR11375_c1_g2_i3_len=1074	PSBQ1_MAIZE	Q:496-882,H:89-217	75.19%ID	E:7e-44	Oxygen-evolving enhancer protein 3-1, chloroplastic	-	0.38	-0.514	0	-2.607	0.142	-0.849	0.044	-1.103	0.646	-0.365 PSBQ1_MAIZE	Oxygen-evolving enhancer protein 3-1, chloroplastic (OEE3) (16 kDa subunit of oxygen evolving system of photosystem II) (OEC 16 kDa subunit)	PSBQ1 PSBQ	Zea mays (Maize)	Chloroplast; Complete proteome; Membrane; Photosynthesis; Photosystem II; Plastid; Reference proteome; Thylakoid; Transit peptide
SRR342029_TR11511_c0_g2_i5_len=1289	SDF2_ARATH	Q:992-357,H:1-215	77.21%ID	E:3e-119	Stromal cell-derived factor 2-like protein	PF02815.16*MIR*MIR domain*165-297*E:4.5e-14	1	0.019	0	-8.501	1	0.055	0.516	-0.287	1	0 SDF2_ARATH	Stromal cell-derived factor 2-like protein (AtSDF2) (SDF2-like protein)	SDF2 At2g25110 F13D4.70	Arabidopsis thaliana (Mouse-ear cress)	Endoplasmic reticulum; Glycoprotein; Plant defense; Reference proteome; Repeat; Signal
SRR342029_TR11911_c0_g3_i5_len=1427	NA	NA	NA	NA	NA	-	0.002	-0.849	0	-2.356	0.493	-0.351	0.253	0.481	0.16	1.19 -	-	-	-	-
SRR342029_TR12216_c0_g3_i1_len=2241	SR54C_ARATH	Q:251-1843,H:35-564	84.02%ID	E:0	Signal recognition particle 54 kDa protein, chloroplastic	PF02881.16*SRP54_N*SRP54-type protein, helical bundle domain*91-188*E:1.2e-19 PF00448.9*Zeta_toxin*Zeta toxin*184-291*E:5e-06 PF00448.19*SRP54*SRP54-type protein, GTPase domain*188-381*E:3.5e-29 PF10158.3.17*APG_kinase*Autophagy/apoptosis kinase*188-227*E:5.6e-05 PF02421.12*Helic_ATPase*Anion-transporting ATPase*188-223*E:5.4e-05 PF01656.20*CobA/CobQ/CobB/MinD/ParA nucleotide binding domain*196-340*E:2e-06 PF02978.16*SRP_SPB*Signal peptide binding domain*412-510*E:2.8e-24	0.05	-0.507	0	-1.352	0.086	-0.571	0.461	-0.245	0.029	-0.554 SR54C_ARATH	Signal recognition particle 54 kDa protein, chloroplastic (54 chloroplast protein) (54CP) (SRP54) (cp SRP54) (FFC)	FFC CPSRP54 At5g03940 F8F6_150	Arabidopsis thaliana (Mouse-ear cress)	3D-structure; Chloroplast; Complete proteome; GTP-binding; Nucleotide-binding; Plastid; RNA-binding; Reference proteome; Ribonucleoprotein; Ribosomal protein; Transit peptide; Transit peptide; rRNA-binding
SRR342029_TR12377_c0_g3_i2_len=984	COMT1_CATRO	Q:982-335,H:127-313	63.32%ID	E:4e-74	Caffeic acid 3-O-methyltransferase	PF00891.15*Methyltransf_2*O-methyltransferase*1-61*E:1.3e-30	0.935	-0.031	0	-1.718	0.798	0.455	0.76	-0.599	0.381	-0.827 COMT1_CATRO	Caffeic acid 3-O-methyltransferase (CAOMT) (COMT) (EC 2.1.1.68) (5-adenosyl-L-methionine:caffeic acid 3-O-methyltransferase)	COMT1	Catharanthus roseus (Madagascar periwinkle) (Vinca rosea)	PATHWAY: Aromatic compound metabolism; phenylpropanoid biosynthesis.
SRR342029_TR13012_c0_g3_i10_len=811	RCD1_DANRE	Q:16-274,H:180-274	65.26%ID	E:2e-36	Cell differentiation protein RCD1 homolog	-	1	0	0.001	-4.67	1	0	1	0	0.892	-0.169 RCD1_DANRE	Cell differentiation protein RCD1 homolog (Rcd-1)	rqcd1 rcd1 si:dkeyp-84a8.6 zgc:85618	Danio rerio (Zebrafish) (Brachydanio rerio)	Activator; Complete proteome; Cytoplasm; Nucleus; RNA-mediated gene silencing; Reference proteome; Repressor; Transcription; Transcription regulation; Translation regulation
SRR342029_TR13132_c0_g3_i1_len=1550	Y4372_ARATH	Q:2-1264,H:355-768	57.83%ID	E:2e-124	Probable LRR receptor-like serine/threonine-protein kinase At4g37250	PF00069.22*Pkinase*Protein kinase domain*116-408*E:1.2e-32 PF07714.14*Pkinase_Tyr*Protein tyrosine kinase*131-268*E:4.1e-21 PF07714.14*Pkinase_Tyr*Protein tyrosine kinase*306-408*E:2.7e-05	0.673	-0.237	0	-2.018	0.133	-1.282	0.038	-1.706	0.003	-2.356 Y4372_ARATH	Probable LRR receptor-like serine/threonine-protein kinase At4g37250 (EC 2.7.11.1)	At4g37250 AP22.22 C7A10.110	Arabidopsis thaliana (Mouse-ear cress)	ATP-binding; Cell cycle; Cell division; Coiled coil; Cytoplasm; Cytoskeleton; Microtubule; Motor protein; Nucleotide-binding; Nucleus; Phosphoprotein; Reference proteome; Repeat; Serine/threonine-protein kinase; Signal; Transferase; Transmembrane; Transmembrane helix
SRR342029_TR13214_c0_g3_i10_len=811	RCD1_DANRE	Q:16-274,H:180-274	65.26%ID	E:2e-36	Cell differentiation protein RCD1 homolog	-	1	0	0.001	-4.67	1	0	1	0	0.892	-0.169

SRR342023_TR5978_c1_g9_i5_len=1181	C7D55_HYOMU	C7D55	60.47%ID	E:1e-76	Premnaspirodiene oxygenase	PF00067.19*p450*Cytochrome P450*2-17I*E:3.8e-08	0.618	0.165	0	-1.866	0.722	0.155	0.761	-0.127	1	0.915	C7D55_HYOMU	Premnaspirodiene oxygenase (HPO) (EC 1.14.13.121) (Cytochrome P450 7D55)	CYP71D55	Hypoxylemon mailicola (Lagopsis henbane)	-	-	-	-	-
SRR342023_TR6064_c0_g1_i1_len=1775	FUCO1_ARATH	O-183-1517;H:39-481	54.41%ID	E:5e-165	Alpha-L-fucosidase 1	PF01120.14*Alpha_L_fuco*Alpha-L-fucosidase*96-359*E:6.5e-36	0.154	-0.462	0	-2.782	1	-1.038	1	-0.952	0.321	0.335	FUCO1_ARATH	Alpha-L-fucosidase 1 (EC 3.2.1.51) (Alpha-L-3/4-fucosidase) (AtFUC1) (Alpha-L-fucoside fucohydrolase)	FUC1 At2g28100 F24D13.11	Arabidopsis thaliana (Mouse-ear cress)	-	-	-	-	-
SRR342023_TR6280_c0_g4_i1_len=1086	NA	NA	NA	NA	NA	PF14309.3*DUF4378*Domain of unknown function (DUF4378)*94-235*E:2.4e-18	1	-0.051	0	-2.402	0.004	-2.068	0.019	-1.465	0.754	-0.177	-	-	-	-	-	-	-	-	-
SRR342023_TR6654_c1_g1_i2_len=2275	Y1154_ARATH	O-417-2348;H:3-643	64.5%ID	E:0	Probable serine/threonine-protein kinase At1g01540	PF00069.22*Pkinase*Protein kinase domain*188-453*E:1.1e-47*PF07714.14*Pkinase_Tyr*Protein tyrosine kinase*188-455*E:3.4e-45	0.024	-0.747	0	-2.042	0.719	0.302	0.597	0.377	0.318	0.488	Y1154_ARATH	Probable serine/threonine-protein kinase At1g01540 (EC 2.7.11.1)	At1g01540 F22L4.8	Arabidopsis thaliana (Mouse-ear cress)	-	-	-	-	-
SRR342023_TR7023_c0_g3_i1_len=3160	THIC_ARATH	O-417-2348;H:3-643	65.74%ID	E:0	Phosphomethylpyrimidine synthase, chloroplastic	PF01894.15*THiC_Rad_SAM*Radical SAM ThC family*166-586*E:7.1e-198	0.196	0.383	0	-1.222	1	0.193	1	0.021	0.401	-0.646	THIC_ARATH	Phosphomethylpyrimidine synthase, chloroplastic (EC 4.1.99.17) (Hydroxymethylpyrimidine phosphate synthase) (HMP-P synthase) (HMP-phosphate synthase) (HMPP synthase) (Protein PYRIMIDINE REQUIRING) (Thiamine biosynthesis protein ThiC) (Protein THIAMINE C)	THIC PY A0g29630 T27A16.27	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Cofactor biosynthesis; thiamine diphosphate biosynthesis.	-	-	-	-
SRR342023_TR7223_c1_g3_i1_len=3785	ATH1_ARATH	Q-2538-3407;H:162-446	55.26%ID	E:9e-86	Homeobox protein ATH1	PF05920.8*POX*Associated with HOX*292-418*E:5.1e-25*PF05920.8*Homeobox_KN*Homeobox KN domain*479-518*E:9e-15*PF00046.26*Homeobox*Homeobox domain*480-518*E:5.3e-06	0.409	-0.403	0	-2.123	0.732	-0.912	0.732	-0.85	0.219	-0.622	ATH1_ARATH	Homeobox protein ATH1	ATH1 At4g32980 F26P21.100	Arabidopsis thaliana (Mouse-ear cress)	-	-	-	-	-
SRR342023_TR7922_c0_g1_i1_len=1250	NDK2_TOBAC	Q:1044-418;H:25-232	77.51%ID	E:2e-109	Nucleoside diphosphate kinase 2, chloroplastic	PF00334.16*NDK*Nucleoside diphosphate kinase*99-232*E:2.5e-54	0.094	-0.444	0.001	-0.967	0.954	-0.032	1	0.017	0.252	-0.304	NDK2_TOBAC	Nucleoside diphosphate kinase 2, chloroplastic (EC 2.7.4.6) (Nucleoside diphosphate kinase II) (NDK II) (NDP kinase II) (NDPK II)	NDPK2	Nicotiana tabacum (Common tobacco)	-	-	-	-	-
SRR342023_TR9121_c5_g1_i1_len=1294	TBB1_AVESA	Q:144-1028;H:70-364	96.61%ID	E:0	Tubulin beta-1 chain	PF00091.22*Tubulin*Tubulin/FtsZ family, GTPase domain*245-E:2e-15*PF03953.14*Tubulin_C*Tubulin C-terminal domain*115-235*E:2.6e-41	1	-0.51	0	-3.284	1	0	1	2.137	0.006	2.464	TBB1_AVESA	Tubulin beta-1 chain (Beta-1-tubulin) (Fragment)	TUBB1 TUB1	Avena sativa (Oat)	-	-	-	-	-
SRR342023_TR9881_c0_g4_i2_len=504	NA	NA	NA	NA	NA	-	0.013	-0.954	0	-1.382	0.423	0.341	0.182	0.534	0.172	-0.397	-	-	-	-	-	-	-	-	-
SRR342023_TR9968_c3_g3_i2_len=3246	TTM3_ARATH	Q:1702-1163;H:22-210	49.74%ID	E:2e-38	Triphosphate tunel metalloenzyme 3	PF01928.18*CYTH*CYTH domain*11-151*E:4.1e-19	1	-0.105	0	-5.567	0.452	0.597	1	0.015	1	-0.784	TTM3_ARATH	Triphosphate tunel metalloenzyme 3 (Adenosinetriphosphatase) (ATPase) (EC 3.6.1.3) (Triphosphatase) (PPPase) (EC 3.6.1.25)	TTM3 At2g11890 F23M2.5	Arabidopsis thaliana (Mouse-ear cress)	-	-	-	-	-
SRR342023_TR10609_c1_g5_i2_len=1032	GCSH_FLAAN	Q:786-269;H:1-162	84.94%ID	E:3e-96	Glycine cleavage system H protein, mitochondrial	PF01597.16*GCV_H*Glycine cleavage H-protein*42-161*E:1.1e-48	0.087	-0.388	0	-0.833	0.005	-0.652	0.017	-0.543	1	0.019	GCSH_FLAAN	Glycine cleavage system H protein, mitochondrial	GDCSH GCDH GCSH	Flaveria anomala (Yellowtops)	-	-	-	-	-
SRR342023_TR10885_c0_g4_i1_len=911	NA	NA	NA	NA	NA	-	0.643	-0.141	0	-1.086	0.475	0.232	0.414	0.272	1	0.787	-	-	-	-	-	-	-	-	-
SRR342023_TR11198_c1_g4_i8_len=939	RK6_ARATH	Q:886-530;H:12-130	71.43%ID	E:1e-81	50S ribosomal protein L6, chloroplastic	PF00347.20*Ribosomal_L6*Ribosomal protein L6*59-131*E:2.2e-13	0.206	-0.469	0	-2.034	1	-0.029	1	0.428	-0.395	1	0	RK6_ARATH	50S ribosomal protein L6, chloroplastic (Protein EMBRYO DEFECTIVE 2394)	RPL6 EMB2394 At1g05190 YUP8H12.20	Arabidopsis thaliana (Mouse-ear cress)	-	-	-	-	-
SRR342023_TR11498_c2_g2_i1_len=2058	GUN17_ARATH	Q:1864-455;K:48-516	81.28%ID	E:0	Endoglucanase 17	PF00759.16*Glycos_hydro_9*Glycosyl hydrolase family 9*70-524*E:1.6e-143	0.037	-0.657	0	-4.669	0.692	-1.179	0.381	-1.441	0.494	-0.275	GUN17_ARATH	Endoglucanase 17 (EC 3.2.1.4) (Endo-1,4-beta glucanase 17) (Cellulase 17)	At4g02290 T2H3.5	Arabidopsis thaliana (Mouse-ear cress)	-	-	-	-	-
SRR342023_TR11922_c1_g10_i1_len=1288	GDL17_ARATH	Q:80-1165;K:6-370	68.94%ID	E:0	GDSL esterase/lipase At1g33811	PF00657.19*Lipase_GDSL*GDSL-like Lipase/Acylhydrolase*36-348*E:1.6e-15	0.662	-0.165	0.001	-2.708	0.004	-1.671	0.002	-1.904	0.149	-0.604	GDL17_ARATH	GDSL esterase/lipase At1g33811 (EC 3.1.1.-) (Extracellular lipase At1g33811)	At1g33811 F14M2.7	Arabidopsis thaliana (Mouse-ear cress)	-	-	-	-	-
SRR342023_TR14167_c2_g4_i3_len=655	NA	NA	NA	NA	NA	-	1	-1.442	0	-1.564	0.83	0.134	0.474	-0.358	0.502	-3.973	-	-	-	-	-	-	-	-	-
SRR342023_TR14167_c2_g4_i4_len=832	NA	NA	NA	NA	NA	-	1	-0.334	0.001	-1.524	0.623	0.296	0.52	0.401	1	-1.496	-	-	-	-	-	-	-	-	-
SRR342023_TR14185_c0_g1_i1_len=1735	TL225_ARATH	Q:373-1020;H:63-278	84.26%ID	E:6e-106	-	PF00805.19*Pentapeptide*Pentapeptide repeats (8 copies)*99-138*E:6.4e-07*PF13599.3*Pentapeptide_4*Pentapeptide repeats (9 copies)*119-194*E:7.8e-07*PF00805.19*Pentapeptide*Pentapeptide repeats (8 copies)*124-160*E:7.8e-09*PF00805.19*Pentapeptide*Pentapeptide repeats (8 copies)*166-199*E:6.7e-07	0.311	-0.39	0	-1.352	0.931	0.08	0.165	0.511	0.008	-1.43	TL203_ARATH	Thylakoid lumenal protein TL20.3, chloroplastic	TL20.3 At1g12250 T28K15.2	Arabidopsis thaliana (Mouse-ear cress)	-	-	-	-	-
SRR342023_TR14202_c2_g1_i5_len=1314	EXPA4_ARATH	Q:857-138;H:18-257	90%ID	E:1e-159	Expansin-A4	PF03330.15*DPBB_1*Lytic transglycolase*68-155*E:1.3e-21*PF03137.18*Pollen_allerg_1*Pollen allergen*166-243*E:1.9e-24	0.548	-0.166	0	-1.151	0.343	0.325	1	-0.03	0.229	0.495	EXPA4_ARATH	Expansin-A4 (AtEXPA4) (Alpha-expansin-4) (AtEXP4) (AtEx4) (Atth-ExpAlpha-1.6)	EXPA4 EXP4 At2g39700 F17A14.7	Arabidopsis thaliana (Mouse-ear cress)	-	-	-	-	-
SRR342023_TR14529_c0_g2_i1_len=1633	NA	NA	NA	NA	NA	-	0.232	-0.576	0	-1.879	0.581	0.084	1	0.848	0.725	-0.167	-	-	-	-	-	-	-	-	-
SRR342023_TR16216_c0_g1_i1_len=1355	NA	NA	NA	NA	NA	PF02234.16*CDP-Alcohol-dependent kinase inhibitor*225-268*E:2.6e-18	0.881	0.072	0	-1.569	0.014	-1.006	0.007	-1.147	0.496	-0.245	-	-	Os11g0244800 LOC_Os11g14010 Os_33509 OSJNBa0004P24 OSJNBa0024M06	-	-	-	-	-	-
SRR342023_TR16373_c7_g4_i1_len=1003	ALF L8_ORYSJ	Q:1002-334;H:49-253	64.16%ID	E:2e-66	PHD finger protein ALFIN-LIKE 8	PF12165.5*DUF3594*Domain of unknown function (DUF3594)*1-88*E:7.1e-43*PF00628.26*PHD*PHD-finger*171-219*E:1.2e-10	0.398	-0.344	0	-1.647	0.895	0.143	0.666	-0.232	1	0	ALF L8_ORYSJ	PHD finger protein ALFIN-LIKE 8	Oryza sativa subsp. japonica (Rice)	-	-	-	-	-	-
SRR342023_TR16460_c1_g9_i1_len=1697	Y5830_ARATH	Q:1443-382;H:303-653	74.16%ID	E:0	Probable inactive receptor kinase At5g58300	PF00069.22*Pkinase*Protein kinase domain*147*E:4.8e-37*PF07714.14*Pkinase_Tyr*Protein tyrosine kinase*148-411*E:1.4e-35	0.599	-0.19	0.001	-1.317	0.581	-0.322	0.484	-0.447	1	0.143	Y5830_ARATH	Probable inactive receptor kinase At5g58300	At5g58300 MCK7.17	Arabidopsis thaliana (Mouse-ear cress)	-	-	-	-	-
SRR342023_TR16591_c0_g3_i1_len=1252	UBE11_ARATH	Q:77-1003;H:772-1080	80.91%ID	E:0	Ubiquitin-activating enzyme E1 1	PF10585.6*UBA_e1_thioCys*Ubiquitin-activating enzyme active site*1-125*E:5.4e-30 *PF00899.18*ThiF*ThiF family*104-184*E:2.9e-10 *PF09358.7*E1_UFD*Ubiquitin fold domain*199-285*E:3.1e-23	1	-0.54	0	-0.188	1	0	0	0.006	-1.06	UBE11_ARATH	Ubiquitin-activating enzyme E1 1 (AtUBA1) (Protein MODIFIER OF SNC1 5)	UBA1 MOS5 At2g30110 T27E13.15	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Protein modification; protein ubiquitination.	-	-	-	-	-
SRR342023_TR16698_c0_g4_i1_len=611	NA	NA	NA	NA	NA	PF03539.12*DUF275*Protein of unknown function (DUF275)*2-79*E:7.7e-17*PF10950.5*DUF2775*Protein of unknown function (DUF2775)*86-157*E:1.6e-15 *PF10950.5*DUF2775*Protein of unknown function (DUF2775)*160-202*E:6.2e-09	0.487	0.304	0	-5.322	1	0	1	0	0.317	0.532	-	-	-	-	-	-	-	-	-
SRR342023_TR17575_c0_g3_i3_len=1298	MENB_ARATH	Q:1109-120;H:4-337	76.65%ID	E:0	1,4-dihydroxy-2-naphthoyl-CoA synthase, peroxisomal	PF03328.17*ECH_1*Enoyl-CoA hydratase/isomerase*80-326*E:3e-75*PF16113.2*ECH_2*Enoyl-CoA hydratase/isomerase*83-259*E:3.2e-21	0.091	-0.463	0	-2.122	0.902	-0.058	0.603	0.174	1	0.013	MENB_ARATH	1,4-dihydroxy-2-naphthoyl-CoA synthase, peroxisomal (DHNS) (EC 4.1.3.36) (Enoyl-CoA hydratase/isomerase 8) (ECHID) (Naphthoate synthase)	MENB At1g60550 F8A5.9	Arabidopsis thaliana (Mouse-ear cress)	-	-	-	-	-
SRR342023_TR18351_c3_g4_i8_len=2801	EFTU2_SOYBN	Q:2336-1044;H:49-479	89.56%ID	E:0	Elongation factor Tu, chloroplastic	PF00009.24*GTP_EFTU*Elongation factor Tu GTP binding domain*85-286*E:4.5e-57*PF03144.22*GTP_EFTU_D2*Elongation factor Tu domain 2*310-378*E:9.6e-19 *PF03143.14*GTP_EFTU_D3*Elongation factor Tu C-terminal domain*383-482*E:6e-35	0.016	-0.554	0	-0.959	0.005	-0.61	0.096	-0.359	0.42	-0.177	EFTU2_SOYBN	Elongation factor Tu, chloroplastic (EF-Tu)	TUFB1	Glycine max (Soybean) (Glycine hispida)	-	-	-	-	-
SRR342023_TR19197_c0_g1_i1_len=1169	CITX2_NICBE	Q:321-854;H:1-181	69.02%ID	E:7e-80	Thioredoxin-like protein CITRX2, chloroplastic (ECO:0000303|PubMed:15131698)	PF00085.17*Thioredoxin*Thioredoxin*72-158*E:9.7e-20 *PF13098.3*Thioredoxin_2*Thioredoxin-like domain*88-172*E:4e-09	0.057	-0.605	0	-1.286	0.657	0.177	1	-0.049	0.248	-0.37	CITX2_NICBE	Thioredoxin-like protein CITRX2, chloroplastic (EC 1.8.-.-) (Cf49-interacting thioredoxin 2) (NbCiTrx2)	CITRX2	Nicotiana benthamiana	-	-	-	-	-
SRR342023_TR19798_c0_g2_i9_len=1952	GCR2_ARATH	Q:1940-1059;H:116-416	71.86%ID	E:5e-150	LanC-like protein GCR2	PF05147.10*LANC_like*Lanthionine synthetase C-like protein*4-298*E:6.1e-84	0.12	-0.681	0	-3.22	1	0.522	1	0.421	0.791	0.066	GCR2_ARATH	LanC-like protein GCR2 (G-protein coupled receptor 2)	GCR2 GPCR At1g52920 F14G24.19	Arabidopsis thaliana (Mouse-ear cress)	-	-	-	-	-
SRR342023_TR19811_c1_g3_i1_len=1011	NA	NA	NA	NA	NA	PF03745.11*DUF309*Domain of unknown function (DUF309)*84-140*E:3.1e-20	0.568	0.191	0	-1.195	0.006	-0.933	0.003	-1.027	0.031	0.699	-	-	-	-	-	-	-	-	-
SRR342023_TR19929_c1_g1_i5_len=852	NA	NA	NA	NA	NA	-	1	0	0	-7.661	1	0	1	0	1	0	-	-	-	-	-	-	-	-	-
SRR342023_TR20482_c2_g7_i2_len=749	RS4_SOLTU	Q:3491;H:101-264	91.46%ID	E:1e-87	40S ribosomal protein S4	PF00900.17*Ribosomal_S4e*Ribosomal family S4e*11-69*E:1.9e-32*PF00467.26*KOW*KOW motif*77-110*E:6.1e-7*PF16121.2*40S_S4_C*40S ribosomal protein S4 C-terminal*112-157*E:2.1e-28	0.634	-0.241	0.001	-1.016	0.013	1.145	0.496	0.417	0.054	-0.472	RS4_SOLTU	40S ribosomal protein S4	RPS4	Solanum tuberosum (Potato)	-	-	-	-	-
SRR342023_TR21200_c1_g6_i8_len=5341	IF2C_PHAVU	Q:2788-4968;H:27-959	80.91%ID	E:0	Translation initiation factor IF-2, chloroplastic	PF01985.18*CRS1_Yhb1*CRS1 / YhbY (CRM) domain*51-133*E:3.5e-24*PF01985.18*CRS1_Yhb1*CRS1 / YhbY (CRM) domain*248-332*E:2.4e-20 PF01985.18*CRS1_Yhb1*CRS1 / YhbY (CRM) domain*459-545*E:6.5e-18	0.031	-1.36	0	-2.272	0.402	1.106	0.76	0.675	0.221	-0.421	IF2C_PHAVU	Translation initiation factor IF-2, chloroplastic (PvIF2cp)	IF2CP	Phaseolus vulgaris (Kidney bean) (French bean)	-	-	-	-	-
SRR342023_TR21417_c0_g1_i1_len=962	NA	NA	NA	NA	NA	PF06364.9*DUF1064*Protein of unknown function (DUF1064)*10-174*E:8.7e-65	1	-0.069	0	-6.514	0.518	0.33	1	-0.062	1	1.687	-	-	-	-	-	-	-	-	-
SRR342023_TR22292_c1_g3_i1_len=744	NA	NA	NA	NA	NA	-	1	0.061	0	-2.792	0.299	-1.407	0.517	-1.245	0.229	-0.439	-	-	-	-	-	-	-	-	-
SRR342023_TR23173_c0_g1_i2_len=2137	SR542_SOLLC	Q:1888-452;H:1-479	84.57%ID	E:0	Signal recognition particle 54 kDa protein 2	PF02881.16*SRP54_N*SRP54-type protein, helical bundle domain*6-83*E:9.8e-16*PF00448.19*SRP54*SRP54-type protein, GTP-bind domain*101-298*E:1.2e-78 PF02492.16*cobW*CobW/HypB/UreG, nucleotide-binding domain*103-254*E:8.2e-07*PF09278.15*RBF_SPB*Signal peptide binding domain*328-422*E:2e-27	1	-1.272	0	-6.595	0.874	0.216	1	0.091	1	0	SR542_SOLLC	Signal recognition particle 54 kDa protein 2 (SRP54)	-	Solanum lycopersicum (Tomato) (Lycopersicon esculentum)	-	-	-	-	-
SRR342023_TR23641_c4_g4_i4_len=1761	F16P1_PEA	Q:1526-306;H:6-407	81.07%ID	E:0	Fructose-1,6-bisphosphatase, chloroplastic	PF00316.17*FBPase*Fructose-1-6-bisphosphatase, N-terminal domain*80-279*E:6.7e-56	0	-1.053	0	-4.03	0.448	0.634	-0.107	0.112	-0.536	F16P1_PEA	Fructose-1,6-bisphosphatase, chloroplastic (FBPase) (EC 3.1.3.11) (D-fructose-1,6-bisphosphate 1-phosphohydrolase)	FBP	Pisum sativum (Garden pea)	PATHWAY: Carbohydrate biosynthesis; Calvin cycle.	-	-	-	-	-
SRR342023_TR24357_c2_g3_i7_len=985	SABP2_TOBAC	Q:562-137;H:120-260	57.75%ID	E:8e-47	Salicylic acid-binding protein 2	-	0.904	-0.135	0	-2.361	0.002	-1.354	0.015	-1.015	0.555	-0.309	SABP2_TOBAC	Salicylic acid-binding protein 2 (NtSABP2) (EC 3.1.1.-) (Methyl salicylate esterase)	SABP2	Nicotiana tabacum (Common tobacco)	-	-	-	-	-
SRR342023_TR24567_c0_g1_i1_len=1091	NA	NA	NA	NA	NA	-	0.828	0.078	0	-1.333	0.203	-0.416	0.606	-0.171	0.572	-0.194	-	-	-	-	-	-	-	-	-
SRR342023_TR24647_c0_g1_i1_len=821	ML423_ARATH	Q:3744;H:17-150	52.21%ID	E:4e-36	MLP-like protein 423	-	0.892	-0.045	0	-2.357	0.002	-1.066	0.001	-1.109	0.001	-0.85	ML423_ARATH	MLP-like protein 423	MLP423 At1g24020 T23E23.17 T23E23_22	Arabidopsis thaliana (Mouse-ear cress)	-	-	-	-	-
SRR342023_TR24795_c0_g5_i1_len=4004	TPL_ARATH	Q:225-3602;H:1-1131	79.51%ID	E:0	Protein TOPLESS	PF00400.29*WD40*WD domain, G-beta repeat*456-490*E:1.8e-05*PF00400.29*WD40*WD domain, G-beta repeat*914-948*E:0.0026	1	-0.172	0	-6.48	0.211	0.761	0.412	0.563	1	0.207	TPL_ARATH	Protein TOPLESS (WUS-interacting protein 1)	TPL WSIP1 At1g15750 F7H2.9	Arabidopsis thaliana (Mouse-ear cress)	-	-	-	-	-
SRR342023_TR24795_c1_g1_i1_len=3098	TGD1_ARATH	Q:1857-940;H:41-347	75.08%ID	E:3e-158	Protein TRIGALACTOSYLDIACYLGLYCEROL 1, chloroplastic (ECO:0000303|PubMed:12743031)	PF02405.13*MlaE*Permease MlaE*130-338*E:8e-69	1	-0.364	0	-4.647	0.35	0.65	0.739	0.279	1	0.349	TGD1_ARATH	Protein TRIGALACTOSYLDIACYLGLYCEROL 1, chloroplastic (ABC transporter I family member 14) (ABC transporter ABCI.14) (AIABC014)	TGD1 ABCI14 At1g19800 F14P1.27	Arabidopsis thaliana (Mouse-ear cress)	-	-	-	-	-
SRR342023_TR25706_c1_g4_i4_len=1138	B561D_ARATH	Q:1065-325;H:141-391	54.76%ID	E:1e-69	Cytochrome b561 and DOMON domain-containing protein At4g12980	PF12146.5*Hydrolase_4*Serine aminopeptidase, S33*105-218*E:1.7e-08 *PF00561.17*Abhydrolase_1*alpha/beta hydrolase fold*107-360*E:1.2e-16 PF12697.4*Abhydrolase_6*Alpha/beta hydrolase family*109-366*E:4.6e-21	0.507	-0.239	0	-1.286	0.29	-0.379	0.405	-0.285	0.502	-0.226	YUGF_BACSU	Uncharacterized hydrolase YugF (EC 3.1.-.-)	yugF BSU31420	Bacillus subtilis (strain 168)	-	-	-	-	-
SRR342023_TR26965_c0_g9_i3_len=1612	NA	NA	NA	NA	NA	PF00450.9*BSP*Peptidase of plants and bacteria*95-305*E:5.2e-17	1	0.035	0	-2.26	0.01	0.914	0.007	-0.967	0.6	-0.332	-	-	-	-	-	-	-	-	-
SRR342023_TR27467_c3_g4_i5_len=5411	POLX_TOBAC	Q:5411-2034;H:221-1323	43.99%ID	E:0	Retrovirus-related Pol polyprotein from transposon TNT 1-94	PF13976.3*gag_pre-integrase*GAG-pre-integrase domain*183-250*E:2.8e-14*PF00665.23*rve*Integrase core domain*266-380*E:6e-26 PF07727.11*RVT_2*Reverse transcriptase (RNA-dependent DNA polymerase)*640-887*E:4.5e-93	0.61	0.196	0	-1.339	0.127	-0.592	0.005	-1.166	0.021	1.038	POLX_TOBAC	Retrovirus-related Pol polyprotein from transposon TNT 1-94 [Includes: Protease (EC 3.4.23.-); Reverse transcriptase (EC 2.7.7.49); Endonuclease]	-	Nicotiana tabacum (Common tobacco)	-	-	-	-	-
SRR342023_TR27467_c3_g4_i8_len=1394	NA	NA	NA	NA	NA	PF06108.9*DUF932*Protein of unknown function (DUF932)*19-54*E:7.6e-08	0	1.571	0	-2.315	0.132	0.762	0.496	0.388	1	-2.002	-	-	-	-	-	-	-	-	-
SRR342023_TR28415_c3_g2_i1_len=1319	NA	NA	NA	NA	NA	PF02544.13*Steroid_dh*3-oxo-5-alpha-steroid 4-dehydrogenase*158-269*E:2.1e-26	0.641	-0.248	0	-2.211	0.019	-0.691	0.076	-0.519	1	0.732	-	-	-	-	-	-	-	-	-
SRR342023_TR28419_c2_g2_i6_len=1513	NA	NA	NA	NA	NA	-	1	-1.159	0	-7.003	1	-0.077	1	-0.113	1	0	-	-	-	-	-	-	-	-	-
SRR342023_TR30149_c2_g5_i1_len=2948	NA	NA	NA	NA	NA	-	1	-0.105	0	-6.401	0.618	-0.264	0.177	-0.663	1	-0.478	-	-	-	-	-	-	-	-	-
SRR342023_TR30634_c0_g2_i1_len=404	NA	NA	NA	NA	NA	-	0.722	-0.133	0	-1.435	0.705	0.223	1	-0.042	0.04	-0.683	-	-	-	-	-	-	-	-	-
SRR342023_TR30649_c0_g5_i2_len=1314	CCD4_ARATH	Q:1260-274;H:266-595	73.49%ID	E:4e-175	Probable carotenoid cleavage dioxygenase 4, chloroplastic	PF03055.12*RPE65*Retinal pigment epithelial membrane protein*3-305*E:3.4e-59	0.167	0.602	0	-1.133	0.01	-0.872	0.132	-0.493	0.8	0.095	CCD4_ARATH	Probable carotenoid cleavage dioxygenase 4, chloroplastic (AtCCD4) (EC 1.14.99.-) (AINCED4)	CCD4 NCED4 At4g19170 T18B16.140	Arabidopsis thaliana (Mouse-ear cress)	-	-	-	-	-
SRR342023_TR30982_c3_g1_i18_len=2351	FKB70_WHEAT	Q:757-1812;H:9-423	47.75%ID	E:3e-117	70 kDa peptidyl-prolyl isomerase	PF00254.20*FKBP_C*FKBP-type peptidyl-prolyl cis-trans isomerase*10-62*E:4.3e-18 PF00254.25*FKBP_C*FKBP-type peptidyl-prolyl cis-trans isomerase*89-149*E:1.4e-21	0.591	-0.314	0	-2.632	0.781	-0.566	1	-0.33	0.079	-1.11	FKB70_WHEAT	70 kDa peptidyl-prolyl isomerase (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPIase) (Rotamase)	FKBP70	Triticum aestivum (Wheat)	-	-	-	-	-
SRR342023_TR30982_c3_g3_i1_len=2169	NA	NA	NA	NA	NA	-	0.684	0.156	0	-2.056	0.136	-0.594	0.014	-0.968	0.606	-0.182	-	-	-	-	-	-	-	-	-
SRR342023_TR31039_c0_g1_i1_len=1134	GTOMC_ORYSJ	Q:34-906;H:73-359	44.67%ID	E:4e-75	Probable tocopherol O-methyltransferase, chloroplastic	PF13489.3*Methyltransf_23*Methyltransferase domain*63-195*E:2.9e-14*PF01209.15*Ubie_methyltran*ubiE/COQ5 methyltransferase family*75-187*E:3.3e-11 PF13847.3*Methyltransf_31*Methyltransferase domain*79-193*E:1.2e-10 PF02353.17*CMAS*Mycolic acid cyclopropane synthetase*79-193*E:4.7e-11 PF08445.7*Methyltransf_15*RNA cap guanine-N2 methyltransferase*82-156*E:7e-07 PF07021.9*MetW*Methionine biosynthesis protein MetW*82-175*E:1.9e-06 PF08241.9*Methyltransf_11*Methyltransferase domain*84-182*E:4.4e-20 PF13649.3*Methyltransf_25*Methyltransferase domain*84-177*E:2e-18 PF08242.9*Methyltransf_12*Methyltransferase domain*84-180*E:1.6e-12	0.451	-0.324	0	-5.074	0.402	-1.071	0.118	-1.852	0.275	-0.382	GTOMC_ORYSJ	Probable tocopherol O-methyltransferase, chloroplastic (EC 2.1.1.95) (Gamma-tocopherol methyltransferase) (Vitamin E pathway gene 4 protein)	VTE4 G-TMT TMT Os02g0701600 LOC_Os02g47310 OJ1111_E07.25	Oryza sativa subsp. japonica (Rice)	PATHWAY: Cofactor biosynthesis; tocopherol biosynthesis.	-	-	-	-	-
SRR342023_TR31168_c1_g1_i1_len=1545	RK5_ARATH	Q:1408-743;H:37-259	76.23%ID	E:1e-121	50S ribosomal protein L5, chloroplastic	PF00673.18*Ribosomal_L5_C*ribosomal L5P family C-terminus*1-82*E:3.1e-27	0.029	-0.533	0	-1.201	0.005	-0.775	0.016	-0.625	1	-0.337	RK5_ARATH	50S ribosomal protein L5, chloroplastic	RPL5 At4g01310 A_IG002N01.3 F2N1.5	Arabidopsis thaliana (Mouse-ear cress)	-	-	-	-	-
SRR342023_TR31533_c1_g4_i1_len=1529	ENOX_SOLLC	Q:710-1285;H:200-388	87.3%ID	E:3e-125	2-methylene-furan-3-one reductase	PF08240.9*ADH_N*Alcohol dehydrogenase GroES-like domain*109-172*E:1.3e-09	0.314	-0.264	0	-0.914	0.019	-0.538	0.08	-0.399	0.294	-0.531	ENOX_SOLLC	2-methylene-furan-3-one reductase (EC 1.3.1.105) (Enone oxidoreductase) (SIEO)	EO QR Solyc05g005480	Solanum lycopersicum (Tomato) (Lycopersicon esculentum)	-	-	-	-	-
SRR646572_TR6692_c0_g1_i22_len=1249	NA	NA	NA	NA	NA	-	0.472	-0.305	0.267	-1.501	0.333	0.633	0.267	0.712	0.206	-0.722	-	-	-	-	-	-	-	-	-
SRR646572_TR12509_c0_g2_i6_len=1712	NA	NA	NA	NA	NA	PF15459.3*RRP14*60S ribosome biogenesis protein Rrp14*38-71*E:4e-05 PF04935.9*SURF6*Surfeit locus protein 6*122-312*E:5.3e-22	0.014	-3.489	0	-6.792	0.005	6.237	1	0	0.502	-1.662	-	-	-	-	-	-	-	-	-
SRR646572_TR20512_c0_g1_i1_len=1371	CP20B_ARATH	Q:152-910;H:1-256	65.12%ID	E:2e-88	-	PF00160.18*Pro_isomerase*Cyclophilin type peptidyl-prolyl cis-trans isomerase/CLD*145-299*E:7.5e-51	0.002	-0.778	0	-1.338	0.105	-1.063	0.211	-0.765	0.068	-0.399	PNSL5_ARATH	Photosynthetic NDH subunit of lumenal location 5, chloroplastic (Cyclophilin of 20 kDa 2) (Peptidyl-prolyl cis-trans isomerase CYP20-2) (PPIase CYP20-2) (EC 5.2.1.8) (Rotamase CYP20-2) (Thylakoid lumen PPIase of 20 kDa) (TLP20)	PNSL5 CYP20-2 At5g13120 T19L5_80	Arabidopsis thaliana (Mouse-ear cress)	-	-	-	-	-
SRR646572_TR30268_c0_g1_i1_len=737	NA	NA	NA	NA	NA	-	0	8.205	0	-10.998	1	0	1	0	1	0	-	-	-	-	-	-	-	-	-
SRR646572_TR34996_c0_g1_i6_len=1831	TIG_ARATH	Q:1734-268;H:1-547	57.59%ID	E:0	Trigger factor-like protein TIG, Chloroplastic	PF05698.11*Trigger_C*Bacterial trigger factor protein (TF) C-terminus*353-510*E:7.5e-20	0.023	-0.707	0	-1.42	1	-0.024	0.865	0.212	0.933	-0.035	TIG_ARATH	Trigger factor-like protein TIG, Chloroplastic (EC 5.2.1.8) (Immunophilin TIG) (Peptidyl-prolyl

SRR9924142_TR43604_c1_g4_i14_len=472	LZ4CY_ARATH	2235;H:64-683	36.00%ID	E-0e-119	Protein LACCASE-LIKE 1, chloroplastic (EC0.000000)	P11261.4:2 OUT:sod domain:0 cellular:cell:cellular:cell (OUT:SOV)	0.00	0.000	0	-0.101	0	-1.191	0.004	-1.21	0.193	-1.21;LZ4CY_ARATH	Protein LACCASE-LIKE 1, chloroplastic (AtLZ4)	LZ4 At4g39090 T10L21.140	cress)	-	-	-
SRR648705_TR43863_c0_g2_i2_len=1257	LQY1_ARATH	Q:165-635;H:1-154	73.42%ID	E-8e-62	Protein disulfide-isomerase LQY1, chloroplastic (ECO:0000303)PubMed:21586683)	0.746	-0.124	0.001	-1.154	0.235	-0.309	0.858	-0.053	0.102	-0.478;LQY1_ARATH	Protein disulfide-isomerase LQY1, chloroplastic (EC 5.3.4.1) (Protein LOW QUANTUM YIELD OF PHOTOSYSTEM II 1)	LQY1 At1g75690 F10A5.12 F10A5.4	Arabidopsis thaliana (Mouse-ear cress)	-	-	Transit peptide
SRR648705_TR44504_c0_g1_i6_len=1846	NA	NA	NA	NA	NA	-	0.402	-0.927	0	-3.162	1	0.854	1	-0.504	0.447	-0.205	-	-	-	-	-	Chloroplast; Complete proteome; Isomerase; Membrane; Metal-binding; Plastid; Reference proteome; Repeat; Thylakoid; Transit peptide; Transmembrane; Transmembrane helix; Zinc
SRR648705_TR45239_c0_g1_i2_len=2021	SR54C_ARATH	Q:2017-728;H:44-471	86.98%ID	E-0	Signal recognition particle 54 kDa protein, chloroplastic	PF02881.16*SRP54_N*SRP54-type protein, helical bundle domain*41-118*E:8.2e-20 PF06414.9*Zeta_toxin*Zeta toxin*133-241*E:2.9e-06 PF00448.19*SRP54*SRP54-type protein, GTPase domain*136-331*E:1.9e-76 PF01583.13*APS_kinase*Adenylylsulphate kinase*136-17?*E:3.6e-05 PF02374.12*ArsA_ATPase*Anion-transporting ATPase*138-173*E:3.9e-05 PF01656.20*CbiA*CobQ/CobB/MinD/ParA nucleotide binding domain*146-290*E:9.3e-07 PF02879.16*SRP_SPB*Signal peptide binding domain*362-434*E:1.3e-17	0.054	-0.662	0	-1.518	0.902	-0.07	0.609	-0.295	0.381	-2.457;SR54C_ARATH	Signal recognition particle 54 kDa protein, chloroplastic (54 chloroplast protein) (54CP) (SRP54) (cpSRP54) (FFC)	FFC CPSRP54 At5g03940 F8F6_150	Arabidopsis thaliana (Mouse-ear cress)	-	-	3D-structure; Chloroplast; Complete proteome; GTP-binding; Nucleotide-binding; Plastid; RNA-binding; Reference proteome; Ribonucleoprotein; Signal recognition particle; Transit peptide
SRR648707_TR102_c0_g1_i20_len=1857	NA	NA	NA	NA	NA	PF07207.8*Lir1*Light regulated protein Lir1*11-130*E:8.9e-47	0.977	-0.014	0	-1.788	0.564	0.549	0.84	0.287	0.475	-0.228	-	-	-	-	-	-
SRR648707_TR340_c0_g1_i1_len=1003	RR9_SPIOL	Q:79-233;H:9-197	73.06%ID	E-3e-90	30S ribosomal protein S9, chloroplastic	PF00380.16*Ribosomal_S9*Ribosomal protein S9/S16*87-208*E:1.7e-41	0.351	-0.275	0	-1.247	0.424	-0.302	0.474	-0.261	0.675	-0.284;RR9_SPIOL	30S ribosomal protein S9, chloroplastic (Fragment)	PRP59	Spinacia oleracea (Spinach)	-	-	3D-structure; Acetylation; Chloroplast; Direct protein sequencing; Plastid; RNA-binding; Ribonucleoprotein; Ribosomal protein; Transit peptide; rRNA-binding
SRR648707_TR968_c0_g1_i1_len=668	NA	NA	NA	NA	NA	-	0.025	-0.547	0	-1.04	0.025	0.751	0.014	0.803	1	-0.008	-	-	-	-	-	-
SRR648707_TR2770_c0_g1_i2_len=3613	EBF1_ARATH	Q:1144-2790;H:78-627	56.86%ID	E-0	EIN3-binding F-box protein 1	PF13516.3*LRR_6*Leucine Rich repeat*142-165*E:0.62	1	0	0	-7.347	1	0	1	0	0.316	-0.627;EBF1_ARATH	EIN3-binding F-box protein 1 (F-box/LRR-repeat protein 6)	EBF1 FBL6 At2g25490 F13B15.15	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Protein modification; protein ubiquitination.	-	Complete proteome; Ethylene signaling pathway; Nucleus; Reference proteome; Ubl conjugation pathway
SRR648707_TR6095_c0_g1_i1_len=568	SUT_SPIOL	Q:268-308;H:431-517	72.41%ID	E-4e-33	Sucrose transport protein	0	0	7.028	0	-2.224	0	7.892	1	0	1	0 SUT_SPIOL	Sucrose transport protein (Sucrose permease) (Sucrose-proton symporter)	Spinacia oleracea (Spinach)	PATHWAY: Glycan biosynthesis; sucrose metabolism.	-	-	Membrane; Sugar transport; Symport; Transmembrane; Transmembrane helix; Transport
SRR648707_TR9041_c1_g1_i5_len=2945	CUL1_ARATH	Q:203-517;H:4-752	79.29%ID	E-0	Cullin-1	PF00888.19*Cullin*Cullin family*19-639*E:1.6e-178 PF10557.6*Cullin_Nedd8*Cullin protein neddylation domain*666-728*E:5.3e-26	0.017	5.883	0	-3.399	0.025	-2.756	0.005	-6.212	1	0.572;CUL1_ARATH	Cullin-1	CUL1 At4g02570 T10P11.26	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Protein modification; protein ubiquitination.	-	Auxin signaling pathway; Cell cycle; Complete proteome; Cytoplasm; Cytoskeleton; Developmental protein; Ethylene signaling pathway; Isopeptide bond; Nucleus; Reference proteome; Ubl conjugation; Ubl conjugation pathway
SRR648707_TR10640_c0_g1_i1_len=1296	RK15_ARATH	Q:1090-410;H:27-250	69.16%ID	E-1e-99	50S ribosomal protein L15, chloroplastic	PF00828.16*Ribosomal_L27A*Ribosomal proteins 50S-L15, 50S-L18e, 60S-L27A*110-237*E:5.1e-30	0.081	-0.4	0	-0.899	0.729	-0.082	0.412	0.195	0.536	-0.141;RK15_ARATH	50S ribosomal protein L15, chloroplastic (CL15)	RPL15 At3g25920 MPE11.32 MPE11.9 MPE11_7	Arabidopsis thaliana (Mouse-ear cress)	-	-	Acetylation; Chloroplast; Complete proteome; Plastid; Reference proteome; Ribonucleoprotein; Ribosomal protein; Transit peptide
SRR648707_TR12461_c0_g1_i1_len=658	PSRP9_ARATH	Q:546-222;H:1-103	54.55%ID	E-3e-23	50S ribosomal protein 6, chloroplastic	0	0.022	-0.565	0	-1.644	0.233	-0.312	0.503	-0.182	0.035	-0.498;PSRP6_ARATH	50S ribosomal protein 6, chloroplastic (CL25) (Plastid-specific 50S ribosomal protein 6) (PSRP-6)	PSRP6 At5g17870 MPI7_10	Arabidopsis thaliana (Mouse-ear cress)	-	-	Chloroplast; Complete proteome; Plastid; Reference proteome; Ribonucleoprotein; Ribosomal protein; Transit peptide
SRR648707_TR1880_c0_g1_i1_len=611	PLPD1_ARATH	Q:1-228;H:489-564	84.21%ID	E-6e-34	Dihydrolipoyl dehydrogenase 1, chloroplastic	0	0.398	-0.388	0	-2.086	0.719	0.388	0.84	-0.178	0.169	-0.546;PLPD1_ARATH	Dihydrolipoyl dehydrogenase 1, chloroplastic (dLPD1) (EC 1.8.1.4) (Dihydrolipoamide dehydrogenase 1) (Protein LIPOAMIDE DEHYDROGENASE 1) (Pyruvate dehydrogenase complex E3 subunit 1) (E3-1) (PDC-E3 1)	PLPD1 At3g16950 K14A17.6	Arabidopsis thaliana (Mouse-ear cress)	-	-	Alternative splicing; Chloroplast; Complete proteome; Disulfide bond; FAD; Flavoprotein; NAD; Oxidoreductase; Plastid; Redox-active center; Reference proteome; Transit peptide
SRR648707_TR18401_c0_g3_i1_len=1728	SPX4_ARATH	Q:1511-618;H:1-503	62.06%ID	E-3e-112	SPX domain-containing protein 4	PF03105.16*SPX*SPX domain*1-59*E:3.6e-11 PF03105.16*SPX*SPX domain*71-114*E:9.5e-07 PF03105.16*SPX*SPX domain*131-168*E:7.5e-09	0.568	-0.201	0	-2.306	0.278	-0.659	0.377	-0.547	0.694	-0.193;SPX4_ARATH	SPX domain-containing protein 4 (Protein SPX DOMAIN GENE 4) (AtSPX4)	SPX4 At5g15330 F8M21_220	Arabidopsis thaliana (Mouse-ear cress)	-	-	Complete proteome; Reference proteome
SRR648707_TR21831_c0_g1_i1_len=1227	NA	NA	NA	NA	NA	PF16697.2*Yop-YscD_cpl*Inner membrane component of TSS, cytoplasmic domain*104-185*E:4.4e-10 PF00498.23*FHA*FHA domain*112-179*E:1.2e-13	0.334	-0.258	0	-0.864	0.824	0.055	0.434	0.194	0.788	-0.071	-	-	-	-	-	-
SRR648707_TR25509_c0_g2_i1_len=942	NA	NA	NA	NA	NA	-	0.73	0.12	0	-2.04	0.001	-0.887	0.313	-0.27	0.398	-0.423	-	-	-	-	-	-
SRR648707_TR28008_c1_g1_i2_len=1388	NA	NA	NA	NA	NA	-	0.258	-0.493	0	-1.955	0.221	-0.515	1	-0.006	0.203	-0.512	-	-	-	-	-	-
SRR648707_TR28966_c0_g1_i1_len=928	TCX2_ARATH	Q:833-243;H:479-674	41.04%ID	E-1e-23	Protein tesmin/TSO1-like CXC 2	0.111	-1.453	0	-7.077	0.381	-1.335	0.692	-0.646	0.044	-1.167;TCX2_ARATH	Protein tesmin/TSO1-like CXC 2 (AtTCX2) (Protein TSO1-like 2) (Protein SOL2)	TCX2 SOL2 At4g14770 dl3425c FCAALL.306	Arabidopsis thaliana (Mouse-ear cress)	-	-	Complete proteome; Developmental protein; Metal-binding; Nucleus; Reference proteome; Zinc
SRR648707_TR34294_c0_g1_i3_len=1245	BH149_ARATH	Q:899-462;H:37-188	50.32%ID	E-3e-34	Transcription factor bHLH149	0.851	0.088	0	-1.711	0.664	-0.159	0.008	-1.002	0.378	-0.339;BH149_ARATH	Transcription factor bHLH149 (ATBS1 interacting factor 4) (Basic helix-loop-helix protein 149) (AtbHLH149) (bHLH 149) (Transcription factor EN 144) (bHLH transcription factor bHLH149)	BHLH149 AIF4 EN 144 At1g09250 T12M8.4	Arabidopsis thaliana (Mouse-ear cress)	-	-	Complete proteome; DNA-binding; Nucleus; Reference proteome; Transcription; Transcription regulation
SRR648707_TR37155_c0_g1_i1_len=2065	Y3913_ARATH	Q:1606-347;H:88-497	50.12%ID	E-9e-127	Uncharacterized protein At3g49140	0.617	-0.19	0.001	-1.236	0.059	-0.717	0.108	-0.618	1	-0.009;Y3913_ARATH	Uncharacterized protein At3g49140	At3g49140 F2K15.2 T2J13.20	Arabidopsis thaliana (Mouse-ear cress)	-	-	Complete proteome; Phosphoprotein; Reference proteome
SRR648707_TR37562_c0_g1_i1_len=1266	PABN2_ARATH	Q:1044-421;H:13-219	84.13%ID	E-1e-85	Polyadenylate-binding protein 2 (ECO:0000303)PubMed:18479511)	PF00076.19*RRM_1*RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)*95-163*E:2.5e-17 PF13893.3*RRM_5*RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)*108-166*E:0.03	0.957	0.041	0	-3.299	0.608	0.21	0	1.175	0.129	4.873;PABN2_ARATH	Polyadenylate-binding protein 2 (AtPabN2) (Poly(A)-binding protein 2) (Nuclear poly(A)-binding protein 2) (Poly(A)-binding protein II) (PABII)	PABN2 At5g65260 MQN23.20	Arabidopsis thaliana (Mouse-ear cress)	-	-	Coiled coil; Complete proteome; Cytoplasm; Nucleus; RNA-binding; Reference proteome
SRR924147_TR403_c0_g1_i1_len=815	NA	NA	NA	NA	NA	PF05768.11*DUF836*Glutaredoxin-like domain (DUF836)*59-145*E:2.3e-20	0.164	-0.538	0	-2.054	0.811	0.306	1	-0.017	0.708	0.161	-	-	-	-	-	-
SRR924147_TR9296_c0_g3_i2_len=1005	RS12_HORVU	Q:199-558;H:24-143	82.5%ID	E-4e-57	40S ribosomal protein S12	PF01248.23*Ribosomal_L7Ae*Ribosomal protein L7Ae/L30e/S12e/Gad045 family*25-118*E:1.8e-26	1	3.289	0	-8.403	0.312	0.765	1	0.083	0.057	1,361;RS12_HORVU	40S ribosomal protein S12	RPS12	Hordeum vulgare (Barley)	-	-	Ribonucleoprotein; Ribosomal protein
SRR924147_TR5604_c0_g1_i1_len=2693	PP222_ARATH	Q:554-2548;H:8-775	67.43%ID	E-0	Pentatricopeptide repeat-containing protein At3g09650, chloroplastic	PF13812.3*PPR_3*Pentatricopeptide repeat domain*224-279*E:4.6e-12 PF13041.3*PPR_2*PPR repeat family*232-280*E:6e-13 PF01535.17*PPR*PPR repeat*236-265*E:0.0005 PF01535.17*PPR*PPR repeat*271-299*E:1.2 PF12854.4*PPR_1*PPR repeat*382-411*E:2.3e-05 PF01535.17*PPR*PPR repeat*387-411*E:0.033 PF17177.1*PPR_long*Pentacotripeptide-repeat region of PROPR*403-504*E:6.6e-07 PF12854.4*PPR_1*PPR repeat*420-450*E:9.6e-07 PF13041.3*PPR_2*PPR repeat family*421-470*E:6.7e-14 PF13812.3*PPR_3*Pentatricopeptide repeat domain*421-468*E:1.6e-07 PF01535.17*PPR*PPR repeat*424-454*E:6.6e-06 PF13041.3*PPR_2*PPR repeat family*457-504*E:3.3e-12 PF01535.17*PPR*PPR repeat*459-486*E:0.00096 PF13812.3*PPR_3*Pentatricopeptide repeat domain*483-539*E:3.2e-09 PF13041.3*PPR_2*PPR repeat family*492-540*E:4.7e-12 PF01535.17*PPR*PPR repeat*498-528*E:0.00016 PF13812.3*PPR_3*Pentatricopeptide repeat domain*517-557*E:6.8e-05 PF01535.17*PPR*PPR repeat*530-557*E:0.000127 PF13812.3*PPR_3*Pentatricopeptide repeat domain*551-606*E:1e-06 PF12854.4*PPR_1*PPR repeat*561-592*E:3.2e-08 PF13041.3*PPR_2*PPR repeat family*564-610*E:3.3e-12 PF01535.17*PPR*PPR repeat*566-596*E:3.1e-08 PF01535.17*PPR*PPR repeat*601-629*E:1.1	1	-2.284	0	-3.973	1	0	1	0	1	-0.006;PP222_ARATH	Pentatricopeptide repeat-containing protein At3g09650, chloroplastic (Protein HIGH CHLOROPHYLL FLUORESCENCE 152)	HCF152 CRM3 At3g09650 F11F8_24	Arabidopsis thaliana (Mouse-ear cress)	-	-	Chloroplast; Complete proteome; Nucleotide-binding; Plastid; RNA-binding; Reference proteome; Repeat; Transit peptide
SRR924147_TR6523_c0_g1_i1_len=887	NA	NA	NA	NA	NA	-	0.017	-5.844	0.001	-6.62	1	0	1	0	0.471	-0.493	-	-	-	-	-	-
SRR924147_TR7995_c0_g1_i1_len=1581	UREG_ARATH	Q:369-1112;H:28-275	92.74%ID	E-7e-168	Urease accessory protein G	PF02492.16*cobW*CobW/HypB/UreG, nucleotide-binding domain*86-254*E:4.2e-32	0.458	-0.272	0	-1.349	0.517	-0.277	0.142	-0.564	0.752	0.091;UREG_ARATH	Urease accessory protein G (AtUREG)	UREG At2g34470	Arabidopsis thaliana (Mouse-ear cress)	-	-	Alternative splicing; Chaperone; Complete proteome; GTP-binding; Nickel insertion; Nucleotide-binding; Reference proteome
SRR924147_TR8351_c0_g1_i1_len=1715	NA	NA	NA	NA	NA	PF04862.9*DUF642*Protein of unknown function (DUF642)*31-188*E:2e-64 PF04862.9*DUF642*Protein of unknown function (DUF642)*201-366*E:9.7e-19	0.041	-0.611	0	-2.27	0.759	-0.248	0.489	-0.487	0.052	-0.63	-	-	-	-	-	-
SRR924147_TR16824_c0_g1_i1_len=1457	RSI1_SOLLC	Q:843-607;H:6-96	65.93%ID	E-3e-31	Protein RSI-1	0.129	-1.005	0	-3.304	1	-0.802	1	-1.266	1	-0.806;RSI1_SOLLC	Protein RSI-1 (TR132)	RSI-1	Solanum lycopersicum (Tomato) (Lycopersicon esculentum)	-	-	Complete proteome; Disulfide bond; Reference proteome; Secreted; Signal
SRR924147_TR19455_c2_g1_i1_len=2387	CHUP1_ARATH	Q:1113-325;H:720-984	59.71%ID	E-2e-97	Protein CHUP1, chloroplastic	0.318	-0.467	0	-3.992	0.076	-2.345	0.076	-2.292	1	-0.166;CHUP1_ARATH	Protein CHUP1, chloroplastic (Protein CHLOROPLAST UNUSUAL POSITIONING 1)	CHUP1 At3g25690 T5M7.14	Arabidopsis thaliana (Mouse-ear cress)	-	-	Alternative splicing; Chloroplast; Coiled coil; Complete proteome; Membrane; Phosphoprotein; Plastid; Plastid outer membrane; Reference proteome; Repeat
SRR924147_TR22073_c0_g2_i1_len=1027	NA	NA	NA	NA	NA	PF17067.2*RPS31*Ribosomal protein S31e*1-94*E:1.1e-31	0.511	-0.192	0	-1.826	0.007	-0.801	0.001	-0.957	0.56	-0.709	-	-	-	-	-	-
SRR924147_TR22093_c2_g5_i1_len=8305	TI214_COFAR	Q:459-1819;H:1067-1873	70.96%ID	E-0	Protein TIC 214 (ECO:0000250)UniProtKB:P56785)	1	-0.059	0	-3.294	0.381	2.002	0.381	2.104	0.149	-0.381;TI214_COFAR	Protein TIC 214 (Translocon at the inner envelope membrane of chloroplasts 214) (AtTIC214)	TIC214 ycf1	Coffea arabica (Arabian coffee)	-	-	Chloroplast; Membrane; Plastid; Plastid inner membrane; Protein transport; Transmembrane; Transmembrane helix; Transport
SRR924147_TR22473_c0_g2_i2_len=853	NA	NA	NA	NA	NA	-	0.228	-1.134	0	-2.954	0.235	-0.949	0.581	-0.383	1	0.028	-	-	-	-	-	-
SRR924147_TR25917_c0_g1_i1_len=741	PATL6_ARATH	Q:66-461;H:27-407	74.07%ID	E-1e-63	Patellin-6	0.635	-0.318	0	-3.111	0.282	0.979	1	-0.135	0.09	-0.685;PATL6_ARATH	Patellin-6	PATL6 At3g51670 T18N14.50	Arabidopsis thaliana (Mouse-ear cress)	-	-	Cell cycle; Cell division; Coiled coil; Complete proteome; Cytoplasm; Lipid-binding; Membrane; Reference proteome; Transport
SRR924147_TR29981_c0_g1_i1_len=950	NA	NA	NA	NA	NA	-	0.44	-0.884	0	-3.584	1	0	-0.403	0.472	0.691	1	-0.299	-	-	-	-	-
SRR924147_TR27509_c0_g1_i1_len=723	SYFM_ARATH	Q:620-309;H:325-429	80.95%ID	E-1e-52	Phenylalanine--tRNA ligase, chloroplastic/mitochondrial (ECO:0000305)	-	0.798	0.523	0	-2.817	0.591	0.355	0.115	0.8	0.016	-1.264;SYFM_ARATH	Phenylalanine--tRNA ligase, chloroplastic/mitochondrial (EC 6.1.1.20) (Phenylalanyl-tRNA synthetase) (PheRS)	At3g58140 F9D24.50	Arabidopsis thaliana (Mouse-ear cress)	-	-	ATP-binding; Acetylation; Aminoacyl-tRNA synthetase; Chloroplast; Complete proteome; Ligase; Mitochondrion; Nucleotide-binding; Plastid; Protein biosynthesis; Reference proteome; Transit peptide
SRR924147_TR31027_c0_g1_i1_len=1067	21KD_DAUCA	Q:695-240;H:28-187	45.62%ID	E-1e-41	21 kDa protein	PF04043.12*PMEI*Plant invertase/pectin methylesterase inhibitor*36-183*E:4.3e-37	0.009	-0.747	0	-2.708	0.059	-1.81	0.111	-1.424	0.594	0.252;21KD_DAUCA	21 kDa protein (1.2 protein)	Daucus carota (Wild carrot)	-	-	Signal
SRR924147_TR34664_c0_g2_i1_len=1368	RK9_ARATH	Q:914-378;H:16-197	73.63%ID	E-6e-58	50S ribosomal protein L9, chloroplastic	PF01281.16*Ribosomal_L9_N*Ribosomal protein L9, N-terminal domain*50-95*E:3e-16 PF03948.15*Ribosomal_L9_C*Ribosomal protein L9, C-terminal domain*111-193*E:1.3e-21	0.051	-0.495	0	-1.103	0.843	-0.077	0.812	0.083	0.076	-0.44;RK9_ARATH	50S ribosomal protein L9, chloroplastic (CL9)	RPL9 At3g44890 F28D10_80	Arabidopsis thaliana (Mouse-ear cress)	-	-	Chloroplast; Complete proteome; Plastid; RNA-binding; Reference proteome; Ribonucleoprotein; Ribosomal protein; Transit peptide; rRNA-binding
SRR924147_TR38112_c0_g2_i1_len=1089	UBC9_ARATH	Q:868-425;H:1-148	95.95%ID	E-7e-100	SUMO-conjugating enzyme UBC9	PF00179.23*UQ_con*Ubiquitin-conjugating enzyme*5-141*E:1e-53	1	0	0	-6.992	1	0	0	0.129	1	-1;UBC9_ARATH	SUMO-conjugating enzyme UBC9 (EC 6.3.2.-) (UBCA T48) (Ubiquitin carrier protein 9) (Ubiquitin-conjugating enzyme E2 9) (Ubiquitin-conjugating enzyme E2-17 kDa) (Ubiquitin-protein ligase 9)	UBC9 UBC4B At4g27960 T13J8.70	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Protein modification; protein sumoylation.	-	ATP-binding; Alternative splicing; Chloroplast; Complete proteome; Ligase; Nucleotide-binding; Reference proteome; Ubl conjugation; Ubl conjugation pathway
SRR924148_TR6830_c0_g2_i1_len=1281	ABS9B_ARATH	Q:91-1248;H:847-1233	59.95%ID	E-8e-149	ABC transporter B family member 9	PF00664.20*ABC_membrane*ABC transporter transmembrane region*6-97*E:1.6e-18 PF00005.24*ABC_tran*ABC transporter*165-331*E:1e-33 PF03283.8*DLC*Dynein light intermediate chain (DLIC)*172-204*E:0.0007 2 PF00004.24*AAA*ATPase family associated with various cellular activities (AAA)*178-375*E:0.00032	0.243	-0.586	0	-1.736	0.719	0.418	0.719	0.4	0.35	-0.451;ABS9B_ARATH	ABC transporter B family member 9 (ABC transporter ABCB.9) (AtABCB9) (Multidrug resistance protein 9) (P-glycoprotein 9)	ABCB9 MDR9 PGP9 At4g18050 F15J5.20	Arabidopsis thaliana (Mouse-ear cress)	-	-	ATP-binding; Complete proteome; Glycoprotein; Membrane; Nucleotide-binding; Reference proteome; Repeat; Transmembrane; Transmembrane helix; Transport
SRR924148_TR7299_c0_g3_i6_len=1191	NA	NA	NA	NA	NA	-	0.86	-0.251	0	-3.225	0.18	-0.919	0.25	-0.802	0.76	0.553	-	-	-	-	-	-
SRR924148_TR12427_c0_g1_i7_len=2086	TSJT1_TOBAC	Q:894-448;H:1-149	64%ID	E-2e-57	Stem-specific protein TSJT1	PF12481.5*DUF3700*Aluminium induced protein*3-228*E:7.1e-84 PF13537.3*GATase_7*Glutamine amidotransferase domain*77-176*E:2.1e-09	0.335	-0.695	0	-2.818	1	0.228	1	-0.213	1	-0.001;TSJT1_TOBAC	Stem-specific protein TSJT1	TSJT1	Nicotiana tabacum (Common tobacco)	-	-	-
SRR924148_TR16923_c1_g1_i2_len=1314	REMO_SOLTU	Q:766-266;H:29-198	79.53%ID	E-1e-66	Remorin	PF03766.10*Remorin_N*Remorin, N-terminal region*33-87*E:2.1e-21 PF03763.10*Remorin_C*Remorin, C-terminal region*92-196*E:1.4e-31	0.297	-0.259	0	-1.098	0.044	-0.572	0.396	0.224	1	-0.262;REMO_SOLTU	Remorin (pp34)	Solanum tuberosum (Potato)	-	-	-
SRR924148_TR19021_c0_g1_i1_len=964	PHI_MYCGS	Q:186-794;H:5-199	35.92%ID	E-7e-24	3-hexulose-6-phosphate isomerase	-	0.272	-0.381	0	-1.17	0.079	-0.913	0.232	-0.567	0.385	0.29;PHI_MYCGS	3-hexulose-6-phosphate isomerase (EC 5.3.1.27) (6-phospho-3-hexuloisomerase) (PHI)	rmpB	Mycobacterium gastri	PATHWAY: One-carbon metabolism; formaldehyde assimilation via RuMP pathway; D-fructose 6-phosphate from D-ribulose 5-phosphate and formaldehyde: step 2/2.	-	Carbohydrate metabolism; Isomerase
SRR924148_TR20412_c0_g1_i13_len=2364	AFC2_ARATH	Q:1071-556;H:253-425	84.97%ID	E-4e-93	Serine/threonine-protein kinase AFC2	0.01	-2.027	0	-7.752	0.545	0.568	0.43	0.706	1	-1.753;AFC2_ARATH	Serine/threonine-protein kinase AFC2 (EC 2.7.12.1)	AFC2 At4g24740 F22K18.60	Arabidopsis thaliana (Mouse-ear cress)	-	-	ATP-binding; Alternative splicing; Complete proteome; Kinase; Nucleotide-binding; Reference proteome; Serine/threonine-protein kinase; Transferase
SRR924148_TR23813_c0_g1_i1_len=655	PB27A_ARATH	Q:183-569;H:43-174	69.92%ID	E-4e-58	Photosystem II repair protein PSB27-H1, chloroplastic	PF13326.3*PSII_Pbs27*Photosystem II Pbs27*59-185*E:1e-30	0.798	-0.369	0.001	-2.634	0.335	-0.769	0.581	-0.473	0.768	0.067;PB27A_ARATH	Photosystem II repair protein PSB27-H1, chloroplastic (Psb27-H1) (Thylakoid lumenal protein PSB27-H1)	PSB27-1 At1g03600 F21B7.14 F21B7.21 F21B7.22 F21B7_140	Arabidopsis thaliana (Mouse-ear cress)	-	-	Chloroplast; Complete proteome; Direct protein sequencing; Membrane; Phosphoprotein; Plastid; Reference proteome; Thylakoid; Transit peptide
SRR924148_TR24436_c0_g2_i1_len=753	ACBP_RICCO	Q:569-315;H:1-85	88.24%ID	E-2e-46	Acyl-CoA-binding protein	0.009	5.955	0.001	-6.655	1	0	1	0	1	0	0 ACBP_RICCO	Acyl-CoA-binding protein (ACBP)	Ricinus communis (Castor bean)	-	-	Lipid-binding; Transport
SRR924148_TR26347_c0_g1_i4_len=1742	GEDH1_OCIBA	Q:1423-707;H:1-242	56.61%ID	E-4e-83	Geraniol dehydrogenase 1	PF08240.9*ADH_N*Alcohol dehydrogenase GroES-like domain*37-146*E:1.6e-23 PF02826.16*2-Hacid_dh_C*D-isomer specific 2-hydroxyacid dehydrogenase, NAD binding domain*177-227*E:1.5e-06	0.138	0.654	0	-2.802	0.026	-1.086	0.018	-1.159	0.823	0.085;GEDH1_OCIBA	Geraniol dehydrogenase 1 (ObaGEDH1) (EC 1.1.1.183)	GEDH1	Ocimum basilicum (Sweet basil)	-	-	Metal-binding; NADP; Oxidoreductase; Zinc
SRR924148_TR28419_c0_g3_i2_len=1336	PIP1_SOLLC	Q:203-1048;H:1-282	85.52%ID	E-3e-179	Probable aquaporin PIP-type pTOM75	PF00230.17*MIP*Major intrinsic protein*45-274*E:3.2e-84	1.97	-0.045	0	-1.305	0	1	0	0.818	0.444	0.317;PIP1_SOLLC	Probable aquaporin PIP-type pTOM75 (Ripening-associated membrane protein) (RAMP)	Solanum lycopersicum (Tomato) (Lycopersicon esculentum)	-	-	Cell membrane; Complete proteome; Membrane; Reference proteome; Repeat; Stress response; Transmembrane; Transmembrane helix; Transport
SRR924148_TR29305_c0_g1_i1_len=2045	NA	NA	NA	NA	NA	-	0.009	-1.127	0	-4.017	0.226	-2.078	0.461	-1.585	0.629	-1.245	-	-	-	-	-	-
SRR924148_TR31545_c0_g1_i2_len=1650	TRPD_ARATH	Q:132-1231;H:304-437	77.61%ID	E-1e-55	Anthranilate phosphoribosyltransferase, chloroplastic	PF00591.18*Glycos_transf_3*Glycosyl transferase family, a/b domain*1-121*E:4.4e-30	0.076	-3.088	0	-4.301	0.005	-5.047	0.005	-5.575	1	0.006;TRPD_ARATH	Anthranilate phosphoribosyltransferase, chloroplastic (EC 2.4.2.18)	PAT1 At5g17990 MCM23.6	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Amino-acid biosynthesis; L-tryptophan biosynthesis; L-tryptophan from chorismate: step 2/5.	-	Amino-acid biosynthesis; Aromatic amino acid biosynthesis; Chloroplast; Complete proteome; Glycosyltransferase; Plastid; Reference proteome; Transferase; Transit peptide; Tryptophan biosynthesis
SRR924148_TR32136_c0_g1_i1_len=1524	PER42_ARATH	Q:1365-376;H:1-330	79.7%ID	E-0	Peroxidase 42	PF00141.20*peroxidase*Peroxidase*48-291*E:4.1e-60	0.219	-0.273	0	-2.176	0.492	-0.189	0.007	-0.786	0	0.948;PER42_ARATH	Peroxidase 42 (Atperox P42) (EC 1.11.1.7) (ATP1a/ATP1b) (PRXR1)	PER42 P42 At4g21960 F1N20.3 T8O5.170	Arabidopsis thaliana (Mouse-ear cress)	-	-	Biological rhythms; Calcium; Complete proteome; Disulfide bond; Glycoprotein; Heme; Hydrogen peroxide; Iron; Metal-binding; Oxidoreductase; Peroxidase; Reference proteome; Secreted; Signal
SRR924148_TR34588_c0_g1_i1_len=966	NA	NA	NA	NA	NA	PF05498.8*RALF*Rapid ALkalinization Factor (RALF)*72-131*E:7.4e-09	1	-0.024	0	-1.954	0.142	0.747	0.114	0.817	0.036	0.505	-	-	-	-	-	-
SRR924148_TR34958_c0_g1_i4_len=1690	PUMP2_ARATH	Q:1062-586;H:146-304	75.47%ID	E-6e-109	Mitochondrial uncoupling protein 2	PF00153.24*Mito_carr*Mitochondrial carrier protein*7-105*E:3e-20	0.707	0.416	0.001	-2.641	0.158	-1.581	0.44	-0.869	0.357	0.687;PUMP2_ARATH	Mitochondrial uncoupling protein 2 (AtPUMP2)	PUMP2 UCP2 At5g58970 K19M22.16	Arabidopsis thaliana (Mouse-ear cress)	-	-	Alternative splicing; Complete proteome; Membrane; Mitochondrion; Mitochondrion inner membrane; Reference proteome; Repeat; Stress response; Transmembrane; Transmembrane helix; Transport
SRR924148_TR35654_c0_g2_i1_len=1485	NA	NA	NA	NA	NA	PF00786.25*PBD*P21-Rho-binding domain*112-143*E:5.4e-09	1	-0.053	0	-4.599	0.038	-1.613	0.017	-1.965	0.684	0.03	-	-	-	-	-	-
SRR924148_TR38039_c1_g2_i1_len=1769	P2SAF_ARATH	Q:369-1346;H:78-403	87.42%ID	E-0	Photosystem II stability/assembly factor HCF136, chloroplastic	PF14870.3*PSII_BNR*Photosynthesis system II assembly factor YCF48*80-401*E:1.6e-122	0.014

SRR342019_TR35470_c2_g2_i5_len=2052	TPT_PEA	Q:71-1291,H:1-402	79.17%ID	E:0	Triose phosphate/phosphate translocator, chloroplastic	PF03151.13*TPT*Triose-phosphate Transporter family*127-414*E:4.8e-111 PF00892.17*EamA*EamA-like transporter family*270-414*E:1.9e-06	0,731	-0,092	0,205	-0,349	0	-0,906	0,005	-0,613	0,012	0,618	TPT_PEA	Triose phosphate/phosphate translocator, chloroplastic (cTPT) (E30) (p36)		Pisum sativum (Garden pea)		Chloroplast; Direct protein sequencing; Membrane; Plastid; Transit peptide; Transmembrane; Transmembrane helix; Transport
SRR342019_TR36227_c6_g10_i1_len=1554	GDT11_ARATH	Q:475-1053,H:112-304	77.32%ID	E:1e-83	GDT1-like protein 1, chloroplastic	PF01169.16*UPF0016*Uncharacterized protein family UPF0016*163-246*E:3.1e-19	0,38	-0,521	0,008	-1,573	0,001	-1,657	0,003	-1,397	1	-0,028	GDT11_ARATH	GDT1-like protein 1, chloroplastic	At1g64150 F22C12.9	Arabidopsis thaliana (Mouse-ear cress)			Chloroplast; Complete proteome; Membrane; Plastid; Reference proteome; Transit peptide; Transmembrane; Transmembrane helix
SRR342019_TR38704_c0_g2_i2_len=2572	COLX_ARATH	Q:299-613,H:10-115	52.83%ID	E:1e-28	Putative zinc finger protein At1g68190	.	1	-0,04	0,118	-1,779	0,001	-4,326	0,016	-2,769	0,282	1,129	COLX_ARATH	Putative zinc finger protein At1g68190	At1g68190 T22E19.18	Arabidopsis thaliana (Mouse-ear cress)			Complete proteome; Metal-binding; Nucleus; Reference proteome; Repeat; Zinc; Zinc-finger
SRR342022_TR4690_c0_g1_i2_len=1962	GLYM_SOLTU	Q:143-1594,H:34-518	91.55%ID	E:0	Serine hydroxymethyltransferase, mitochondrial	PF00464.16*SHMT*Serine hydroxymethyltransferase*1-362*E:8e-195	0,747	0,08	0,352	0,213	0	-0,799	0,003	-0,652	0,195	0,284	GLYM_SOLTU	Serine hydroxymethyltransferase, mitochondrial (SHMT) (EC 2.1.2.1) (Glycine hydroxymethyltransferase) (Serine methylase)		Solanum tuberosum (Potato)	PATHWAY: One-carbon metabolism; tetrahydrofolate interconversion.	Complete proteome; Mitochondrion; One-carbon metabolism; Pyridoxal phosphate; Reference proteome; Transferase; Transit peptide
SRR342022_TR8241_c0_g2_i2_len=2500	PPR68_ARATH	Q:808-2489,H:14-679	58.02%ID	E:0	Pentatricopeptide repeat-containing protein At1g31920	PF13041.2*PPR_2*PPR repeat family*95-143*E:4.1e-11 PF13812.3*PPR_3*Pentatricopeptide repeat domain*95-141*E:9e-06 PF01535.17*PPR*PPR repeat*99-126*E:0.0015 PF01535.17*PPR*PPR repeat*170-193*E:0.0022 PF01535.17*PPR*PPR repeat*199-223*E:0.0007 PF01535.17*PPR*PPR repeat*273-299*E:2.8e-03 PF01535.17*PPR*PPR repeat*302-331*E:2.9e-05 PF13812.3*PPR_3*Pentatricopeptide repeat domain*322-382*E:0.0002 PF01535.17*PPR*PPR repeat*336-362*E:0.00036 PF01535.17*PPR*PPR repeat*374-398*E:0.029 PF14432.3*DYW_deaminase*DYW family of nucleic acid deaminases*472-678*E:4.1e-23 PF14306.3*PUA_2*PUA-like domain*69-231*E:3e-46 PF01747.14*ATP-sulfurylase*ATP-sulfurylase*240-463*E:4.5e-65	0,16	-1,32	0,129	-4,898	0,001	-1,333	0,005	-1,081	0,608	0,229	PPR68_ARATH	Pentatricopeptide repeat-containing protein At1g31920	PCMP-H11 At1g31920 F5M6.8	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Reference proteome; Repeat
SRR342022_TR9956_c0_g1_i2_len=2205	APS2_ARATH	Q:346-1782,H:1-475	75.57%ID	E:0	ATP sulfurylase 2	PF01747.14*ATP-sulfurylase*ATP-sulfurylase*240-463*E:4.5e-65	0,626	-0,249	0,739	-0,266	0	-1,202	0,003	-0,755	0,629	-0,19	APS2_ARATH	ATP sulfurylase 2 (EC 2.7.7.4)	APS2 ASA1 MET3-1 At1g19920 F6F9.2	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Sulfur metabolism; hydrogen sulfide biosynthesis; sulfite from sulfate: step 1/3.	ATP-binding; Alternative initiation; Chloroplast; Complete proteome; Cytoplasm; Nucleotide-binding; Nucleotidyltransferase; Plastid; Reference proteome; Transferase; Transit peptide
SRR342022_TR11785_c0_g2_i3_len=2432	LUT1_ARATH	Q:2216-708,H:33-539	81.85%ID	E:0	Carotene epsilon-monooxygenase, chloroplastic	PF00067.19*p450*Cytochrome P450*99-521*E:9.8e-81	1	-0,01	0,12	-0,662	0	-1,462	0,001	-1,19	0,784	-0,148	LUT1_ARATH	Carotene epsilon-monooxygenase, chloroplastic (EC 1.14.99.45) (Cytochrome P450 97C1) (Protein LUTEIN DEFICIENT 1)	CYP97C1 LUT1 At3g53130 T4D2.60	Arabidopsis thaliana (Mouse-ear cress)		Carotenoid biosynthesis; Chloroplast; Complete proteome; Heme; Iron; Membrane; Metal-binding; Monooxygenase; Oxidoreductase; Plastid; Reference proteome; Transit peptide
SRR342022_TR16045_c5_g2_i5_len=1592	ALJ3F1_ARATH	Q:151-461,H:1-484	50.62%ID	E:2e-151	Aldehyde dehydrogenase family 3 member F1	PF00171.19*Aldedh*Aldehyde dehydrogenase family*16-357*E:2e-67	0,29	-0,421	0,034	-1,014	0	-2,065	0,064	-0,98	0,121	0,804	ALJ3F1_ARATH	Aldehyde dehydrogenase family 3 member F1 (EC 1.2.1.3)	ALDH3F1 Atlg36250 F23E13.140	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; NAD; Oxidoreductase; Reference proteome
SRR342022_TR17158_c1_g3_i13_len=1510	GPPL2_ARATH	Q:368-920,H:66-220	85.81%ID	E:5e-114	Haloacid dehalogenase-like hydrolase domain-containing protein At3g48420	.	0,527	-0,182	0,484	-0,19	0	-0,899	0,015	-0,596	0,914	-0,041	GPPL2_ARATH	Haloacid dehalogenase-like hydrolase domain-containing protein At3g48420 (EC 3.1.3.-)	At3g48420 T29H11.60	Arabidopsis thaliana (Mouse-ear cress)			3D-structure; Chloroplast; Complete proteome; Hydrolase; Magnesium; Metal-binding; Plastid; Reference proteome; Transit peptide
SRR342023_TR5684_c1_g2_i7_len=777	NA	NA	NA	NA	NA	NA	0,258	1,033	0,452	-0,553	0	-1,407	0,025	-0,801	0,166	-0,772	.		.				
SRR342023_TR6740_c3_g1_i3_len=679	RTNLA_ARATH	Q:362-679,H:70-175	72.64%ID	E:1e-49	Reticulon-like protein B1	PF02453.14*Reticulon*Reticulon*70-152*E:2e-25	1	0	1	0	0	-7,727	0,9	-0,134	1	0	RTNLA_ARATH	Reticulon-like protein B1 (AIRTNLB1) (VirB2-interacting protein 1)	RTNLB1 BTI1 At4g23630 F8D16.100	Arabidopsis thaliana (Mouse-ear cress)			Acetylation; Cell membrane; Complete proteome; Endoplasmic reticulum; Membrane; Reference proteome; Transmembrane; Transmembrane helix
SRR342023_TR11601_c0_g1_i1_len=687	NA	NA	NA	NA	NA	NA	0,78	0,856	1	-0,021	0	-0,962	0,006	-0,638	0,178	0,81	.		.				
SRR342023_TR13950_c0_g1_i2_len=554	RK12_NICSY	Q:45-461,H:1-127	71.76%ID	E:1e-35	50S ribosomal protein L12, chloroplastic	PF16320.2*Ribosomal_L12_N*Ribosomal protein L7/L12 dimerisation domain*62-109*E:7.3e-14	0,002	-0,69	0,793	-0,071	0	-0,895	0,015	-0,571	0,927	0,076	RK12_NICSY	50S ribosomal protein L12, chloroplastic (CL12)		Nicotiana sylvestris (Wood tobacco) (South American tobacco)		Chloroplast; Plastid; Ribonucleoprotein; Ribosomal protein; Transit peptide
SRR342023_TR16855_c0_g1_i1_len=869	PSAEA_NICSY	Q:310-672,H:21-141	69.92%ID	E:1e-35	Photosystem I reaction center subunit IV A, chloroplastic	PF02432.14*PSI_PsaE*Photosystem I reaction centre subunit IV / PsaE*82-141*E:2.2e-30	0,246	0,242	0,019	-0,488	0,001	-0,688	0,002	-0,651	0,807	0,052	PSAEA_NICSY	Photosystem I reaction center subunit IV A, chloroplastic (PSI-E A) (Cleaved into: Photosystem I reaction center subunit IV A isoform 2)	PSAEA	Nicotiana sylvestris (Wood tobacco) (South American tobacco)		Chloroplast; Direct protein sequencing; Membrane; Photosynthesis; Photosystem I; Plastid; Thylakoid; Transit peptide
SRR342023_TR19508_c3_g13_i7_len=2221	BASS2_ARATH	Q:205-909,H:1-224	64.68%ID	E:3e-84	Sodium/pyruvate cotransporter BASS2, chloroplastic	PF13193.3*SBF_like*SBF-like CPA transporter family (DUF4137)*136-233*E:1.3e-06 PF01758.13*SBF*Sodium Bile acid symporter family*143-230*E:3.2e-30	0,11	-0,498	0,234	-0,517	0	-1,169	0,027	-0,625	0,051	0,524	BASS2_ARATH	Sodium/pyruvate cotransporter BASS2, chloroplastic (Bile acid transporter 1) (Bile acid-sodium symporter family protein 2)	BASS2 BAT1 SBF1 At2g26900 F12CD20.6	Arabidopsis thaliana (Mouse-ear cress)			Acetylation; Chloroplast; Complete proteome; Membrane; Plastid; Reference proteome; Transit peptide; Transmembrane; Transmembrane helix; Transport
SRR342023_TR22755_c1_g2_i2_len=451	NA	NA	NA	NA	NA	.	0,61	-0,176	0,943	0,044	0	-0,903	0,131	-0,352	0,062	0,613	.		.				
SRR342023_TR23453_c2_g8_i11_len=3617	HEM11_CUCSA	Q:1610-3307,H:1-552	81.27%ID	E:0	Glutamyl-tRNA reductase 1, chloroplastic	PF05201.12*GluRR_N*Glutamyl-tRNAGlu reductase, N-terminal domain*121-271*E:1.3e-08 PF01488.15*Shikimate_DH*Shikimate / quinate 5-dehydrogenase*287-428*E:5.2e-44 PF02423.12*OCD_Mu_crystal*Ornithine cyclodeaminase/mu-crystallin family*299-382*E:3.5e-05 PF03807.14*F420_oxidored*NAD(P) oxidoreductase coenzyme F420-dependent*304-393*E:4.3e-07 PF00346.12*NAD_binding_2*NAD binding domain of 6-phosphogluconate dehydrogenase*304-435*E:9.8e-06 PF00745.11*GluR_dimer*Glutamyl-tRNAGlu reductase, dimerisation domain*442-546*E:2.8e-29	0,895	0,048	0,382	-0,24	0,001	-0,787	0,03	-0,497	1	0,018	HEM11_CUCSA	Glutamyl-tRNA reductase 1, chloroplastic (GluTR) (EC 1.2.1.70)	HEMA1	Cucumis sativus (Cucumber)	PATHWAY: Porphyrin-containing compound metabolism; protoporphyrin-IX biosynthesis; 5-aminolevulinate from L-glutamyl-tRNA(Glu): step 1/2.	Chlorophyll biosynthesis; Chloroplast; NADP; Oxidoreductase; Plastid; Porphyrin biosynthesis; Transit peptide
SRR342023_TR25894_c1_g3_i4_len=2328	RK2B_COFAR	Q:1983-1585,H:1-133	97.74%ID	E:6e-82	50S ribosomal protein L2-B, chloroplastic	PF03947.15*Ribosomal_L2_C*Ribosomal Proteins L2, C-terminal domain*111-179*E:5e-50	0,018	-0,574	0,021	-0,568	0	-0,993	0,002	-0,748	1	-0,683	RK2B_COFAR	50S ribosomal protein L2-B, chloroplastic	rpl2-B	Coffea arabica (Arabian coffee)			Chloroplast; Plastid; Ribonucleoprotein; Ribosomal protein
SRR346572_TR29356_c0_g1_i1_len=2714	LACS9_ARATH	Q:2235-151,H:1-691	77.12%ID	E:0	Long chain acyl-CoA synthetase 9, chloroplastic	PF00501.25*AMP-binding*AMP-binding enzyme*97-562*E:2.5e-105	0,415	-0,348	0,493	-0,315	0	-1,069	0,002	-0,829	0,258	0,839	LACS9_ARATH	Long chain acyl-CoA synthetase 9, chloroplastic (EC 6.2.1.3)	LACS9 At1g77590 T3M16.18	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Lipid metabolism; fatty acid metabolism.	ATP-binding; Chloroplast; Complete proteome; Fatty acid metabolism; Ligase; Lipid metabolism; Magnesium; Nucleotide-binding; Plastid; Reference proteome
SRR346572_TR30105_c1_g1_i4_len=662	NA	NA	NA	NA	NA	.	0,79	-0,132	0,255	0,635	0	-7,044	0,471	-0,522	0,36	0,421	.		.				
SRR346596_TR10671_c0_g1_i11_len=2200	G3PB_PEA	Q:1804-479,H:10-451	87.56%ID	E:0	Glyceraldehyde-3-phosphate dehydrogenase B, chloroplastic	PF00044.21*Gp_dh_N*Glyceraldehyde 3-phosphate dehydrogenase, NAD binding domain*67-239*E:1.7e-52 PF02800.17*Gp_dh_C*Glyceraldehyde 3-phosphate dehydrogenase, C-terminal domain*244-401*E:2.5e-65 PF02672.12*CP12*CP12 domain*430-451*E:3.3e-05	0,212	-1,009	1	0,06	0	-1,725	0,014	-0,703	0,299	1,476	G3PB_PEA	Glyceraldehyde-3-phosphate dehydrogenase B, chloroplastic (EC 1.2.1.13) (NADP-dependent glyceraldehydephosphate dehydrogenase subunit B)	GAPB GPB1	Pisum sativum (Garden pea)	PATHWAY: Carbohydrate biosynthesis; Calvin cycle.	Calvin cycle; Chloroplast; NADP; Oxidoreductase; Plastid; Transit peptide
SRR346596_TR12961_c0_g1_i1_len=1507	PSBO_SOLTU	Q:1369-371,H:1-332	88.59%ID	E:0	Oxygen-evolving enhancer protein 1, chloroplastic	PF01716.15*MSP*Manganese-stabilising protein / photosystem II polypeptide*146-378*E:1.4e-98	0,43	-0,212	0,658	-0,135	0	-0,887	0,017	-0,583	0,188	0,663	PSBO_SOLTU	Oxygen-evolving enhancer protein 1, chloroplastic (OEE1) (33 kDa subunit of oxygen evolving system of photosystem II) (33 kDa thylakoid membrane protein) (OEC 33 kDa subunit)	PSBO	Solanum tuberosum (Potato)		Chloroplast; Complete proteome; Manganese; Membrane; Photosynthesis; Photosystem II; Plastid; Reference proteome; Thylakoid; Transit peptide
SRR346596_TR16995_c0_g1_i9_len=2470	NA	NA	NA	NA	NA	.	1	-0,135	0,118	2,005	0	-1,296	0,004	-1,023	0,254	4,465	.		.				
SRR346596_TR29262_c0_g2_i3_len=6439	RK2A_COFAR	Q:6012-5191,H:1-274	98.91%ID	E:6e-168	50S ribosomal protein L2-A, chloroplastic	PF01193.21*RNA_pol_L*RNA polymerase Rpb3/Rpb11 dimerisation domain*35-225*E:6.3e-14 PF01000.23*RNA_pol_A_bac*RNA polymerase Rpb3/Rpo4A insert domain*845-1015*E:3.6e-15	0,101	-0,474	0,013	-0,769	0	-1,319	0,001	-1,017	0,002	-0,797	RK2A_COFAR	50S ribosomal protein L2-A, chloroplastic	rpl2-A	Coffea arabica (Arabian coffee)			Chloroplast; Plastid; Ribonucleoprotein; Ribosomal protein
SRR346604_TR11901_c0_g1_i5_len=2671	PSY_CAPAN	Q:599-1723,H:1-368	78.4%ID	E:0	Bifunctional 15-cis-phytoene synthase, chromoplastic [EC:0.0000303/PubMed:16578535]	PF00494.16*SQS_PSY*Squalene/phytoene synthase*150-378*E:1.7e-65	0,878	-0,172	0,472	-0,715	0	-1,566	0,019	-0,934	0,052	1,482	PSY_CAPAN	Bifunctional 15-cis-phytoene synthase, chromoplastic (EC 2.5.1.32) (Geranylgeranyl pyrophosphate geranylgeranyltransferase) (Phytoene synthase)	PSY1	Capsicum annuum (Bell pepper)	PATHWAY: Carotenoid biosynthesis; phytoene biosynthesis; all-trans-phytoene from geranylgeranyl diphosphate: step 1/1. [EC:0.0000305].	Carotenoid biosynthesis; Chromoplast; Isoprene biosynthesis; Multifunctional enzyme; Plastid; Transferase; Transit peptide
SRR346604_TR12580_c1_g2_i21_len=1460	NA	NA	NA	NA	NA	.	1	-0,391	0,502	-2,92	0	-1,841	0,002	-1,58	0,76	0,679	.		.				
SRR346604_TR24623_c0_g1_i1_len=2952	ATPD_TOBAC	Q:1536-2288,H:1-247	73.71%ID	E:3e-120	ATP synthase delta chain, chloroplastic	PF02536.11*mTERF*mTERF*139-347*E:3.5e-20	0,631	-0,204	0,024	-0,782	0	-1,038	0,003	-0,844	0,459	-0,178	ATPD_TOBAC	ATP synthase delta chain, chloroplastic (F-ATPase delta chain)	ATPD	Nicotiana tabacum (Common tobacco)			ATP synthesis; CF(1); Chloroplast; Hydrogen ion transport; Ion transport; Membrane; Plastid; Thylakoid; Transit peptide; Transport
SRR346604_TR37356_c1_g4_i4_len=1915	PPCK1_ARATH	Q:1849-1061,H:26-268	52.83%ID	E:2e-91	Phosphoenolpyruvate carboxylase kinase 1	PF00069.22*Kinase*Protein kinase domain*33-286*E:9.7e-30 PF00774.14*Pkinase_Tyr*Protein tyrosine kinase*36-285*E:2e-29 PF14531.3*Kinase-like*Kinase-like*118-271*E:4.3e-07	1	-0,586	0,461	-1,379	0	-2,699	0,002	-1,981	0,629	1,226	PPCK1_ARATH	Phosphoenolpyruvate carboxylase kinase 1 (AtPPCK1) (EC 2.7.11.1)	PPCK1 At1g08650 F22O13.13	Arabidopsis thaliana (Mouse-ear cress)			ATP-binding; Alternative splicing; Complete proteome; Kinase; Nucleotide-binding; Pyruvate; Reference proteome; Serine/threonine-protein kinase; Transferase
SRR348705_TR13253_c0_g2_i2_len=3854	ALFC2_ARATH	Q:3324-2134,H:1-398	88.72%ID	E:0	Probable fructose-bisphosphate aldolase 2, chloroplastic	PF00274.16*Glycolytic*Fructose-bisphosphate aldolase class-I*53-297*E:2.1e-158	0,552	-0,233	1	0,031	0	-0,925	0,019	-0,515	0	2,167	ALFC2_ARATH	Probable fructose-bisphosphate aldolase 2, chloroplastic (EC 4.1.2.13)	FBA2 At4g38970 F19H22.70	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Carbohydrate degradation; glycolysis; D-glyceraldehyde 3-phosphate and glycerone phosphate from D-glucose: step 4/4.	Alternative splicing; Calmodulin-binding; Cell membrane; Complete proteome; Ion channel; Ion transport; Ligand-gated ion channel; Membrane; Nucleotide-binding; Plant defense; Reference proteome; Transmembrane; Transmembrane helix; Transport; cAMP; cAMP-binding; cGMP; cGMP-binding
SRR348705_TR15129_c0_g1_i1_len=3951	IF2C_ARATH	Q:3472-476,H:1-1010	68.34%ID	E:0	Translation initiation factor IF-2, chloroplastic	PF00009.24*GTP_EFTU*Elongation factor Tu GTP binding domain*481-641*E:4e-33 PF01926.20*MMR_HSR1*50S ribosome-binding GTPase*482-550*E:6e-08 PF00575.19*Rae*Ras family*482-640*E:2.4e-06 PF11987.5*IF-2*Translation-initiation factor 2*786-837*E:3.5e-29	0,263	-0,374	0,387	-0,496	0	-0,933	0,028	-0,574	0,059	1,229	IF2C_ARATH	Translation initiation factor IF-2, chloroplastic	At1g17220 F20D23.8	Arabidopsis thaliana (Mouse-ear cress)		Chloroplast; Complete proteome; GTP-binding; Initiation factor; Nucleotide-binding; Plastid; Protein biosynthesis; Reference proteome; Transit peptide
SRR348705_TR16698_c0_g1_i4_len=2213	GLO1_ARATH	Q:838-1944,H:1-367	91.33%ID	E:0	Peroxisomal (S)-2-hydroxy-acid oxidase GLO1	PF01070.16*FMN_dh*Nitroalkane dehydrogenase*13-355*E:1.8e-137 PF00478.22*IMPDH*IMP dehydrogenase / GMP reductase domain*265-311*E:4.5e-06	0,528	-0,152	0,771	-0,068	0	-0,801	0,005	-0,583	0,611	0,113	GLO1_ARATH	Peroxisomal (S)-2-hydroxy-acid oxidase GLO1 (EC 1.1.3.15) (Glycolate oxidase 1) (AtGLO1) (GOX 1) (Short chain alpha-hydroxy acid oxidase GLO1)	GLO1 At3g14420 MAO2.2	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Photosynthesis; photorespiration; glycine from 2-phosphoglycolate: step 2/3.	Acetylation; Alternative splicing; Complete proteome; Direct protein sequencing; FMN; Flavoprotein; Glycolate pathway; Oxidoreductase; Peroxisome; Photorespiration; Reference proteome
SRR348705_TR34107_c0_g1_i1_len=1400	RRFC_SPIOL	Q:1066-353,H:34-271	72.27%ID	E:1e-110	Ribosome-recycling factor, chloroplastic	PF01765.16*RRF*Ribosome recycling factor*109-270*E:1e-61	0,031	-0,559	0,213	-0,353	0	-1,121	0,004	-0,764	0,18	0,572	RRFC_SPIOL	Ribosome-recycling factor, chloroplastic (RRF) (CpFrr) (RRFHCP) (Ribosome-releasing factor, chloroplastic)	RRF RRFHCP	Spinacia oleracea (Spinach)			Chloroplast; Coiled coil; Direct protein sequencing; Plastid; Protein biosynthesis; Transit peptide
SRR348707_TR5440_c0_g1_i1_len=1710	SAT3_ARATH	Q:138-1319,H:10-391	60.1%ID	E:2e-153	Serine acetyltransferase 3, mitochondrial	PF00132.21*Hexapep*Bacterial transferase hexapeptide (six repeats)*268-308*E:0.0016 PF00132.21*Hexapep*Bacterial transferase hexapeptide (six repeats)*317-357*E:2e-10 PF14602.3*Hexapep_2*Hexapeptide repeat of succinyl-transferase*319-351*E:2.5e-06 PF13436.3*Glycoziper_OmpA*Glycine-zipper domain*332-348*E:0.75	1	-0,03	1	-0,115	0	-1,193	0,06	-0,474	0,026	1,096	SAT3_ARATH	Serine acetyltransferase 3, mitochondrial (AtSAT-3) (AtSERAT2;2) (SAT-m) (EC 2.3.1.30)	SAT3 SAT3 SATA At3g13110 MJG19.6	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Amino-acid biosynthesis; L-cysteine biosynthesis; L-cysteine from L-serine: step 1/2.	Acyltransferase; Amino-acid biosynthesis; Complete proteome; Mitochondrion; Reference proteome; Transferase; Transit peptide
SRR348707_TR18338_c0_g1_i2_len=2862	TKTC_SOLTU	Q:186-2414,H:1-740	87.37%ID	E:0	Transketolase, chloroplastic	PF00456.18*Transketolase_N*Transketolase, thiamine diphosphate binding domain*86-417*E:1.7e-154 PF02779.21*Transket_pyr*Transketolase, pyrimidine binding domain*435-635*E:6.5e-44 PF02780.17*Transketolase_C*Transketolase, C-terminal domain*630-736*E:2e-13	0,04	-0,511	0,059	-0,5	0	-0,873	0,022	-0,508	0,469	0,165	TKTC_SOLTU	Transketolase, chloroplastic (TK) (EC 2.2.1.1)		Solanum tuberosum (Potato)	PATHWAY: Carbohydrate biosynthesis; Calvin cycle.	Calcium; Chloroplast; Complete proteome; Magnesium; Membrane; Metal-binding; Plastid; Reference proteome; Thiamine pyrophosphate; Thylakoid; Transferase; Transit peptide
SRR348707_TR37651_c0_g1_i1_len=521	ADF1_PETHY	Q:250-519,H:1-90	90%ID	E:2e-40	Actin-depolymerizing factor 1	.	0,017	5,775	0,502	4,201	0,001	-1,947	1	-0,025	1	-1,088	ADF1_PETHY	Actin-depolymerizing factor 1 (ADF-1)	ADF1	Petunia hybrida (Petunia)		Actin-binding
SRR924147_TR2070_c0_g1_i1_len=1487	NA	NA	NA	NA	NA	PF04982.10*HPP*HPP family*140-249*E:2.1e-21	0,594	-0,272	0,526	-0,305	0,001	-1,018	0,02	-0,685	0,848	-0,259	.		.				
SRR924147_TR5931_c0_g2_i1_len=2431	RHM1_ARATH	Q:153-2156,H:1-669	84.3%ID	E:0	Trifunctional UDP-glucose 4,6-dehydratase/UDP-4-keto-6-deoxy-D-glucose 3,5-epimerase/UDP-4-keto-L-rhamnose-reductase RHM1 (ECO:0000305/PubMed:17190829)	PF01370.16*Epimerase*NAD dependent epimerase/dehydratase family*9-251*E:2.7e-64 PF02719.10*Polysac_synt_2*Polysaccharide biosynthesis protein*9-276*E:1.3e-18 PF16363.3*GDP_Man_Dehyd*GDP-mannose 4,6 dehydratase*9-165*E:7.5e-39 PF03015.13*Sdr*Male sterility protein*11-191*E:5.6e-19 PF04321.14*RmlD_sub_bind*RmlD substrate binding domain*385-557*E:3.7e-12 PF01370.18*Epimerase*NAD dependent epimerase/dehydratase family*442-545*E:8.5e-11	0,555	-0,352	0,023	-1,638	0	-2,076	0,002	-1,83	0,376	-0,49	RHM1_ARATH	Trifunctional UDP-glucose 4,6-dehydratase/UDP-4-keto-6-deoxy-D-glucose 3,5-epimerase/UDP-4-keto-L-rhamnose-reductase RHM1 (Protein REPRESSOR OF LRX1 1) (Rhamnose biosynthetic enzyme 1) (AtRHM1) [Includes: UDP-glucose 4,6-dehydratase (EC 4.2.1.76); UDP-4-keto-6-deoxy-D-glucose 3,5-epimerase/UDP-4-keto-L-rhamnose 4-keto-reductase (EC 1.1.1.-) (EC 5.1.3.-)]	RHM1 ROL1 At1g78570 T30F21.10	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Carbohydrate biosynthesis. (ECO:0000305).	Cell wall biogenesis/degradation; Complete proteome; Cytoplasm; Isomerase; Lyase; Multifunctional enzyme; NAD; NADP; Oxidoreductase; Reference proteome; Ubl conjugation
SRR924147_TR14324_c0_g2_i1_len=2081	PLGG1_ARATH	Q:1762-329,H:37-612	74.9%ID	E:0	Plastidial glycolate/glycerate translocator 1, chloroplastic	PF04172.13*LrgB*LrgB-like family*285-508*E:1.4e-40	0,968	0,021	0,205	0,325	0	-0,997	0,003	-0,744	0,13	0,473	PLGG1_ARATH	Plastidial glycolate/glycerate translocator 1, chloroplastic (Bacterial membrane protein LrgB-like protein) (AtLrgB)	PLGG1 At1g32080 F22L3.12 T12D21.2	Arabidopsis thaliana (Mouse-ear cress)		Acetylation; Chloroplast; Complete proteome; Membrane; Photorespiration; Plastid; Reference proteome; Transit peptide; Transmembrane; Transmembrane helix; Transport
SRR924147_TR26451_c0_g1_i1_len=1795	NA	NA	NA	NA	NA	.	1	-0,015	0,29	-0,504	0	-0,893	0,012	-0,614	0,05	-0,734	.		.				
SRR924148_TR15509_c0_g1_i1_len=2062	UVR8_ARATH	Q:939-412,H:171-345	40.68%ID	E:5e-32	Ultraviolet-B receptor UVR8	PF13540.3*RCC1_2*Regulator of chromosome condensation (RCC1) repeat*375-433*E:4.3e-10 PF13540.3*RCC1_2*Regulator of chromosome condensation (RCC1) repeat*433-459*E:2.7e-06 PF00415.15*RCC1*Regulator of chromosome condensation (RCC1) repeat*446-497*E:2.2e-12 PF13540.3*RCC1_2*Regulator of chromosome condensation (RCC1) repeat*487-513*E:5e-10 PF00415.15*RCC1*Regulator of chromosome condensation (RCC1) repeat*500-548*E:3.2e-12	1	-0,601	1	0,506	0,001	-1,295	0,001	-1,262	1	-0,173	UVR8_ARATH	Ultraviolet-B receptor UVR8 (Protein UV-B RESISTANCE 8) (RCC1 domain-containing protein UVR8)	UVR8 At5g63860 MGI19.7	Arabidopsis thaliana (Mouse-ear cress)		3D-structure; Acetylation; Chromosome; Complete proteome; Cytoplasm; Nucleus; Photoreceptor protein; Receptor; Reference proteome; Repeat; Sensory transduction
SRR924148_TR28214_c0_g1_i1_len=855	PSAN_ARATH	Q:185-688,H:1-168	69.19%ID	E:2e-60	Photosystem I reaction center subunit N, chloroplastic	PF05479.8*PsaN*Photosystem I reaction centre subunit N (PSAN or PSI-N)*104-232*E:1.3e-48	1	-3,475	1	-3,504	0	-8,016	0,915	0,091	0,085	-0,751	PSAN_ARATH	Photosystem I reaction center subunit N, chloroplastic (PSI-N)	PSAN At5g64040 MHJ24.2	Arabidopsis thaliana (Mouse-ear cress)			Acetylation; Chloroplast; Complete proteome; Direct protein sequencing; FMN; Membrane; Photosynthesis; Photosystem I; Plastid; Reference proteome; Thylakoid; Transit peptide
SRR924148_TR30734_c0_g1_i1_len=2758	DXS_CAPAN	Q:2382-226,H:1-719	87.24%ID	E:0	Probable 1-deoxy-D-xylulose-5-phosphate synthase, chloroplastic	PF13292.3*DXP_synthase_N*1-deoxy-D-xylulose-5-phosphate synthase*76-361*E:5.5e-114 PF00676.17*E1_dh*Dehydrogenase E1 component*187-247*E:4.1e-05 PF02779.21*Transket_pyr*Transketolase, pyrimidine binding domain*398-559*E:3.1e-44 PF02780.17*Transketolase_C*Transketolase, C-terminal domain*577-700*E:9.8e-31	0,037	-0,525	0,017	0,677	0	-1,074	0,23	-0,307	0,09	0,934	DXS_CAPAN	Probable 1-deoxy-D-xylulose-5-phosphate synthase, chloroplastic (1-deoxyxylulose-5-phosphate synthase) (DXP synthase) (DXPS) (EC 2.2.1.7) (Cap TKT2)	TKT2	Capsicum annuum (Bell pepper)	PATHWAY: Metabolic intermediate biosynthesis; 1-deoxy-D-xylulose 5-phosphate biosynthesis; 1-deoxy-D-xylulose 5-phosphate from D-glyceraldehyde 3-phosphate and pyruvate: step 1/1.	Chloroplast; Isoprene biosynthesis; Magnesium; Metal-binding; Plastid; Thiamine biosynthesis; Thiamine pyrophosphate; Transferase; Transit peptide

MsDamaged24h_MsIntact24h

Transcript (CDF97)	Uniprot homolog	BLASTX Position	BLASTX %Identity	BLASTX evalue	Uniprot descr	Pfam	PValue_Ms6h	logFC_Ms6h	PValue_Ms8h	logFC_Ms8h	PValue_MsDamaged24h	logFC_MsDamaged24h	PValue_MsIntact24h	logFC_MsIntact24h	PValue_Mst1wk	logFC_Mst1wk	Entry name	Protein names	Gene names	Organism	Pathway	Keywords
SRR1144633_TR11351_c0_g2_i1_len=1413	NA	NA	NA	NA	NA	PF11250.5*FAF*Fantastic Four meristem regulator*160-209*E:1.6e-16	0,211	-0,822	0,076	-2,604	0	-3,524	0	-3,785	0,035	-1,615	.	.	.	.	.	.
SRR1144633_TR11707_c0_g3_i4_len=1279	CB12_SOLLC	Q:1094-297,H:1-265	89.85%ID	E:5e-174	Chlorophyll a-b binding protein 7, chloroplastic	PF00504.18*Chloroa_b-bind*Chlorophyll A-B binding protein*75-241*E:1e-61	0,229	-0,27	0,001	-0,753	0	-1,123	0	-0,918	0,412	0,549	CB12_SOLLC	Chlorophyll a-b binding protein 7, chloroplastic (LHCI type II CAB-7)	CAB7

SRR1722228_TR12197_c0_g1_i1_len=[illegible]	COPT12_ARATH	130	[illegible]	[illegible]	Copper transporter 2	PF04148:12 Sc*Cc*Copper transporter family *1*1 [illegible]	1	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	COPT12_ARATH	Copper transporter 2 (AtCOPT12)	COPT12 At3g20650 TM1 [illegible]	Arabidopsis thaliana (Mouse-ear cress)	.	.	Transmembrane helix; Transport
SRR1722238_TR59710_c0_g1_i1_len=1451	NA	NA	NA	NA	NA	PF01190:14*Pollen_Ole_e_I*Pollen proteins Ole e I like*43-132*E:2.1e-20	1	-0,055	0,009	-1,705	0	-1,186	0	-1,775	0,038	0,555.	.	.	.	.	.	.	.	.
SRR1722238_TR68398_c0_g1_i1_len=2711	CYP37_ARATH	Q:2372-1167;H:54-456	69.48%ID	E0	Peptidyl-prolyl cis-trans isomerase CYP37, chloroplast	PF00160:18*Pro_isomerase*Cyclophilin type peptidyl-prolyl cis-trans isomerase;CLD:351-501*E:1e-125	0,268	-0,43	0,077	-0,66	0	-1,664	0	-1,695	1	0,028 CYP37_ARATH	Peptidyl-prolyl cis-trans isomerase CYP37, chloroplastic (PPIase CYP37) (EC 5.2.1.8) (Rotamase CYP37) (Thylakoid lumen PPIase of 38 kDa) (TLP38) (p38)	CYP37 At3g15520 MJK13.18	Arabidopsis thaliana (Mouse-ear cress)	.	Chloroplast; Complete proteome; Direct protein sequencing; Isomerase; Plastid; Reference proteome; Rotamase; Thylakoid; Transit peptide
SRR1722238_TR79167_c0_g1_i1_len=2232	C71A2_SOLME	Q:235-1617;H:46-505	53.22%ID	E9e-168	Cytochrome P450 71A2	PF00067:19*p450*Cytochrome P450*45-494*E:2.9e-101	1	2,093	1	-0,047	0	-2,119	0	-2,231	0,026	2,134 C71A2_SOLME	Cytochrome P450 71A2 (EC 1.14.--.-) (CYPLXXIA2) (Cytochrome P-450EGA)	CYP71A2 CYPEG4	Solanum melongena (Eggplant) (Aubergine)	.	.	.	.	Heme; Iron; Membrane; Metal-binding; Monooxygenase; Oxidoreductase; Transmembrane; Transmembrane helix
SRR1722238_TR80429_c0_g3_i1_len=634	NA	NA	NA	NA	NA	.	1	0,064	0,044	-1,933	0	-2,072	0	-2,077	1	-0,213.	.	.	.	.	.	.	.	.
SRR1722238_TR88044_c0_g1_i4_len=2084	CYP38_ARATH	Q:336-1565;H:23-437	78.95%ID	E0	Peptidyl-prolyl cis-trans isomerase CYP38, chloroplastic	PF00160:18*Pro_isomerase*Cyclophilin type peptidyl-prolyl cis-trans isomerase;CLD:272-431*E:1.8e-24	0,177	-0,356	0,105	-0,449	0	-1,384	0	-0,974	0,539	0,176 CYP38_ARATH	Peptidyl-prolyl cis-trans isomerase CYP38, chloroplastic (PPIase CYP38) (EC 5.2.1.8) (Rotamase CYP38) (Thylakoid lumen PPIase)	CYP38 At3g01480 FAP13.3	Arabidopsis thaliana (Mouse-ear cress)	.	3D-structure; Alternative splicing; Chloroplast; Complete proteome; Direct protein sequencing; Isomerase; Plastid; Reference proteome; Rotamase; Thylakoid; Transit peptide
SRR1722238_TR90509_c0_g1_i1_len=1757	NA	NA	NA	NA	NA	.	1	-0,394	0,381	-1,863	0	-4,72	0	-4,86	1	0,248.	.	.	.	.	.	.	.	.
SRR1721857_TR3570_c0_g1_i1_len=2452	KTNA1_ARATH	Q:240-1775;H:8-523	85.11%ID	E0	Katanin p60 ATPase-containing subunit A1 (EC0:0000235)HAMAP-Rule:MF_03023)	PF05496:9*RuvB_N*Holliday junction DNA helicase ruvB N-terminus*268-337*E:8.2e-05 PF00004:26*AAA*ATPase family associated with various cellular activities (AAA)*269-406*E:1e-37 PF09336:7*Vps4_C*Vps4 C terminal oligomerisation domain*470-615*E:4e-11	1	-0,039	0,009	4,606	0	-5,64	0	-6,23	1	-0,061 KTNA1_ARATH	Katanin p60 ATPase-containing subunit A1 (Katanin p60 subunit A1) (EC 3.6.4.3) (CAD ATPase) (Katanin-1) (Atp60) (Protein BOTERO 1) (Protein ECTOPIC ROOT HAIR 3) (Protein FAT ROOT) (Protein FRAGILE FIBER 2) (AtAAA1) (p60 katanin)	AAA1 BOT1 ERH3 FRA2 FTR KSS KTN1 LUE1 At1g80350 F5I6.10	Arabidopsis thaliana (Mouse-ear cress)	.	ATP-binding; Complete proteome; Cytoplasm; Cytoskeleton; Hydrolase; Microtubule; Nucleotide-binding; Reference proteome
SRR1721857_TR4760_c0_g1_i1_len=1809	G3PA2_ARATH	Q:1487-333;H:14-399	87.6%ID	E0	Glyceraldehyde-3-phosphate dehydrogenase GAPA2, chloroplastic	PF00044:21*Gp_dh_N*Glyceraldehyde 3-phosphate dehydrogenase, NAD binding domain*69-219*E:8.7e-51 PF02800:17*Gp_dh_C*Glyceraldehyde 3-phosphate dehydrogenase, C-terminal domain*224-380*E:5.4e-67	0,125	-0,334	0,001	-0,698	0	-0,947	0	-0,732	1	0,003 G3PA2_ARATH	Glyceraldehyde-3-phosphate dehydrogenase GAPA2, chloroplastic (EC 1.2.1.13) (NADP-dependent glyceraldehyde-phosphate dehydrogenase A subunit 2)	GAPA2 At1g12900 F13K23.15	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Carbohydrate biosynthesis; Calvin cycle.	Alternative splicing; Calvin cycle; Chloroplast; Complete proteome; NADP; Oxidoreductase; Plastid; Reference proteome; Transit peptide
SRR1721857_TR5192_c0_g1_i1_len=4027	CP26B_ARATH	Q:3305-2616;H:85-312	66.09%ID	E2e-95	Peptidyl-prolyl cis-trans isomerase CYP26-2, chloroplastic	PF07967:10*cl5C3HC*C3HC zinc finger-like*17*4.29*E:2.1e-33	0,298	-0,584	0,006	-1,768	0	-1,431	0,001	-1,219	0,634	0,249 CP26B_ARATH	Peptidyl-prolyl cis-trans isomerase CYP26-2, chloroplastic (PPIase CYP26-2) (EC 5.2.1.8) (Cyclophilin of 26 kDa 2) (Cyclophilin-26-2)	CYP26-2 At1g74070 F2P9.6	Arabidopsis thaliana (Mouse-ear cress)	.	Chaperone; Chloroplast; Complete proteome; Cyclosporin; Isomerase; Plastid; Reference proteome; Rotamase; Thylakoid; Transit peptide
SRR1721857_TR8714_c0_g2_i1_len=562	AX15A_SOYBN	Q:416-213;H:12-79	66.18%ID	E1e-26	Auxin-induced protein 15A	.	1	-0,214	0,027	-2,165	0	-2,731	0	-1,974	0,84	-0,289 AX15A_SOYBN	Auxin-induced protein 15A	.	Glycine max (Soybean) (Glycine hispida)	.	.	.	.	Auxin signaling pathway; Complete proteome; Reference proteome
SRR1721857_TR11355_c0_g2_i1_len=2197	NA	NA	NA	NA	NA	PF09713:7*A_thal_3526*Plant protein 1589 of unknown function (A_thal_3526)*117*8.6*E:4e-23	0,472	-0,613	0,003	-2,551	0,001	-3,285	0,001	-3,058	1	0,468.	.	.	.	.	.	.	.	.
SRR1721857_TR12704_c0_g1_i1_len=1898	GLK1_ARATH	Q:214-1575;H:1-418	40.17%ID	E7e-65	Transcription activator GLK1	PF00249:28*Myb_DNA-binding*Myb-like DNA-binding domain*174-223*E:5e-08	0,486	-0,286	0,211	-0,513	0	-1,342	0	-1,541	0,587	0,28 GLK1_ARATH	Transcription activator GLK1 (GBF'S PRO-RICH REGION-INTERACTING factor 1) (Golden2-like protein 1) (AtGLK1)	GLK1 GPR11 At2g20570 F23N11.11	Arabidopsis thaliana (Mouse-ear cress)	.	Activator; Alternative splicing; Complete proteome; DNA-binding; Nucleus; Reference proteome; Transcription; Transcription regulation
SRR1721857_TR20667_c0_g1_i1_len=2351	AAP7_ARATH	Q:1300-182;H:82-465	55.99%ID	E3e-129	Probable amino acid permease 7	PF01490:15*Aa_trans*Transmembrane amino acid transporter protein*7-358*E:3.1e-70	0,832	0,209	0,175	-0,936	0	-2,316	0	-2,3	0,299	-1,173 AAP7_ARATH	Probable amino acid permease 7 (Amino acid transporter AAP7)	AAP7 At5g23810 MRO11.15	Arabidopsis thaliana (Mouse-ear cress)	.	Alternative splicing; Amino-acid transport; Cell membrane; Complete proteome; Membrane; Reference proteome; Symport; Transmembrane helix; Transport
SRR1721857_TR2768_c0_g2_i1_len=1410	DIV_ARTMA	Q:290-943;H:23-219	47.06%ID	E1e-43	Transcription factor DIVARICATA	PF00249:28*Myb_DNA-binding*Myb-like DNA-binding domain*8-55*E:3.2e-07 PF00249:28*Myb_DNA-binding*Myb-like DNA-binding domain*134-178*E:9.7e-11	0,464	-0,347	0,001	-1,614	0,001	-1,489	0	-1,948	0,229	0,55 DIV_ARTMA	Transcription factor DIVARICATA	DIV1 At2g36290 F4N21.9	Antirrhinum majus (Garden snapdragon)	.	.	.	.	DNA-binding; Developmental protein; Nucleus; Transcription; Transcription regulation
SRR1721857_TR12445_c0_g1_i1_len=2716	AAT_AQUAE	Q:176-247;H:151-394	30.12%ID	E5e-25	Aspartate aminotransferase	PF00155:18*Aminotran_1_2*Aminotransferase class I and II*17-170*E:5e-20	1	-0,058	0,175	1,012	0,001	-1,829	0	-2,057	0,093	-0,787 AAT_AQUAE	Aspartate aminotransferase (AspAT) (EC 2.6.1.1) (Transaminase A)	aspC aq_1969	Aquifex aeolicus (strain VF5)	.	.	.	.	Aminotransferase; Complete proteome; Cytoplasm; Pyridoxal phosphate; Reference proteome; Transferase
SRR1721857_TR30443_c0_g1_i2_len=4726	CAPP2_MESCR	Q:2149-113;H:283-660	87.78%ID	E0	Phosphoenolpyruvate carboxylase 2	PF00311:14*PEPcase*Phosphoenolpyruvate carboxylase*3-681*E:9.2e-257	0,798	-0,344	0,088	-1,771	0	-2,332	0	-1,603	1	0,251 CAPP2_MESCR	Phosphoenolpyruvate carboxylase 2 (PEPC 2) (PEPCase 2) (EC 4.1.1.31)	PPC2	Mesembryanthemum crystallinum (Common ice plant) (Cryophytum crystallinum)	PATHWAY: Photosynthesis; C3 acid pathway.	Allosteric enzyme; Carbon dioxide fixation; Cytoplasm; Lyase; Magnesium; Photosynthesis
SRR1721857_TR30492_c0_g1_i3_len=1760	NA	NA	NA	NA	NA	.	1	0,054	0,066	-1,746	0	-2,493	0	-2,628	1	0,296.	.	.	.	.	.	.	.	.
SRR1721857_TR36126_c0_g1_i1_len=947	NA	NA	NA	NA	NA	PF05349.9*GATA-N*GATA-type transcription activator, N-terminal*51-123*E:0.00012	1	0,872	0,031	1,444	0	-1,323	0	-1,166	0,848	-0,201.	.	.	.	.	.	.	.	.
SRR1721857_TR40607_c0_g1_i23_len=4029	GLGL1_ARATH	Q:3802-2240;H:1-522	75.95%ID	E0	Glucose-1-phosphate adenylyltransferase large subunit 1, chloroplastic	PF00483:20*NTP_transferase*Nucleotidyl transferase*90-367*E:5.1e-74	0,484	-0,193	0,392	-0,233	0	-1,37	0	-1,128	0,45	0,213 GLGL1_ARATH	Glucose-1-phosphate adenylyltransferase large subunit 1, chloroplastic (EC 2.7.7.27) (ADP-glucose pyrophosphorylase) (ADP-glucose synthase) (AGPase S) (Alpha-D-glucose-1-phosphate adenyl transferase)	ADG2 APL1 At5g19220 T24G5.120	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Glycan biosynthesis; starch biosynthesis.	ATP-binding; Allosteric enzyme; Chloroplast; Complete proteome; Nucleotide-binding; Nucleotidyltransferase; Phosphoprotein; Plastid; Reference proteome; Starch biosynthesis; Transferase; Transit peptide
SRR1721858_TR21646_c0_g2_i1_len=1981	NA	NA	NA	NA	NA	.	0,321	0,384	0	6,352	0	-7,616	0	-7,616	0,164	-0,513.	.	.	.	.	.	.	.	.
SRR1721858_TR36366_c0_g1_i4_len=2547	NADB_ARATH	Q:349-2259;H:6-642	74.7%ID	E0	L-aspartate oxidase, chloroplastic	PF00890:21*FAD_binding_2*FAD binding domain*88-472*E:3.7e-90 PF01266:21*DAO*FAD dependent oxidoreductase*88-216*E:3.2e-07 PF02910:17*Succ_DH_flav_C*Fumarate reductase flavoprotein C-term*529-618*E:3e-15	1	-0,057	1	0,92	0	-1,839	0	-2,023	1	0,372 NADB_ARATH	L-aspartate oxidase, chloroplastic (EC 1.4.3.16) (Protein FLAGELLIN-INSENSITIVE 4)	AO FIN4 At5g14760 T9L3.60	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Cofactor biosynthesis; NAD(+) biosynthesis; iminoaspartate from L-aspartate (oxidase route): step 1/1.	Chloroplast; Complete proteome; FAD; Flavoprotein; Oxidoreductase; Plastid; Pyridine nucleotide biosynthesis; Reference proteome; Transit peptide
SRR1721859_TR441_c0_g2_i1_len=1790	PSBS_SOLSG	Q:937-158;H:1-271	80.29%ID	E6e-86	Photosystem II 22 kDa protein, chloroplastic	PF05054:18*Chlorox_b-bind*Chlorophyll A-B binding protein*84-211*E:7e-09	0,949	-0,016	0,012	-0,548	0	-1,053	0,001	-0,73	0,059	0,456 PSBS_SOLSG	Photosystem II 22 kDa protein, chloroplastic (CP22)	PSBS	Solanum sogarandinum	.	.	.	.	Chloroplast; Membrane; Photosynthesis; Photosystem II; Plastid; Repeat; Thylakoid; Transit peptide; Transmembrane; Transmembrane helix
SRR1721859_TR1756_c0_g1_i1_len=541	NA	NA	NA	NA	NA	.	0,62	0,243	0,636	-0,177	0	-1,212	0	-1,209	0,618	0,203.	.	.	.	.	.	.	.	.
SRR1721859_TR5788_c0_g3_i2_len=847	HSP21_IPONI	Q:564-788;H:79-155	74.03%ID	E1e-24	17.2 kDa class II heat shock protein	.	0,365	-0,518	0,258	-0,92	0,001	-1,35	0	-1,641	0,6	-0,337 HSP21_IPONI	17.2 kDa class II heat shock protein	SHSP-1	Ipomoea nil (Japanese morning glory) (Pharbitis nil)	.	.	.	.	Cytoplasm; Stress response
SRR1721859_TR7367_c0_g1_i2_len=912	RBS_MALSP	Q:673-173;H:17-183	85.03%ID	E7e-104	Ribulose bisphosphate carboxylase small chain, chloroplastic	PF12338.5*RbcS*Ribulose-1,5-bisphosphate carboxylase small subunit*44*E:4.4e-23 PF00101.17*RuBisCO_small*Ribulose bisphosphate carboxylase, small chain*71-179*E:1.3e-39	0	1,039	0,001	0,716	0	-1,471	0	-1,312	0,006	-0,585 RBS_MALSP	Ribulose bisphosphate carboxylase small chain, chloroplastic (RuBisCO small subunit) (EC 4.1.1.39)	RBCS	Malus sp. (Crab apple)	.	.	.	.	Calvin cycle; Carbon dioxide fixation; Chloroplast; Lyase; Monooxygenase; Oxidoreductase; Photorespiration; Photosynthesis; Plastid; Transit peptide
SRR1721859_TR7961_c1_g2_i1_len=3066	RVE1_ARATH	Q:255-761;H:34-189	58.82%ID	E4e-38	Protein REVEILLE 1	PF00249:28*Myb_DNA-binding*Myb-like DNA-binding domain*57-100*E:4.8e-13	1	-0,482	1	-0,191	0	-0,062	0	-2,049	0,643	0,572 RVE1_ARATH	Protein REVEILLE 1	RVE1 At5g17300 MKP11.15	Arabidopsis thaliana (Mouse-ear cress)	.	.	.	.	Biological rhythms; Complete proteome; DNA-binding; Nucleus; Reference proteome; Transcription; Transcription regulation
SRR1721859_TR9527_c0_g1_i1_len=580	NA	NA	NA	NA	NA	.	0,854	0,236	0,051	-1,039	0	-1,461	0	-1,807	0,193	0,705.	.	.	.	.	.	.	.	.
SRR1721859_TR10426_c0_g1_i1_len=783	NA	NA	NA	NA	NA	.	1	0	1	0,105	0	-3,119	0,001	-2,833	1	-0,496.	.	.	.	.	.	.	.	.
SRR1721859_TR16022_c0_g1_i2_len=2497	NIR_BETPN	Q:208-1441;H:36-583	85.4%ID	E0	Ferredoxin--nitrite reductase, chloroplastic	PF03460:14*NIR_SIR_ferr*Nitrite/Sulfite reductase ferredoxin-like half domain*129-194*E:5.4e-18 PF01077:19*NIR_SIR*Nitrite and sulphite reductase 4Fe-4S domain*204-361*E:2.7e-37 PF03460:14*NIR_SIR_ferr*Nitrite/Sulfite reductase ferredoxin-like half domain*388-449*E:6.6e-21 PF01077:19*NIR_SIR*Nitrite and sulphite reductase 4Fe-4S domain*468-572*E:5.7e-10	0,269	-0,375	0,725	-0,108	0	-1,5	0	-1,294	0,876	-0,084 NIR_BETPN	Ferredoxin--nitrite reductase, chloroplastic (EC 1.7.7.1)	NIR1	Betula pendula (European white birch) (Betula verrucosa)	PATHWAY: Nitrogen metabolism; nitrate reduction (assimilation).	4Fe-4S; Chloroplast; Electron transport; Heme; Iron; Iron-sulfur; Metal-binding; Nitrate assimilation; Oxidoreductase; Plastid; Transit peptide; Transport
SRR1721859_TR19852_c0_g1_i9_len=1061	PPCK1_ARATH	Q:149-943;H:15-279	53.93%ID	E4e-100	Phosphoenolpyruvate carboxylase kinase 1	PF00069:22*Pkinase*Protein kinase domain*9-266*E:1.5e-72 PF07714:14*Pkinase_Tyr*Protein tyrosine kinase*12-261*E:2e-29 PF14531:3*Kinase-like*Kinase-like*84-247*E:4.3e-07	1	-0,544	0,059	-1,583	0	-2,378	0	-1,855	0,057	1,449 PPCK1_ARATH	Phosphoenolpyruvate carboxylase kinase 1 (AtPPCK1) (EC 2.7.11.1)	PPCK1 At1g08650 F22O13.13	Arabidopsis thaliana (Mouse-ear cress)	.	.	.	.	ATP-binding; Alternative splicing; Complete proteome; Kinase; Nucleotide-binding; Pyruvate; Reference proteome; Serine/threonine-protein kinase; Transferase
SRR1721859_TR21359_c0_g2_i1_len=1148	NA	NA	NA	NA	NA	.	0,34	0,529	0,017	5,728	0	-9,307	0	-9,307	1	-0,222.	.	.	.	.	.	.	.	.
SRR1721859_TR32386_c0_g2_i1_len=1517	NA	NA	NA	NA	NA	.	0	1,484	0,117	0,335	0	-1,273	0	-1,148	0,75	-0,077.	.	.	.	.	.	.	.	.
SRR1721859_TR42336_c0_g3_i1_len=1314	UGT6_CATRO	Q:161-1312;H:1-384	64.25%ID	E0	7-deoxyloganetin glucosyltransferase	PF00201:15*UDPGT*UDP-glucuronosyl and UDP-glucosyl transferase*237-384*E:3.9e-11	1	1,414	1	-1,228	0	-1,46	0	-2,099	1	-1,736 UGT6_CATRO	7-deoxyloganetin glucosyltransferase (EC 2.4.1.324) (Iridoid 1-O-glucosyltransferase) (UDP-glucose glucosyltransferase 6) (CrUGT6) (UDP-glycosyltransferase 85A23)	UGT85A23 UGT6	Catharanthus roseus (Madagascar periwinkle) (Vinca rosea)	.	.	.	.	Transferase
SRR1721859_TR45607_c0_g1_i2_len=2019	FED2E_SOYBN	Q:148-1733;H:1-382	76.29%ID	E0	Omega-6 fatty acid desaturase, endoplasmic reticulum isozyme 2	PF03407:21*FA_desaturase*Fatty acid desaturase*91-351*E:1.5e-32	0,708	-0,166	0,003	-2,613	0	-0,708	0,796	-0,147 FDE2_SOYBN	Omega-6 fatty acid desaturase, endoplasmic reticulum isozyme 2 (EC 1.14.19.-)	FAD2-2	Glycine max (Soybean) (Glycine hispida)	PATHWAY: Lipid metabolism; polyunsaturated fatty acid biosynthesis.	Complete proteome; Endoplasmic reticulum; Fatty acid biosynthesis; Fatty acid metabolism; Lipid biosynthesis; Lipid metabolism; Membrane; Oxidoreductase; Reference proteome; Transmembrane; Transmembrane helix
SRR3420117_TR13432_c0_g1_i1_len=716	IAA17_ARATH	Q:604-29;H:3-218	50.69%ID	E2e-60	Auxin-responsive protein IAA17	PF02309.13*AUX_IAA*AUX/IAA family*31-201*E:3.3e-58	1	-0,038	0	3,613	0	-2,94	0	-2,596	1	-0,12 IAA17_ARATH	Auxin-responsive protein IAA17 (Auxin response 3) (Indoleacetic acid-induced protein 17)	IAA17 AXR3 At1g04250 F19P19.31	Arabidopsis thaliana (Mouse-ear cress)	.	3D-structure; Auxin signaling pathway; Complete proteome; Nucleus; Phosphoprotein; Reference proteome; Repressor; Transcription; Transcription regulation
SRR3420117_TR13773_c0_g2_i1_len=635	GCSH_FLAAN	Q:212-686;H:1-127	41.32%ID	E6e-46	Glycine cleavage system H protein, mitochondrial	PF01597:16*GCV_H*Glycine cleavage H-protein*42-125*E:1.4e-31	0,632	-0,107	0,038	-0,456	0	-1,071	0	-0,9	1	-0,011 GNOM_ARATH	ARF guanine-nucleotide exchange factor GNOM (Pattern formation protein EMB30) (Protein EMBRYO DEFECTIVE 30) (Protein MIZU-KUSSEE2) (Protein VASCULAR NETWORK 7)	GDCSH GCDH GCSH	Flaveria anomala (Yellowtops)	.	.	.	.	Lipoyl; Mitochondrion; Transit peptide
SRR3420117_TR18746_c0_g1_i4_len=1332	NA	NA	NA	NA	NA	PF05512.8*AWPM-19*AWPM-19-like family*15-155*E:1.4e-52	1	0,065	0,04	-1,436	0	-1,978	0	-2,076	0,84	-0,33.	.	.	.	.	.	.	.	.
SRR3420117_TR19184_c1_g1_i3_len=1339	TL29_SOLLC	Q:106-1128;H:1-345	75.43%ID	E0	Thylakoid lumenal 29 kDa protein, chloroplastic	PF00141.20*peroxidase*Peroxidase*128-300*E:1.2e-24	0,662	-0,103	0,236	-0,274	0	-1,129	0	-1,092	0,366	0,21 TL29_SOLLC	Thylakoid lumenal 29 kDa protein, chloroplastic (TL29) (EC 1.--.--) (LeAPx09) (P29)	CLEB3J9	Solanum lycopersicum (Tomato) (Lycopersicon esculentum)	.	.	.	.	Chloroplast; Complete proteome; Oxidoreductase; Plastid; Reference proteome; Thylakoid; Transit peptide
SRR3420117_TR19226_c0_g1_i1_len=7059	VGA_BPS13	Q:236-3798;H:1-522	98.47%ID	E0	A' protein	PF05840.10*Phage_GPA*Bacteriophage replication gene A protein (GPA)*84-405*E:1.1e-77	0,131	-0,372	0,467	0,188	0	-1,313	0	-1,091	0,091	-0,457 VGA_BPS13	A' protein (GPA)	A	Enterobacteria phage S13 (Bacteriophage S13)	.	.	.	.	Alternative initiation; Complete proteome; DNA-binding; Endonuclease; Hydrolase; Metal-binding; Nuclease; Zinc; Zinc-finger
SRR3420117_TR21437_c0_g1_i1_len=1377	NA	NA	NA	NA	NA	.	1	-1,303	0,254	-2,556	0	-4,129	0	-4,982	1	-0,642.	.	.	.	.	.	.	.	.
SRR3420117_TR23313_c2_g1_i3_len=2140	GLYK_ARATH	Q:443-1549;H:87-455	73.24%ID	E0	D-glycerate 3-kinase, chloroplastic	PF02595.14*Glycerate_kin*Glycerate kinase*1-416*E:5.7e-08 PF06203.11*CCT*CCT motif*359-401*E:3.9e-18	0,451	0,328	0	4,222	0	-6,62	0	-6,674	0,099	-0,831 GLYK_ARATH	D-glycerate 3-kinase, chloroplastic (AtGLYK) (EC 2.7.1.31)	GLYK At1g80380 F5I6.13	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Photosynthesis; photorespiration; 3-phospho-D-glycerate from glycine: step 4/4.	ATP-binding; Alternative splicing; Chloroplast; Complete proteome; Glycolate pathway; Kinase; Nucleotide-binding; Photorespiration; Plastid; Reference proteome; Transferase; Transit peptide
SRR3420117_TR24328_c0_g3_i3_len=574	NU50B_ARATH	Q:396-672;H:320-378	72.88%ID	E5e-22	Nuclear pore complex protein NUP50B	PF00638.15*Ran_BP1*Ran binding protein domain*121-173*E:1e-07	0,163	-0,689	0,001	6,638	0	-6,728	0	-6,728	0,196	0,517 NU50B_ARATH	Nuclear pore complex protein NUP50B (Nucleoporin 50B)	NUP50B AtG15970 MSL1.1	Arabidopsis thaliana (Mouse-ear cress)	.	Acetylation; Complete proteome; Nuclear pore complex; Nucleus; Phosphoprotein; Protein transport; Reference proteome; Repeat; Translocation; Transport; mRNA transport
SRR3420117_TR24903_c0_g4_i1_len=3970	PSAA_EUCGG	Q:3431-1182;H:1-750	99.33%ID	E0	Photosystem I P700 chlorophyll a apoprotein A1 (EC0:0000235)HAMAP-Rule:MF_00458)	PF00223.16*PsaA_PsaB*Photosystem I psaA/psaB protein*1-750*E:0	0,058	0,819	0	2,022	0	-1,767	0	-1,43	1	-0,304 PSAA_EUCGG	Photosystem I P700 chlorophyll a apoprotein A1 (EC 1.97.1.12) (PSI-A) (PsaA)	psaA	Eucalyptus globulus subsp. globulus (Tasmanian blue gum)	.	4Fe-4S; Chlorophyll; Chloroplast; Chromophore; Electron transport; Iron; Iron-sulfur; Magnesium; Membrane; Metal-binding; Oxidoreductase; Photosynthesis; Photosystem I; Plastid; Thylakoid; Transmembrane; Transmembrane helix; Transport
SRR3420117_TR28976_c3_g2_i2_len=667	NA	NA	NA	NA	NA	PF00403.23*HMA*Heavy-metal-associated domain*36-92*E:1.4e-10	0,067	-0,634	0,001	-1,677	0	-2,727	0	-2,421	0,008	0,906.	.	.	.	.	.	.	.	.
SRR3420119_TR1943_c2_g2_i9_len=1293	CAHC_TOBAC	Q:1188-202;H:1-321	77.27%ID	E4e-159	Carbonic anhydrase, chloroplastic	PF00484.16*Pro_CA*Carbonic anhydrase*156-313*E:2.8e-39	0,013	-0,562	0,047	0,434	0	-2,118	0	-1,833	0,059	0,45 CAHC_TOBAC	Carbonic anhydrase, chloroplastic (EC 4.2.1.1) (Carbonate dehydratase)	.	Nicotiana tabacum (Common tobacco)	.	.	.	.	Chloroplast; Lyase; Plastid; Transit peptide; Zinc
SRR3420119_TR10041_c4_g1_i3_len=1246	NA	NA	NA	NA	NA	.	1	1,044	0,021	-1,237	0	-1,589	0	-1,86	0,748	0,225.	.	.	.	.	.	.	.	.
SRR3420119_TR12494_c1_g4_i3_len=2852	NA	NA	NA	NA	NA	.	0,675	-0,133	0,831	0,065	0	-0,997	0,001	-0,83	1	0,361.	.	.	.	.	.	.	.	.
SRR3420119_TR15470_c2_g3_i11_len=2865	GLNA2_DAUCA	Q:1206-2411;H:1-403	89.08%ID	E0	Glutamine synthetase, chloroplastic	PF03951.16*Gln-synt_N*Glutamine synthetase, beta-Grasp domain*81-156*E:2.2e-10 PF00120.21*Gln-synt_C*Glutamine synthetase, catalytic domain*185-406*E:7.7e-16	1	-0,036	0,2	-0,698	0,001	-1,112	0,001	-1,142	0,716	0,106 GLNA2_DAUCA	Glutamine synthetase, chloroplastic (EC 6.3.1.2) (GS2) (Glutamate--ammonia ligase)	GLN2	Daucus carota (Wild carrot)	.	.	.	.	ATP-binding; Chloroplast; Ligase; Nucleotide-binding; Plastid; Transit peptide
SRR3420119_TR18767_c0_g1_i2_len=1818	RCA2_LARTR	Q:909-1691;H:175-435	87.74%ID	E1e-166	Ribulose bisphosphate carboxylase/oxygenase activase 2, chloroplastic	PF00004.26*AAA*ATPase family associated with various cellular activities (AAA)*2-117*E:9.3e-09	0,56	-1,007	0,118	-2,264	0	-1,644	0	-1,819	0,111	1,248 RCA2_LARTR	Ribulose bisphosphate carboxylase/oxygenase activase 2, chloroplastic (RA 2) (RuBisCO activase 2) (RuBisCO activase beta form)	RCA2	Larrea tridentata (Creosote bush) (Zygophyllum tridentatum)	.	.	.	.	ATP-binding; Chloroplast; Nucleotide-binding; Plastid; Transit peptide
SRR3420119_TR20493_c2_g2_i1_len=2173	NA	NA	NA	NA	NA	.	0,488	0,261	1	0,064	0,001	-1,111	0	-1,152	1	-0,499.	.	.	.	.	.	.	.	.
SRR3420119_TR27542_c2_g1_i2_len=1750	CB5_ARATH	Q:882-1601;H:92-280	70.42%ID	E4e-94	Chlorophyll a-b binding protein CP26, chloroplastic	PF12698.4*Chlorophyll a-b binding protein*109-195*E:1.7e-09	0,798	0,492	0,088	-1,655	0,001	-1,759	0	-2,105	0,581	0,453 CB5_ARATH	Chlorophyll a-b binding protein CP26, chloroplastic (LHCB5) (LHCIIc) (Lightharvesting complex II protein 5)	LHCB5 At4g10340 F24G24.140	Arabidopsis thaliana (Mouse-ear cress)	.	Chlorophyll; Chloroplast; Chromophore; Complete proteome; Membrane; Metal-binding; Phosphoprotein; Photosynthesis; Photosystem I; Photosystem II; Plastid; Reference proteome; Thylakoid; Transit peptide; Transmembrane; Transmembrane helix
SRR3420119_TR31144_c1_g1_i7_len=1420	FER_CAPAN	Q:364-1201;H:1-144	73.29%ID	E2e-57	Ferredoxin, chloroplastic	PF00111.18*Fer2*2Fe-2S iron-sulfur cluster binding domain*12-63*E:6.2e-20	0,212	-0,573	0,9	0,123	0	-2,948	0	-2,274	0,35	0,362 FER_CAPAN	Ferredoxin, chloroplastic (PFLP)	AP1	Capsicum annuum (Bell pepper)	.	2Fe-2S; Chloroplast; Electron transport; Iron; Iron-sulfur; Metal-binding; Phosphoprotein; Plastid; Transit peptide; Transport
SRR3420119_TR34140_c1_g1_i2_len=629	GC1_ARATH	Q:624-73;H:40-223	80.43%ID	E2e-101	Epimerase family protein SDR39U1 homolog, chloroplastic (EC0:0000305)	PF05368.10*NmrA*NmrA-like family*10-68*E:6.5e-06 PF01370:18*Epimerase*NAD dependent epimerase/dehydratase family*11-148*E:3.1e-13 PF10073.16*3Beta_HSD*3-beta hydroxysteroid dehydrogenase/isomerase family*12-129*E:1.9e-05 PF07993.9*NAD_binding_4*Male sterility protein*12-43*E:0.00012 PF13460.3*NAD_binding_10*NAD(P)H-binding*14-130*E:2.4e-08	0,292	-0,348	0,953	0,035	0	-1,788	0	-1,575	0,226	1,97 GC1_ARATH	Epimerase family protein SDR39U1 homolog, chloroplastic (EC 1.1.1.-) (Protein GIANT CHLOROPLAST 1) (Protein SULA homolog) (AtSulA)	GC1 SULA At2g21280 F3K23	Arabidopsis thaliana (Mouse-ear cress)	.	Chloroplast; Complete proteome; Membrane; NADP; Oxidoreductase; Plastid; Plastid inner membrane; Reference proteome; Transit peptide
SRR3420119_TR37

SRR646572_TR18050_c0_g2_i2_len=1105	CB5_ARATH	Q:461-3,H:93-245	90.85%ID	E:4e-82	Chlorophyll a-b binding protein CP26, chloroplastic	.	0,091	-0,413	0,002	-0,798	0	-1,023	0,001	-0,75	0,861	0,068 CB5_ARATH	Chlorophyll a-b binding protein CP26, chloroplastic (LHCB5) (LHCIIc) (Light-harvesting complex II protein 5)	LHCB5 At4g10340 F24G24.140	Arabidopsis thaliana (Mouse-ear cress)	.	.	Chlorophyll; Chloroplast; Chromophore; Complete proteome; Magnesium; Membrane; Metal-binding; Phosphoprotein; Photosynthesis; Photosystem I; Photosystem II; Plastid; Reference proteome; Thylakoid; Transit peptide; Transmembrane; Transmembrane helix
SRR646572_TR19460_c0_g1_i1_len=711	RBS_MALSP	Q:462-229,H:106-183	87.18%ID	E:1e-44	Ribulose bisphosphate carboxylase small chain, chloroplastic	.	0,865	0,172	0,008	-1,272	0	-2,239	0	-1,748	0,663	0,4 RBS_MALSP	Ribulose bisphosphate carboxylase small chain, chloroplastic (RuBisCO small subunit) (EC 4.1.1.39)	RBCS	Malus sp. (Crab apple)	.	.	Calvin cycle; Carbon dioxide fixation; Chloroplast; Lyase; Monooxygenase; Oxidoreductase; Photorespiration; Photosynthesis; Plastid; Transit peptide
SRR646572_TR27490_c0_g1_i1_len=1330	BCA1_ARATH	Q:327-1202,H:53-347	78.64%ID	E:3e-157	Beta carbonic anhydrase 1, chloroplastic	PF00484.16^Pro_CA^Carbonic anhydrase^83-240^E:1.5e-39	0,381	2,455	0,798	0,431	0	-2,539	0	-2,089	1	0,018 BCA1_ARATH	Beta carbonic anhydrase 1, chloroplastic (AtbCA1) (AtbetaCA1) (EC 4.2.1.1) (Beta carbonate dehydratase 1) (Protein SALICYLIC ACID-BINDING PROTEIN 3) (AtSABP3)	BCA1 CA1 SABP3 At3g01500 F4P13.5	Arabidopsis thaliana (Mouse-ear cress)	.	.	Acetylation; Alternative splicing; Cell membrane; Chloroplast; Complete proteome; Lyase; Membrane; Phosphoprotein; Plastid; Reference proteome; Sviotroylation; Transit peptide; Zinc
SRR646572_TR29313_c0_g2_i4_len=2971	RUS5_ARATH	Q:376-1140,H:61-304	61.71%ID	E:7e-82	Protein root UVB sensitive 5 (ECO:0000303|PubMed:19515790)	PF04884.11^DUF647^Vitamin B6 photo-protection and homoeostasis^115-201^E:3.1e-23	0,443	-0,425	0,022	-1,387	0	-2,158	0	-2,008	0,892	-0,077 RUS5_ARATH	Protein root UVB sensitive 5	RUS5 At5g01510 F7A7.30	Arabidopsis thaliana (Mouse-ear cress)	.	.	Complete proteome; Reference proteome
SRR646572_TR29450_c0_g1_i1_len=531	NA	NA	NA	NA	NA	NA	1	-0,012	0,002	-1,043	0	-1,34	0	-1,024	0,535	-0,208 .	.	.	.	.	.	.
SRR646572_TR34084_c2_g1_i1_len=1480	ALFC2_ARATH	Q:170-1324,H:12-397	86.27%ID	E:0	Probable fructose-bisphosphate aldolase 2, chloroplastic	PF00274.16^Glycolytic^Fructose-bisphosphate aldolase class-I^98-442^E:7.2e-157	1	0,04	0,009	1,072	0	-0,928	0	-0,981	0,984	-0,014 ALFC2_ARATH	Probable fructose-bisphosphate aldolase 2, chloroplastic (EC 4.1.2.13)	FBA2 At4g38970 F19H22.70	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Carbohydrate degradation; glycolysis; D-glyceraldehyde 3-phosphate and glycerone phosphate from D-glucose; step 4/4.	.	Alternative splicing; Chloroplast; Complete proteome; Glycolysis; Lyase; Methylation; Phosphoprotein; Plastid; Reference proteome; Schiff base; Transit peptide
SRR646596_TR3897_c1_g3_i2_len=581	NA	NA	NA	NA	NA	.	1	1,121	0,044	1,121	0	-6,664	0	-6,664	1	-0,695 .	.	.	.	.	.	.
SRR646596_TR10573_c0_g2_i1_len=775	ERG16_ARATH	Q:427-38,H:69-198	80.77%ID	E:2e-68	Squalene epoxidase 3	PF0149.16^FAD_binding_3^FAD binding domain^102-248^E:2e-06	0,377	-0,561	1	-3,4	0	-2,122	0,001	-1,95	1	0,56 ERG16_ARATH	Squalene epoxidase 3 (AtSQE3) (EC 1.14.13.132)	SQE3 At4g37760 T28I19.4	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Terpene metabolism; lanosterol biosynthesis; lanosterol from farnesyl diphosphate; step 2/3.	.	Complete proteome; FAD; Flavoprotein; Membrane; NADP; Oxidoreductase; Reference proteome; Transmembrane; Transmembrane helix
SRR646596_TR19878_c0_g1_i1_len=1367	PSBP_SPIOL	Q:366-1181,H:1-267	76.36%ID	E:7e-142	Oxygen-evolving enhancer protein 2, chloroplastic	PF01789.13^PsbP^PsbP*62-271*E:6.5e-41	0,614	-0,105	0,492	-0,143	0	-0,889	0	-0,767	0,003	0,614 PSBP_SPIOL	Oxygen-evolving enhancer protein 2, chloroplastic (OEE2) (23 kDa subunit of oxygen evolving system of photosystem II) (23 kDa thylakoid membrane protein) (OEC 23 kDa subunit)	PSBP	Spinacia oleracea (Spinach)	.	.	3D-structure; Chloroplast; Direct protein sequencing; Membrane; Photosynthesis; Photosystem II; Plastid; Thylakoid; Transit peptide
SRR646604_TR2665_c0_g1_i1_len=528	NA	NA	NA	NA	NA	NA	1	0	1	-1,059	0,001	-2,618	0	-3,443	1	-3,232 .	.	.	.	.	.	.
SRR646604_TR5745_c0_g1_i1_len=2839	ROGF8_ARATH	Q:1698-889,H:75-412	58.03%ID	E:2e-117	Rho guanine nucleotide exchange factor 8	PF03759.10^PRONE^PRONE (Plant-specific Rop nucleotide exchanger)^1-24^E:4.1e-06 PF03759.10^PRONE^PRONE (Plant-specific Rop nucleotide exchanger)^55-262^E:3.7e-64	1	-0,52	1	-1,128	0	-2,463	0	-2,657	1	0,931 ROGF8_ARATH	Rho guanine nucleotide exchange factor 8 (AtRopGEF8) (Rho of plants guanine nucleotide exchange factor 8)	ROPGEF8 At3g24620 MOB24.21	Arabidopsis thaliana (Mouse-ear cress)	.	.	3D-structure; Cell membrane; Complete proteome; Guanine-nucleotide releasing factor; Membrane; Reference proteome
SRR646604_TR7503_c0_g2_i1_len=1569	CP41B_ARATH	Q:197-1213,H:1-378	76.46%ID	E:0	Chloroplast stem-loop binding protein of 41 kDa b, chloroplastic	PF01370.18^Epimerase^NAD dependent epimerase/dehydratase family^56-251^E:2.5e-07 PF13460.3^NAD_binding_10^NAD(P)H-binding^60-212^E:7.6e-09	1	0,003	0,541	0,174	0	-1,053	0	-0,838	0,014	0,683 CP41B_ARATH	Chloroplast stem-loop binding protein of 41 kDa b, chloroplastic (CSP41-b) (Heteroglycan-interacting protein 1.3) (Protein CHLOROPLAST RNA BINDING) (Protein CbsB)	CSP41B CRB HP1.3 At1g09340 T31J12.6	Arabidopsis thaliana (Mouse-ear cress)	.	.	Carbohydrate metabolism; Chloroplast; Complete proteome; Cytoplasm; Phosphoprotein; Plastid; Polysaccharide degradation; RNA-binding; Reference proteome; Transit peptide; rRNA processing; rRNA-binding
SRR646604_TR18421_c0_g1_i1_len=3370	NA	NA	NA	NA	NA	.	0,502	3,976	0,189	1,771	0	-1,927	0	-4,999	0,395	-0,6 .	.	.	.	.	.	.
SRR646604_TR20460_c0_g2_i1_len=2073	U83A1_ARATH	Q:488-1855,H:9-462	47.85%ID	E:2e-150	UDP-glycosyltransferase 83A1	PF00201.15^UDPGT^UDP-glucoronosyl and UDP-glucosyl transferase^268-422^E:1.1e-18	1	-0,137	1	0,163	0	-2	0	-1,789	0,76	0,55 U83A1_ARATH	UDP-glycosyltransferase 83A1 (EC 2.4.1.-)	UGT83A1 At3g02100 F1C9.11	Arabidopsis thaliana (Mouse-ear cress)	.	.	Complete proteome; Glycosyltransferase; Reference proteome; Transferase
SRR646604_TR21542_c0_g2_i1_len=1070	CUT1A_ARATH	Q:299-763,H:13-164	66.45%ID	E:1e-58	Protein CURVATURE THYLAKOID 1A, chloroplastic	PF14159.3^CAAD^CAAD domains of cyanobacterial aminoacyl-tRNA synthetases^85-168^E:3.4e-32 PF06813.10^Nodulin-like^Nodulin-like^8-266^E:6.1e-60 PF07690.13^MFS_1^Major Facilitator Superfamily^331-524^E:1.4e-09	0,395	-0,2	0,089	-0,386	0	-1,157	0	-0,976	0,988	0,004 CUT1A_ARATH	Protein CURVATURE THYLAKOID 1A, chloroplastic	CURT1A At4g01150 A_IG002N01.18 F2N1.18	Arabidopsis thaliana (Mouse-ear cress)	.	.	.
SRR646604_TR22841_c0_g3_i2_len=2346	NA	NA	NA	NA	NA	.	1	-0,135	0,461	-1,53	0	-2,147	0	-1,792	1	-0,056 .	.	.	.	.	.	.
SRR646604_TR23835_c0_g1_i1_len=1385	NA	NA	NA	NA	NA	.	0,395	-0,617	0,035	-1,592	0,001	-0,924	0	-1,11	0,043	0,954 .	.	.	.	.	.	.
SRR646604_TR32441_c0_g1_i8_len=2560	TPT_SPIOL	Q:230-1166,H:88-399	78.59%ID	E:0	Triose phosphate/phosphate translocator, chloroplastic	PF03151.13^TPT^Triose-phosphate Transporter family^1-165^E:6e-68	0,254	4,468	0,009	-6,042	0	-7,305	0	-7,305	1	0 TPT_SPIOL	Triose phosphate/phosphate translocator, chloroplastic (cTPT) (E29) (p36)	.	Spinacia oleracea (Spinach)	.	.	Chloroplast; Direct protein sequencing; Membrane; Plastid; Transit peptide; Transmembrane; Transmembrane helix; Transport
SRR646604_TR32633_c0_g2_i1_len=828	GAT22_ARATH	Q:257-610,H:117-230	40.3%ID	E:2e-21	Putative GATA transcription factor 22	PF00320.24^GATA^GATA zinc finger^174-207^E:9e-17	0,447	-0,293	0,071	-0,923	0	-2,64	0	-3,155	0,005	-1,079 GAT22_ARATH	Putative GATA transcription factor 22	GATA22 At4g26150 F20B18.260	Arabidopsis thaliana (Mouse-ear cress)	.	.	Complete proteome; DNA-binding; Metal-binding; Nucleus; Reference proteome; Transcription; Transcription regulation; Zinc; Zinc-finger
SRR646604_TR34940_c0_g3_i1_len=1403	PSBO_SOLTU	Q:212-1210,H:1-332	88.59%ID	E:0	Oxygen-evolving enhancer protein 1, chloroplastic	PF01716.15^MSP^Manganese-stabilising protein / photosystem II polypeptide^100-332^E:9.6e-99	0,308	-0,216	0,003	-0,625	0	-0,996	0,001	-0,704	0,037	0,436 PSBO_SOLTU	Oxygen-evolving enhancer protein 1, chloroplastic (OEE1) (33 kDa subunit of oxygen evolving system of photosystem II) (33 kDa thylakoid membrane protein) (OEC 33 kDa subunit)	PSBO	Solanum tuberosum (Potato)	.	.	Chloroplast; Complete proteome; Manganese; Membrane; Photosynthesis; Photosystem II; Plastid; Reference proteome; Thylakoid; Transit peptide
SRR646604_TR38081_c0_g3_i1_len=1533	ALFC_ORYSJ	Q:282-1292,H:50-386	91.1%ID	E:0	Fructose-bisphosphate aldolase, chloroplastic	PF00274.16^Glycolytic^Fructose-bisphosphate aldolase class-I^13-351^E:1.4e-154	1	0,542	0,254	-4,808	0	-1,582	0	-2,808	1	0,618 ALFC_ORYSJ	Fructose-bisphosphate aldolase, chloroplastic (ALDP) (EC 4.1.2.13)	Os11g0171300 LOC_Os11g07020 Os1_33121	Oryza sativa subsp. japonica (Rice)	PATHWAY: Carbohydrate degradation; glycolysis; D-glyceraldehyde 3-phosphate and glycerone phosphate from D-glucose; step 4/4.	.	Chloroplast; Complete proteome; Direct protein sequencing; Glycolysis; Lyase; Plastid; Reference proteome; Schiff base; Transit peptide
SRR646604_TR38541_c1_g1_i8_len=1674	CB5_ARATH	Q:155-3,H:195-245	94.12%ID	E:2e-29	Chlorophyll a-b binding protein CP26, chloroplastic	.	1	0,189	0,017	-2,249	0	-2,064	0	-2,479	1	0,09 CB5_ARATH	Chlorophyll a-b binding protein CP26, chloroplastic (LHCB5) (LHCIIc) (Light-harvesting complex II protein 5)	LHCB5 At4g10340 F24G24.140	Arabidopsis thaliana (Mouse-ear cress)	.	.	Chlorophyll; Chloroplast; Chromophore; Complete proteome; Magnesium; Membrane; Metal-binding; Phosphoprotein; Photosynthesis; Photosystem I; Photosystem II; Plastid; Reference proteome; Thylakoid; Transit peptide; Transmembrane; Transmembrane helix
SRR648705_TR269_c3_g5_i8_len=2682	GNOM_ARATH	Q:1242-1454,H:176-246	49.3%ID	E:5e-23	ARF guanine-nucleotide exchange factor GNOM	.	1	-0,061	0,019	-1,608	0	-1,628	0	-1,912	0,848	0,142 GNOM_ARATH	ARF guanine-nucleotide exchange factor GNOM (Pattern formation protein EMB30) (Protein EMBRYO DEFECTIVE 30) (Protein MIZU-KUSSEI2) (Protein VASCULAR NETWORK 1)	GN EMB30 GBF3 MIZ2 VAN7 At1g13980 F16A14.20 F7A19.7	Arabidopsis thaliana (Mouse-ear cress)	.	.	Cell membrane; Complete proteome; GPI-anchor; Glycoprotein; Lipoprotein; Membrane; Reference proteome; Transport
SRR648705_TR18110_c0_g1_i1_len=1031	IAA17_ARATH	Q:245-820,H:3-218	51.15%ID	E:1e-59	Auxin-responsive protein IAA17	PF02309.13^AUX_IAA^AUX/IAA family^31-202^E:6.3e-59	1	0,038	0	7,058	0	-7,593	0	-9,345	0,786	0,1 IAA17_ARATH	Auxin-responsive protein IAA17 (Auxin response 3) (Indoleacetic acid-induced protein 17)	IAA17 AXR3 At1g04250 F19P19.31	Arabidopsis thaliana (Mouse-ear cress)	.	.	3D-structure; Auxin signaling pathway; Complete proteome; Nucleus; Phosphoprotein; Reference proteome; Repressor; Transcription; Transcription regulation
SRR648705_TR10096_c0_g1_i1_len=2966	FRO7_ARATH	Q:240-7281,H:32-747	61.2%ID	E:0	Ferric reduction oxidase 7, chloroplastic	PF01794.16^Ferric_reduct^Ferric reductase like transmembrane component^190-317^E:1.1e-18 PF08022.9^FAD_binding_8^FAD-binding domain^347-453^E:3.6e-16 PF08030.9^NAD_binding_6^Ferric reductase NAD binding domain^460-719^E:2.5e-18	1	0,016	0,043	-2,95	0	-1,039	0	-1,026	0,24	0,528 FRO7_ARATH	Ferric reduction oxidase 7, chloroplastic (AtFRO7) (EC 1.16.1.7) (Ferric-chelate reductase 7)	FRO7 At5g49740 K2I5.10	Arabidopsis thaliana (Mouse-ear cress)	.	.	Chloroplast; Complete proteome; Electron transport; FAD; Flavoprotein; Ion transport; Iron; Membrane; Metal-binding; NAD; Oxidoreductase; Plastid; Reference proteome; Transit peptide; Transmembrane; Transmembrane helix; Transport
SRR648705_TR11407_c0_g1_i1_len=1223	U83A1_ARATH	Q:3-902,H:168-460	48.03%ID	E:9e-96	UDP-glycosyltransferase 83A1	PF00201.15^UDPGT^UDP-glucoronosyl and UDP-glucosyl transferase^115-279^E:6.9e-24	1	0,6	1	-1,14	0	-2,972	0	-3,154	1	2,791 U83A1_ARATH	UDP-glycosyltransferase 83A1 (EC 2.4.1.-)	UGT83A1 At3g02100 F1C9.11	Arabidopsis thaliana (Mouse-ear cress)	.	.	Complete proteome; Glycosyltransferase; Reference proteome; Transferase
SRR648705_TR12859_c0_g1_i1_len=1421	LBD39_ARATH	Q:301-636,H:1-112	82.14%ID	E:3e-58	LOB domain-containing protein 39	PF03195.11^DUF260^Protein of unknown function DUF260^12-100^E:9.5e-27	0,298	-0,678	0,493	-0,364	0	-2,319	0	-2,292	0,419	0,437 LBD39_ARATH	LOB domain-containing protein 39 (ASYMMETRIC LEAVES 2-like protein 41) (AS2-like protein 41)	LBD39 ASL41 At4g37540 F19F18.30	Arabidopsis thaliana (Mouse-ear cress)	.	.	Complete proteome; Reference proteome
SRR648705_TR13461_c0_g1_i1_len=1371	LBD37_ARATH	Q:1125-472,H:1-219	56.5%ID	E:3e-73	LOB domain-containing protein 37	PF03195.11^DUF260^Protein of unknown function DUF260^12-101^E:9.8e-26	0,865	-0,145	0,03	1,068	0	-1,492	0	-1,636	1	0,044 LBD37_ARATH	LOB domain-containing protein 37 (ASYMMETRIC LEAVES 2-like protein 39) (AS2-like protein 39)	LBD37 ASL39 At5g67420 K8K14.16	Arabidopsis thaliana (Mouse-ear cress)	.	.	Complete proteome; Reference proteome
SRR648705_TR16901_c0_g2_i1_len=2423	DIT1_ARATH	Q:836-1969,H:180-657	89.68%ID	E:0	Dicarboxylate transporter 1, chloroplastic	PF00939.16^Na_sulph_symp^Sodium:sulfate symporter transmembrane region^1-297^E:4.3e-67	0,231	-0,4	0,624	0,185	0	-1,864	0	-1,737	0,845	0,079 DIT1_ARATH	Dicarboxylate transporter 1, chloroplastic (2-oxoglutarate/malate translocator 1) (AtpOMT1)	DIT1 At5g12860 T24H18.30	Arabidopsis thaliana (Mouse-ear cress)	.	.	Alternative splicing; Chloroplast; Complete proteome; Membrane; Plastid; Plastid inner membrane; Reference proteome; Transit peptide; Transmembrane; Transmembrane helix; Transport
SRR648705_TR20491_c0_g1_i1_len=2010	C75A1_PETHY	Q:1723-308,H:33-498	35.92%ID	E:6e-94	Flavonoid 3',5'-hydroxylase 1	PF00067.19^p450^Cytochrome P450^35-497^E:1.1e-96	1	1,364	1	0,856	0	-1,784	0	-1,947	0,18	0,843 C75A1_PETHY	Flavonoid 3',5'-hydroxylase 1 (F3'5'H) (EC 1.14.13.88) (CYPLXXVA1) (Cytochrome P450 75A1)	CYP75A1 HF1	Petunia hybrida (Petunia)	PATHWAY: Pigment biosynthesis; anthocyanin biosynthesis.	.	Endoplasmic reticulum; Heme; Iron; Metal-binding; Microsome; Monooxygenase; NADP; Oxidoreductase
SRR648705_TR23645_c0_g1_i1_len=2118	PEAMT_SPIOL	Q:1746-295,H:10-493	80.58%ID	E:0	Phosphoethanolamine N-methyltransferase	PF13489.3^Methyltransf_23^Methyltransferase domain^46-167^E:2.2e-07 PF13847.3^Methyltransf_31^Methyltransferase domain^54-167^E:5e-11 PF05891.9^Methyltransf_PK^AdoMet dependent proline dimethyltransferase^54-192^E:5.9e-10 PF03601.8^Nod5^Nodulation protein S (Nod5)^54-156^E:2.8e-07 PF03848.11^TehB^Tellurite resistance protein TehB^55-154^E:1.2e-05 PF13649.3^Methyltransf_25^Methyltransferase domain^57-152^E:7e-14 PF08241.9^Methyltransf_11^Methyltransferase domain^58-156^E:4e-14 PF08242.9^Methyltransf_12^Methyltransferase domain^58-154^E:7.4e-08 PF01739.15^CheR^CheR methyltransferase, SAM binding domain^97-156^E:6.6 0.0022 PF00891.15^Methyltransf_2^O-methyltransferase^255-424^E:0.00026 PF02353.17^CMAS^Mycolic acid cyclopropane synthetase^266-462^E:1.2e-17 PF05175.11^MTS^Methyltransferase small domain^271-354^E:0.00015 PF13489.3^Methyltransf_23^Methyltransferase domain^272-426^E:1.2e-22 PF01209.15^Ubie_methyltran^ubiE/COQ5 methyltransferase family^272-389^E:1.9e-10 PF07021.9^MetW^Methionine biosynthesis protein MetW^280-364^E:0.00011 PF13847.3^Methyltransf_31^Methyltransferase domain^282-387^E:6e-20 PF13649.3^Methyltransf_25^Methyltransferase domain^286-379^E:2.8e-19 PF08241.9^Methyltransf_11^Methyltransferase domain^287-383^E:5.3e-18 PF08242.9^Methyltransf_12^Methyltransferase domain^287-380^E:5.1e-13 PF01739.15^CheR^CheR methyltransferase, SAM binding domain^328-383^E:0.00019	0,351	-0,238	0,011	-0,754	0	-1,855	0	-1,735	0,597	0,147 PEAMT_SPIOL	Phosphoethanolamine N-methyltransferase (EC 2.1.1.103)	PEAMT	Spinacia oleracea (Spinach)	PATHWAY: Phospholipid metabolism; phosphatidylcholine biosynthesis; phosphocholine from phosphoethanolamine; step 1/1.	Cytoplasm; Lipid biosynthesis; Lipid metabolism; Methyltransferase; Phospholipid biosynthesis; Phospholipid metabolism; Repeat; Sadenosyl-L-methionine; Stress response; Transferase
SRR648705_TR24334_c0_g1_i1_len=200	NA	NA	NA	NA	NA	PF07386.8^DUF1499^Protein of unknown function (DUF1499)^91-218^E:1.6e-29	0,611	-0,345	0,623	-0,419	0	-1,638	0	-1,665	0,37	-0,407 .	.	.	.	.	.	.
SRR648705_TR29032_c0_g1_i3_len=1237	NA	NA	NA	NA	NA	.	1	-0,186	0,76	-0,602	0	-1,732	0	-1,663	0,84	-0,166 .	.	.	.	.	.	.
SRR648705_TR29776_c0_g1_i1_len=1598	CHSY_CATRO	Q:260-1426,H:1-389	99.74%ID	E:0	Chalcone synthase	PF00195.16^Chal_sti_synt_N^Chalcone and stilbene synthases, N-terminal domain^5-228^E:5.6e-125 PF02797.13^Chal_sti_synt_C^Chalcone and stilbene synthases, C-terminal domain^238-387^E:6.7e-95 PF08541.7^ACP_syn_III^3-Oxoacyl-[acyl-carrier-protein (ACP)] synthase III^162-227^E:1.7e-05 PF02797.12^Chal_sti_synt_C^Chalcone and stilbene synthases, C-terminal domain^238-387^E:6.7e-72 PF08541.7^ACP_syn_III_C^3-Oxoacyl-[acyl-carrier-protein (ACP)] synthase III C terminal^30-138^E:5e-07	0,117	-0,892	0,195	1,302	0	-2,023	0	-1,511	0,581	0,401 CHSY_CATRO	Chalcone synthase (EC 2.3.1.74) (Naringenin-chalcone synthase)	CHS	Catharanthus roseus (Madagascar periwinkle) (Vinca rosea)	PATHWAY: Secondary metabolite biosynthesis; flavonoid biosynthesis.	.	Acyltransferase; Flavonoid biosynthesis; Transferase
SRR648705_TR37308_c0_g1_i1_len=506	NA	NA	NA	NA	NA	.	0,083	-0,369	0,003	-0,69	0	-0,917	0	-0,948	0	0,925 .	.	.	.	.	.	.
SRR648705_TR42657_c0_g2_i1_len=2999	U83A1_ARATH	Q:1730-291,H:9-462	48.05%ID	E:7e-141	UDP-glycosyltransferase 83A1	PF00201.15^UDPGT^UDP-glucoronosyl and UDP-glucosyl transferase^115-275^E:4.4e-19	1	-0,026	0,228	-1,121	0,001	-1,526	0	-1,651	0,407	-0,675 U83A1_ARATH	UDP-glycosyltransferase 83A1 (EC 2.4.1.-)	UGT83A1 At3g02100 F1C9.11	Arabidopsis thaliana (Mouse-ear cress)	.	.	Complete proteome; Glycosyltransferase; Reference proteome; Transferase
SRR648707_TR693_c0_g1_i2_len=3595	CAPP2_ARATH	Q:580-3483,H:1-963	87.1%ID	E:0	Phosphoenolpyruvate carboxylase 2	PF00311.14^PEPcase^Phosphoenolpyruvate carboxylase^163-968^E:0	0,355	-0,326	0,684	0,221	0	-2,213	0	-1,384	0	1,399 CAPP2_ARATH	Phosphoenolpyruvate carboxylase 2 (AtPPC2) (PEPC 2) (PEPCase 2) (EC 4.1.1.31)	PPC2 At2g42600 F14N22.13	Arabidopsis thaliana (Mouse-ear cress)	.	.	Allosteric enzyme; Carbon dioxide fixation; Complete proteome; Cytoplasm; Lyase; Magnesium; Phosphoprotein; Photosynthesis; Reference proteome; Ubl conjugation
SRR648707_TR6353_c0_g2_i1_len=797	RK21_ARATH	Q:502-50,H:57-210	63.29%ID	E:1e-47	50S ribosomal protein L21, chloroplastic	PF00829.18^Ribosomal_L21p^Ribosomal prokaryotic L21 protein^98-198^E:2.2e-31	0,1	-0,47	0,076	-0,587	0	-1,396	0	-1,279	0,597	-0,504 RK21_ARATH	50S ribosomal protein L21, chloroplastic (CL21)	RPL21 At1g35680 F15O4.7	Arabidopsis thaliana (Mouse-ear cress)	.	.	Chloroplast; Complete proteome; Plastid; RNA-binding; Reference proteome; Ribonucleoprotein; Ribosomal protein; Transit peptide; rRNA-binding
SRR648707_TR10843_c0_g1_i3_len=1060	NA	NA	NA	NA	NA	.	0,086	-0,936	0,008	-2,99	0	-2,423	0	-3,216	0,129	-0,648 .	.	.	.	.	.	.
SRR648707_TR22709_c0_g2_i8_len=2493	NA	NA	NA	NA	NA	.	1	0	1	0	0	-6,954	0	-6,954	0,066	5,363 .	.	.	.	.	.	.
SRR924147_TR32482_c0_g1_i1_len=2162	GLNA2_DAUCA	Q:1631-426,H:1-403	89.08%ID	E:0	Glutamine synthetase, chloroplastic	PF03951.16^Gln-synt_N^Glutamine synthetase, beta-Grasp domain^91-156^E:2.2e-10 PF00120.21^Gln-synt_C^Glutamine synthetase, catalytic domain^185-406^E:7.7e-16	0,619	-0,114	0,321	-0,22	0	-1,057	0,001	-0,727	1	0,016 GLNA2_DAUCA	Glutamine synthetase, chloroplastic (EC 6.3.1.2) (GS2) (Glutamate--ammonia ligase)	GLN2	Daucus carota (Wild carrot)	.	.	ATP-binding; Chloroplast; Ligase; Nucleotide-binding; Plastid; Transit peptide
SRR924148_TR2003_c0_g1_i1_len=1287	NA	NA	NA	NA	NA	PF03168.10^LEA_2^Late embryogenesis abundant protein^149-235^E:2.1e-10	1	0,098	0,008	4,13	0	-5,667	0	-5,661	1	0,143 .	.	.	.	.	.	.
SRR924148_TR7756_c1_g3_i2_len=734	PPCK2_ARATH	Q:647-354,H:7-104	43.43%ID	E:4e-22	Phosphoenolpyruvate carboxylase kinase 2	PF00069.22^Pkinase^Protein kinase domain^34-141^E:9.5e-18 PF07714.14^Pkinase_Tyr^Protein tyrosine kinase^37-128^E:6.4e-09	1	0,149	0,129	-5,178	0	-2,512	0	-1,668	1	-0,297 PPCK2_ARATH	Phosphoenolpyruvate carboxylase kinase 2 (AtPPCK2) (EC 2.7.11.1)	PPCK2 At3g04530 T27C4.19	Arabidopsis thaliana (Mouse-ear cress)	.	.	ATP-binding; Complete proteome; Kinase; Nucleotide-binding; Pyruvate; Reference proteome; Serine/threonine-protein kinase; Transferase
SRR924148_TR11150_c1_g1_i1_len=348	NA	NA	NA	NA	NA	.	0,643	0,436	0,09	0,962	0,001	-1,052	0	-1,308	0,537	0,341 .	.	.	.	.	.	.
SRR924148_TR16153_c1_g1_i1_len=3622	COB22_ARATH	Q:3333-562,H:1-926	84.02%ID	E:0	Coatomer subunit beta'-2	PF00400.29^WD40^WD domain, G-beta repeat^91-127^E:8e-06 PF00400.29^WD40^WD domain, G-beta repeat^133-171^E:0.00013 PF00400.29^WD40^WD domain, G-beta repeat^175-215^E:5.6e-06 PF00400.29^WD40^WD domain, G-beta repeat^220-256^E:6.6e-09 PF04053.11^Coatomer_WDAD^Coatomer WD associated region^319-763^E:7.2e-167 PF00400.29^WD40^WD domain, G-beta repeat^91-127^E:8e-06 PF00400.29^WD40^WD domain, G-beta repeat^133-171^E:0.00013 PF00400.29^WD40^WD domain, G-beta repeat^175-215^E:5.6e-06 PF00400.29^WD40^WD domain, G-beta repeat^220-256^E:6.6e-09 PF04053.11^Coatomer_WDAD^Coatomer WD associated region^319-763^E:7.2e-167 PF12338.5^RbcS^Ribulose-1,5-bisphosphate carboxylase small subunit^242^E:6.5e-21 PF00101.17^RuBisCO_small^Ribulose bisphosphate carboxylase, small chain^69-179^E:1.2e-39 PF05368.10^NmrA^NmrA-like family^37-210^E:1.8e-05 PF13460.3^NAD_binding_10^NAD(P)H-binding^101-309^E:9.9e-15	1	0,006	0	2,883	0	-2,642	0	-2,99	0,547	-0,414 COB22_ARATH	Coatomer subunit beta'-2 (Beta'-coat protein 2) (Beta'-COP 2)	At1g52360 F19K6.16	Arabidopsis thaliana (Mouse-ear cress)	.	.	Alternative splicing; Complete proteome; Cytoplasm; Cytoplasmic vesicle; ER-Golgi transport; Golgi apparatus; Membrane; Protein transport; Reference proteome; Repeat; Transport; WD repeat
SRR924148_TR16153_c1_g1_i4_len=3587	COB22_ARATH	Q:3298-527,H:1-926	84.02%ID	E:0	Coatomer subunit beta'-2	PF00400.29^WD40^WD domain, G-beta repeat^91-127^E:8e-06 PF00400.29^WD40^WD domain, G-beta repeat^133-171^E:0.00013 PF00400.29^WD40^WD domain, G-beta repeat^175-215^E:5.6e-06 PF00400.29^WD40^WD domain, G-beta repeat^220-256^E:6.6e-09 PF04053.11^Coatomer_WDAD^Coatomer WD associated region^319-763^E:7.2e-167 PF12338.5^RbcS^Ribulose-1,5-bisphosphate carboxylase small subunit^242^E:6.5e-21 PF00101.17^RuBisCO_small^Ribulose bisphosphate carboxylase, small chain^69-179^E:1.2e-39 PF05368.10^NmrA^NmrA-like family^37-210^E:1.8e-05 PF13460.3^NAD_binding_10^NAD(P)H-binding^101-309^E:9.9e-15	0,724	-0,203	0,001	5,566	0	-5,874	0	-4,508	0,679	-0,432 COB22_ARATH	Coatomer subunit beta'-2 (Beta'-coat protein 2) (Beta'-COP 2)	At1g52360 F19K6.16	Arabidopsis thaliana (Mouse-ear cress)	.	.	Alternative splicing; Complete proteome; Cytoplasm; Cytoplasmic vesicle; ER-Golgi transport; Golgi apparatus; Membrane; Protein transport; Reference proteome; Repeat; Transport; WD repeat
SRR924148_TR23140_c0_g1_i1_len=983	RBS_MALSP	Q:223-762,H:1-183	81.42%ID	E:2e-107	Ribulose bisphosphate carboxylase small chain, chloroplastic	.	0,111	-0,331	0,008	-0,551	0	-0,866	0,001	-0,717	0,772	-0,06 RBS_MALSP	Ribulose bisphosphate carboxylase small chain, chloroplastic (RuBisCO small subunit) (EC 4.1.1.39)	RBCS	Malus sp. (Crab apple)	.	.	Calvin cycle; Carbon dioxide fixation; Chloroplast; Lyase; Monooxygenase; Oxidoreductase; Photorespiration; Photosynthesis; Plastid; Transit peptide
SRR924148_TR25547_c0_g1_i1_len=2219	NA	NA	NA	NA	NA	.	0,61	-0,117	0,332	-0,229	0	-1,404	0	-1,096	0,292	0,247 .	.	.	.	.	.	.
SRR924148_TR39696_c0_g1_i1_len=657	NA	NA	NA	NA	NA	.	1	-0,579	0,254	2,727	0	-4,782	0	-4,366	1	0,161 .	.	.	.	.	.	.

MsIntact24h

| Transcript (CDF97) | Uniprot homolog | BLASTX Position | BLASTX %Identity | BLASTX evalue | Uniprot descr | Pfam | PValue_Ms6h | logFC_

SRR1271859_TR30155_c0_g2_i1_len=615	CCB12_ORYSJ	[illegible]	45,87%|	E:4e-23	Cyclin-B1-2	PF0534 8*UMP1*Proteasome maturation factor UMP1*74-173*E:2.1e-24	0,352	-0,907	0,76	-0,774	0,258	-0,921	0,001	-6,644	0,461	-1,35	CCB12_ORYSJ	Cyclin-B1-2 (G2/mitotic-specific cyclin-B1-2) (CycB1;2)	[illegible] LOC_Os02g55720	Oryza sativa subsp. japonica (Rice)		Cell cycle; Cell division; Complete proteome; Cyclin; Reference proteome
SRR1271859_TR33928_c0_g1_i6_len=3089	GLYC7_ARATH	Q 615-1589,H:28-354	67,89%|	E:1e-144	Serine hydroxymethyltransferase 7	PF00464.16*SHMT*Serine hydroxymethyltransferase*138-373*E:2e-94	1	1,992	0,129	-4,893	0,442	-2,205	0,001	-6,852	0,524	0,54	GLYC7_ARATH	Serine hydroxymethyltransferase 7 (AtSHMT7) (EC 2.1.2.1) (Glycine hydroxymethyltransferase 7) (Serine methylase 7)	SHM7 SHMT7 At1g36370 F7F23.9	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: One-carbon metabolism; tetrahydrofolate interconversion.	Complete proteome; Cytoplasm; One-carbon metabolism; Pyridoxal phosphate; Reference proteome; Transferase
SRR1271859_TR38747_c1_g1_i1_len=1778	NA	NA	NA	NA	NA	PF06273.8*eIF-4B*Plant specific eukaryotic initiation factor 4B*172-233*E:1.5e-34 PF06273.8*eIF-4B*Plant specific eukaryotic initiation factor 4B*174-369*E:1.3e-17	0,05	-0,811	0,35	-0,344	0,002	-1,246	0	-1,522	0,217	-0,481						
SRR1271859_TR42941_c0_g1_i4_len=672	IMB1_ARATH	Q:106-300;H:806-876	83,08%|	E:2e-25	Importin subunit beta-1 (ECO:0000305)		0,282	-1,115	0,18	0,9	0,505	-0,532	0,001	-3,087	1	0	IMB1_ARATH	Importin subunit beta-1 (Karyopherin subunit beta-1) (ATKPNB1)	KPNB1 At5g53480 MNC6.1	Arabidopsis thaliana (Mouse-ear cress)		Acetylation; Complete proteome; Cytoplasm; Nucleus; Protein transport; Reference proteome; Repeat; Stress response; Transport
SRR342017_TR725_c0_g1_i1_len=1166	ZFP8_ARATH	Q:835-38;H:8-257	36,82%|	E:1e-32	Zinc finger protein 8	PF13912.3*zf-C2H2_6*C2H2-type zinc finger*101-125*E:0.00012	0,704	0,195	0,902	-0,13	0,007	-1,055	0	-1,667	0,472	-0,314	ZFP8_ARATH	Zinc finger protein 8	ZFP8 At2g41940 T6D20.16	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Developmental protein; Differentiation; Metal-binding; Reference proteome; Transcription; Transcription regulation; Zinc; Zinc-finger
SRR342017_TR4609_c1_g1_i1_len=2199	GERS_OCIBA	Q:515-2110;H:44-566	64,98%|	E:0	Geraniol synthase, chloroplastic	PF03936.13*terpene_synth_C*Terpene synthase family, metal binding domain*345-612*E:1.3e-95 PF03936.13*terpene_synth_C*Terpene synthase family, metal binding domain*345-612*E:1.3e-95	0,17	0,508	0,679	-0,373	0,051	-0,855	0,001	-1,648	1	-1,594	GERS_OCIBA	Geraniol synthase, chloroplastic (ObGES) (EC 3.1.7.11)	GES	Ocimum basilicum (Sweet basil)	PATHWAY: Secondary metabolite biosynthesis; terpenoid biosynthesis.	Chloroplast; Hydrolase; Manganese; Metal-binding; Plastid; Transit peptide
SRR342017_TR14008_c0_g2_i4_len=854	NA	NA	NA	NA	NA		0,212	0,959	0,214	-0,817	1	-0,216	0,001	-6,656	0,381	0,854						
SRR342017_TR20766_c0_g2_i5_len=849	NA	NA	NA	NA	NA		1	0,221	0,016	-2,805	0,006	-0,984	0	-1,434	1	0,303						
SRR342019_TR2921_c1_g1_i5_len=1413	ADHX_ORYSI	Q:182-1297,H:3-377	44,83%|	E:3e-94	Alcohol dehydrogenase class-3	PF08240.9*ADH_N*Alcohol dehydrogenase GroES-like domain*39-162*E:1.6e-22 PF00107.23*ADH_zinc_N*Zinc-binding dehydrogenase*206-326*E:8.1e-22	0,028	0,553	0,1	0,981	0,071	-0,491	0	-1,865	0,287	0,287	ADHX_ORYSI	Alcohol dehydrogenase class-3 (EC 1.1.1.1) (Alcohol dehydrogenase class-III) (Glutathione-dependent formaldehyde dehydrogenase) (FALDH) (FDH) (GSH-FDH) (EC 1.1.1.-) (S-(hydroxymethyl)glutathione dehydrogenase) (EC 1.1.1.284)	ADHIII Osi_009236	Oryza sativa subsp. indica (Rice)		Complete proteome; Cytoplasm; Metal-binding; NAD; Oxidoreductase; Reference proteome; Zinc
SRR342019_TR1776_c0_g1_i1_len=1811	DDC_CATRO	Q:1360-184;H:112-500	98,46%|	E:0	Aromatic-L-amino-acid decarboxylase	PF00282.16*Pyridoxal_deC*Pyridoxal-dependent decarboxylase conserved domain*4-333*E:5e-102	0,011	0,59	0	3,432	0,937	0,028	0	-1,39	1	0,323	DDC_CATRO	Aromatic-L-amino-acid decarboxylase (AADC) (EC 4.1.1.28) (DOPA decarboxylase) (Tryptophan decarboxylase)	TDC	Catharanthus roseus (Madagascar periwinkle) (Vinca rosea)		Decarboxylase; Lyase; Pyridoxal phosphate
SRR342019_TR7619_c0_g1_i5_len=1469	PTR53_ARATH	Q:284-1102,H:41-314	67,85%|	E:2e-119	Protein NRT1/ PTR FAMILY 2.11	PF00854.18*PTR2*POT family*94-262*E:1.9e-33	1	0,176	0,319	1,07	0,055	-1,547	0	-2,327	0,832	0,182	PTR53_ARATH	Protein NRT1/ PTR FAMILY 2.11 (AtNPF2.11) (Nitrate transporter 1.10) (Protein GLUCOSINOLATE TRANSPORTER-2)	NPF2.11 GTR2 NRT1.10 At5g62680 MRG21.10	Arabidopsis thaliana (Mouse-ear cress)		Cell membrane; Complete proteome; Membrane; Reference proteome; Transmembrane; Transmembrane helix; Transport
SRR342019_TR8417_c2_g4_i1_len=939	RL27_PEA	Q:81-485;H:1-135	77,04%|	E:1e-59	60S ribosomal protein L27	PF01777.15*Ribosomal_L27e*Ribosomal L27e protein family*52-135*E:1.3e-33	0,001	-1,035	0,041	0,659	0,026	-0,848	0	-1,47	0,781	-0,081	RL27_PEA	60S ribosomal protein L27	RPL27	Pisum sativum (Garden pea)		Ribonucleoprotein; Ribosomal protein
SRR342019_TR11109_c3_g4_i1_len=1813	NA	NA	NA	NA	NA		1	-0,006	1	-0,435	0,011	-1,301	0,001	-1,799	0,44	0,788						
SRR342019_TR23065_c0_g1_i2_len=1821	NA	NA	NA	NA	NA		0,689	-0,217	0,38	-0,466	0,048	-0,791	0	-2,083	1	1,045						
SRR342019_TR29967_c2_g2_i1_len=1549	IRIS_CATRO	Q:138-1301,H:1-388	99,74%|	E:0	Iridoid synthase		0,001	0,89	0,277	-0,528	0,645	-0,158	0	-1,344	0,348	0,244	IRIS_CATRO	Iridoid synthase (EC 1.3.1.99)		Catharanthus roseus (Madagascar periwinkle) (Vinca rosea)		Cytoplasm; NAD; Oxidoreductase
SRR342019_TR36227_c6_g7_i2_len=893	C7BL3_CICIN	Q:838-245,H:290-486	42,93%|	E:1e-57	Costunolide synthase	PF00067.19*p450*Cytochrome P450*3-185*E:2.1e-49	0	1,586	0	1,968	0,001	0,852	0,001	-0,994	0,16	1,341	C7BL3_CICIN	Costunolide synthase (CiCOS) (EC 1.14.13.120) (Cytochrome P450 71BL3)	CYP71BL3 COS	Cichorium intybus (Chicory)		Heme; Iron; Membrane; Metal-binding; Monooxygenase; NADP; Oxidoreductase; Transmembrane; Transmembrane helix; Transport
SRR342019_TR3223_c0_g1_i1_len=1823	TL29_SOLLC	Q:18-121-1381;H:74-220	82,31%|	E:4e-71	Thylakoid lumenal 29 kDa protein, chloroplastic	PF01141.20*peroxidase*Peroxidase*24-117*E:9.6e-18	0,967	-0,022	0,027	-0,579	0,001	-0,905	0	-1,082	1	0,71	TL29_SOLLC	Thylakoid lumenal 29 kDa protein, chloroplastic (TL29) (EC 1.--.-) (LeAPx09) (P29)	CLEB3J9	Solanum lycopersicum (Tomato) (Lycopersicon esculentum)		Chloroplast; Complete proteome; Oxidoreductase; Plastid; Reference proteome; Thylakoid; Transit peptide
SRR342022_TR17554_c1_g1_i34_len=3871	RUS5_ARATH	Q:349-5-2941,H:61-226	59,16%|	E:5e-69	Protein root UVB sensitive 5 (ECO:0000303|PubMed:19515790)	PF04884.11*DUF647*Vitamin B6 photo-protection and homoeostasis*115-201*E:3.1e-23	1	0,084	0,01	-2,397	0,002	-2,282	0,001	-2,705	1	0,34	RUS5_ARATH	Protein root UVB sensitive 5	RUS5 At5g01510 F7A7.30	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Reference proteome
SRR342022_TR19437_c5_g6_i2_len=1467	RS8_ORYSJ	Q:936-277,H:1-220	90,91%|	E:9e-103	40S ribosomal protein S8	PF01201.19*Ribosomal_S8e*Ribosomal protein S8e*1-198*E:2.1e-58	1	0,095	1	0,005	0,004	-2,047	0,001	-2,559	0,56	0,863	RS8_ORYSJ	40S ribosomal protein S8	RPS8 Os02g0489400 LOC_Os02g28810 OSJNBa0048K16.2 P0483C08.42	Oryza sativa subsp. japonica (Rice)		Complete proteome; Reference proteome; Ribonucleoprotein; Ribosomal protein
SRR342022_TR21505_c2_g2_i7_len=801	NRT31_ARATH	Q:147-698,H:1-200	52,88%|	E:1e-58	High-affinity nitrate transporter 3.1	PF16974.2*NAR2*High-affinity nitrate transporter accessory*27-199*E:9.2e-81	0,372	0,397	0,573	0,245	0,003	-1,464	0	-1,961	0,702	-0,173	NRT31_ARATH	High-affinity nitrate transporter 3.1 (Protein WOUND-RESPONSIVE 3)	NRT3.1 NAR2.1 NAR2.2 WR3 At5g50200 K6A12.6	Arabidopsis thaliana (Mouse-ear cress)		Cell membrane; Complete proteome; Membrane; Nitrate assimilation; Reference proteome; Signal; Transmembrane; Transmembrane helix
SRR342022_TR26124_c1_g2_i3_len=2520	GUN6_ARATH	Q:2340-1243;H:24-389	78,14%|	E:0	Endoglucanase 6	PF00759.16*Glyco_hydro_9*Glycosyl hydrolase family 9*23-384*E:2.8e-109	0,223	0,305	0,041	-0,554	0,009	-0,715	0	-1,499	0,034	3,638	GUN6_ARATH	Endoglucanase 6 (EC 3.2.1.4) (Endo-1,4-beta-glucanase 6)	At1g64390 F15H21.9	Arabidopsis thaliana (Mouse-ear cress)		Carbohydrate metabolism; Cell wall biogenesis/degradation; Cellulose degradation; Complete proteome; Glycoprotein; Glycosidase; Hydrolase; Polysaccharide degradation; Reference proteome; Secreted; Signal
SRR342022_TR2576_c2_g1_i3_len=3812	NA	NA	NA	NA	NA	PF14364.3*DUF4408*Domain of unknown function (DUF4408)*82-111*E:9.6e-11 PF05553.8*DUF761*Cotton fibre expressed protein*419-454*E:4.2e-15	0,823	0,172	0,094	-1,136	0,002	-1,529	0,001	-1,78	0,372	-0,394						
SRR342022_TR28746_c0_g3_i3_len=926	CTL2_ARATH	Q:91-897,H:50-319	80,74%|	E:3e-165	Chitinase-like protein 2	PF00182.16*Glyco_hydro_19*Chitinase class I*2-184*E:4.3e-53	0,065	0,493	0,035	0,586	1	0,005	0,001	-0,915	0,948	0,023	CTL2_ARATH	Chitinase-like protein 2 (AtCTL2)	CTL2 At3g16920 K14A17.4	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Disulfide bond; Glycoprotein; Reference proteome; Secreted; Signal
SRR342022_TR28971_c0_g1_i1_len=2771	NA	NA	NA	NA	NA	PF14576.3*SEO_N*Sieve element occlusion N-terminus*123-409*E:1.1e-113 PF14577.3*SEO_C*Sieve element occlusion C-terminus*575-805*E:3.2e-106	0,873	-0,096	0,007	-1,22	0,01	-1,439	0,001	-2,116	0,533	0,232						
SRR342022_TR30524_c3_g6_i6_len=1343	C72A1_CATRO	Q:3-1019,H:186-524	98,23%|	E:0	Secologanin synthase	PF00067.19*p450*Cytochrome P450*3-312*E:2.3e-72	0,081	0,501	0,002	1,01	0,043	-0,735	0	-1,492	0,337	0,294	C72A1_CATRO	Secologanin synthase (SLS) (EC 1.3.3.9) (CYPLXIII) (Cytochrome P450 72A1)	CYP72A1 CYP72 P450CR3	Catharanthus roseus (Madagascar periwinkle) (Vinca rosea)	PATHWAY: Alkaloid biosynthesis; secologanin biosynthesis.	Alkaloid metabolism; Heme; Iron; Membrane; Metal-binding; Monooxygenase; NADP; Oxidoreductase; Transmembrane; Transmembrane helix; Vacuole
SRR342023_TR3118_c2_g10_i2_len=2508	GNOM_ARATH	Q:1421-1633;H:176-246	49,3%|	E:4e-23	ARF guanine-nucleotide exchange factor GNOM		1	0,183	0,692	-0,879	0,001	-2,453	0	-2,963	0,132	1,289	GNOM_ARATH	ARF guanine-nucleotide exchange factor GNOM (Pattern formation protein EMB30) (Protein EMBRYO DEFECTIVE 30) (Protein MIZU-KUSSEIZI) (Protein VASCULAR NETWORK 7)	GN EMB30 GBF3 MIZ2 VAN7 At1g13980 F16A14.20 F7A19.7	Arabidopsis thaliana (Mouse-ear cress)		Cell adhesion; Cell membrane; Complete proteome; Cytoplasm; ER-Golgi transport; Endocytosis; Endosome; Guanine-nucleotide releasing factor; Membrane; Polymorphism; Protein transport; Reference proteome; Transport
SRR342023_TR4852_c2_g10_i3_len=1933	GATL3_ARATH	Q:222-1181,H:28-345	92,98%|	E:7e-161	Probable galacturonosyltransferase-like 3	PF01501.17*Glyco_transf_8*Glycosyl transferase family 8*66-322*E:8.2e-51	0,876	-0,084	0,001	-1,41	0,002	-1,284	0	-1,487	0,001	-1,093	GATL3_ARATH	Probable galacturonosyltransferase-like 3 (EC 2.4.1.-)	GATL3 At1g13250 T6J4.1 T6J4.2	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Glycan metabolism; pectin biosynthesis.	Cell wall biogenesis/degradation; Complete proteome; Glycoprotein; Glycosyltransferase; Golgi apparatus; Membrane; Reference proteome; Signal-anchor; Transferase; Transmembrane; Transmembrane helix
SRR342023_TR7827_c3_g7_i1_len=523	NA	NA	NA	NA	NA		1	0,313	1	-0,59	0,014	-0,953	0,001	-1,319	0,461	-1,105						
SRR342023_TR9043_c0_g1_i3_len=898	Y2309_ARATH	Q:333-563,H:1-78	80,77%|	E:3e-36	Uncharacterized protein At2g23090		1	-0,032	0,694	-0,385	0,002	-1,418	0	-1,783	1	0,501	Y2309_ARATH	Uncharacterized protein At2g23090	At2g23090 F21P24.15	Arabidopsis thaliana (Mouse-ear cress)		3D-structure; Complete proteome; Reference proteome
SRR342023_TR11065_c2_g5_i2_len=2038	SC35_ARATH	Q:3-206,H:41-108	88,24%|	E:2e-31	Serine/arginine-rich splicing factor SC35	PF00076.19*RNA_1*RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)*1-47*E:1.2e-12	1	-0,157	1	0,028	0,004	-1,665	0	-2,39	1	-0,746	SC35_ARATH	Serine/arginine-rich splicing factor SC35 (At-SC35) (AtSC35) (SC35-like splicing factor)	SC35 At5g64200 M5J1.4	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Nucleus; Phosphoprotein; RNA-binding; Reference proteome; Spliceosome; mRNA processing; mRNA splicing
SRR342023_TR11459_c2_g1_i1_len=2199	NA	NA	NA	NA	NA	PF14365.3*DUF4409*Domain of unknown function (DUF4409)*56-174*E:6e-44	1	-0,019	0,335	-0,66	0,002	-1,422	0	-2,183	0,35	0,368						
SRR342023_TR11270_c0_g1_i1_len=1202	NA	NA	NA	NA	NA		0,667	0,163	0,139	-0,595	1	0,023	0	-1,283	0,003	1,164						
SRR342023_TR16728_c0_g2_i1_len=1861	NA	NA	NA	NA	NA	PF05757.8*PsbQ*Oxygen evolving enhancer protein 3 (PsbQ)*73-140*E:8e-14	0,892	0,175	0,077	-0,971	0,003	-1,452	0,001	-1,875	0,188	0,68						
SRR342023_TR17003_c0_g1_i1_len=1169	NA	NA	NA	NA	NA	PF04570.11*zfLZ*zinc-finger of the FCS-type, C2-C2*176-222*E:7.3e-22	0,329	0,395	0,006	0,941	0,07	-0,641	0	-1,421	0,033	0,692						
SRR342023_TR25614_c1_g6_i1_len=732	METK1_CATRO	Q:589-2,H:1-196	99,49%|	E:2e-141	S-adenosylmethionine synthase 1	PF00438.17*S-AdoMet_synt_N*S-adenosylmethionine synthetase, N-terminal domain*4-101*E:1.9e-43 PF02772.13*S-AdoMet_synt_M*S-adenosylmethionine synthetase, central domain*117-196*E:1e-32	0,103	1,59	0,502	3,834	0,001	-3,746	0	-6,815	0	1,31	METK1_CATRO	S-adenosylmethionine synthase 1 (AdoMet synthase 1) (EC 2.5.1.6) (Methionine adenosyltransferase 1) (MAT 1)	SAMS1	Catharanthus roseus (Madagascar periwinkle) (Vinca rosea)	PATHWAY: Amino-acid biosynthesis; S-adenosyl-L-methione biosynthesis; S-adenosyl-L-methionine from L-methionine: step 1/1.	ATP-binding; Cobalt; Cytoplasm; Magnesium; Manganese; Metal-binding; Nucleotide-binding; One-carbon metabolism; Potassium; Transferase
SRR342023_TR27467_c3_g4_i3_len=6071	POLX_TOBAC	Q:6071-2694;H:221-1323	43,99%|	E:0	Retrovirus-related Pol polyprotein from transposon TNT 1-94	PF13976.3*gag_pre-integrase*GAG-pre-integrase domain*183-250*E:2.8e-14 PF00665.23*rve*Integrase core domain*266-380*E:6e-26 PF07727.11*RVT_2*Reverse transcriptase (RNA-dependent DNA polymerase)*640-887*E:4.5e-93	0,215	0,367	0	8,263	0,003	-0,974	0,001	-1,086	1	1,661	POLX_TOBAC	Retrovirus-related Pol polyprotein from transposon TNT 1-94 [Includes: Protease (EC 3.4.23.-); Reverse transcriptase (EC 2.7.7.49); Endonuclease]	Nicotiana tabacum (Common tobacco)			Aspartyl protease; Endonuclease; Hydrolase; Metal-binding; Nuclease; Nucleotidyltransferase; Protease; RNA-directed DNA polymerase; Transferase; Transposable element; Zinc; Zinc-finger
SRR346572_TR11888_c0_g1_i1_len=742	NA	NA	NA	NA	NA	PF07107.8*M412*Wound-induced protein M412*44-142*E:2.9e-32	0,781	0,354	0,502	-2,12	0,005	-0,953	0	-2,599	1	0						
SRR346572_TR14902_c0_g1_i1_len=1338	YAB1_ARATH	Q:957-316,H:17-229	58,93%|	E:5e-71	Axial regulator YABBY 1	PF04690.10*YABBY*YABBY protein*27-191*E:1.8e-69	0,696	0,146	0,528	-0,342	0,003	-0,907	0	-1,502	1	0,033	YAB1_ARATH	Axial regulator YABBY 1 (FI-54) (Protein ABNORMAL FLORAL ORGANS) (Protein FILAMENTOUS FLOWER) (Protein antherless)	YAB1 AFO AT FIL At2g45190 F4L23.30	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; DNA-binding; Developmental protein; Metal-binding; Nucleus; Reference proteome; Zinc; Zinc-finger
SRR346572_TR21604_c0_g1_i1_len=1763	NA	NA	NA	NA	NA		0,076	-2,16	0,16	-1,373	0,001	-3,234	0	-4,699	0,228	-1,274						
SRR346572_TR27988_c0_g1_i5_len=2261	EID1_ARATH	Q:1055-2026,H:1-336	61,81%|	E:2e-137	Phytochrome A-associated F-box protein	PF00646.30*F-box*F-box domain*12-56*E:0.0003	1	0,275	1	0,751	0,003	-1,498	0	-1,899	0,692	1,004	EID1_ARATH	Phytochrome A-associated F-box protein (Empfindlicher im dunkelroten Licht protein 1)	EID1 At4g02440 T14P8.22	Arabidopsis thaliana (Mouse-ear cress)	PATHWAY: Protein modification; protein ubiquitination.	Complete proteome; Nucleus; Phytochrome signaling pathway; Reference proteome; Ubl conjugation pathway
SRR346596_TR34139_c0_g1_i1_len=1578	ADHX_ORYSI	Q:104-1219,H:3-377	44,83%|	E:2e-93	Alcohol dehydrogenase class-3	PF08240.9*ADH_N*Alcohol dehydrogenase GroES-like domain*39-162*E:1.6e-22 PF00107.23*ADH_zinc_N*Zinc-binding dehydrogenase*206-326*E:8.1e-22	0,004	1,062	0,52	0,428	1	0,031	0	-1,995	0,083	-0,766	ADHX_ORYSI	Alcohol dehydrogenase class-3 (EC 1.1.1.1) (Alcohol dehydrogenase class-III) (Glutathione-dependent formaldehyde dehydrogenase) (FALDH) (FDH) (GSH-FDH) (EC 1.1.1.-) (S-(hydroxymethyl)glutathione dehydrogenase) (EC 1.1.1.284)	ADHIII Osi_009236	Oryza sativa subsp. indica (Rice)		Complete proteome; Cytoplasm; Metal-binding; NAD; Oxidoreductase; Reference proteome; Zinc
SRR346604_TR21311_c0_g1_i5_len=3248	CTPA2_ARATH	Q:1341-1790;H:272-421	72,67%|	E:4e-62	Carboxyl-terminal-processing peptidase 2, chloroplastic		1	-0,625	1	-0,61	0,007	-1,36	0,001	-1,808	1	0,094	CTPA2_ARATH	Carboxyl-terminal-processing peptidase 2, chloroplastic (EC 3.4.21.102) (D1 C-terminal processing protease 2) (Photosystem II D1 protein processing peptidase 2)	CTPA2 At4g17740 dl4905c FCAALL.169	Arabidopsis thaliana (Mouse-ear cress)		Alternative splicing; Chloroplast; Complete proteome; Chloroplastic (EC 3.4.21.102) (D1 C-terminal processing protease 2) (Photosystem II D1 protein processing peptidase 2); Hydrolase; Plastid; Protease; Reference proteome; Serine protease; Thylakoid; Transit peptide
SRR346604_TR21350_c0_g4_i1_len=1610	NA	NA	NA	NA	NA		1	-0,149	1	0,44	0,002	-0,723	0	-1,665	1	0,665						
SRR346604_TR28960_c0_g2_i1_len=840	NA	NA	NA	NA	NA		0,007	-0,894	0,038	-0,978	0,005	-1,118	0,001	-1,346	1	1,234						
SRR348705_TR23678_c0_g1_i1_len=2285	ERG1_PANGI	Q:495-1847,H:89-539	81,82%|	E:0	Squalene monooxygenase	PF01494.16*FAD_binding_3*FAD binding domain*61-373*E:3.6e-18 PF08491.7*SE*Squalene epoxidase*213-485*E:4.3e-120	0,153	-0,73	0,014	-2,758	0,001	-1,467	0	-1,62	1	0,049	ERG1_PANGI	Squalene monooxygenase (EC 1.14.13.132) (Squalene epoxidase) (SE)		Panax ginseng (Korean ginseng)	PATHWAY: Terpene metabolism; lanosterol biosynthesis; lanosterol from farnesyl diphosphate: step 2/3.	FAD; Flavoprotein; Membrane; NADP; Oxidoreductase; Transmembrane; Transmembrane helix
SRR348705_TR35052_c0_g1_i1_len=1056	PR1_MEDTR	Q:665-255,H:40-173	57,25%|	E:5e-48	Pathogenesis-related protein PR-1	PF00188.23*CAP*Cysteine-rich secretory protein family*65-185*E:8.4e-24	0,239	1,254	1	-0,8	0,01	-1,157	0	-4,108	0,001	1,713	PR1_MEDTR	Pathogenesis-related protein PR-1	PR-1	Medicago truncatula (Barrel medic) (Medicago tribuloides)		Disulfide bond; Pathogenesis-related protein; Plant defense; Signal
SRR348705_TR40514_c0_g1_i4_len=2436	AB22G_ARATH	Q:76-1920,H:53-679	75,47%|	E:0	ABC transporter G family member 22	PF00005.24*ABC_tran*ABC transporter*156-307*E:1.5e-29 PF01061.21*ABC2_membrane*ABC-2 type transporter*476-648*E:1.9e-27	1	-0,518	0,254	-2,303	0,002	-1,371	0	-1,783	0,258	0,486	AB22G_ARATH	ABC transporter G family member 22 (ABC transporter ABCG.22) (AtABCG22) (White-brown complex homolog protein 23) (AtWBC23)	ABCG22 WBC23 At5g06530 F15M7.6	Arabidopsis thaliana (Mouse-ear cress)		ATP-binding; Alternative splicing; Complete proteome; Membrane; Nucleotide-binding; Reference proteome; Transmembrane; Transmembrane helix; Transport
SRR348705_TR41515_c3_g1_i2_len=682	RS8_ORYSJ	Q:2-57,H:5-195	92,67%|	E:6e-93	40S ribosomal protein S8	PF01201.19*Ribosomal_S8e*Ribosomal protein S8e*1-190*E:2.3e-53	0,44	-1,033	0,739	0,285	0,155	-1,049	0	-6,953	0,692	-0,749	RS8_ORYSJ	40S ribosomal protein S8	RPS8 Os02g0489400 LOC_Os02g28810 OSJNBa0048K16.2 P0483C08.42	Oryza sativa subsp. japonica (Rice)		Complete proteome; Reference proteome; Ribonucleoprotein; Ribosomal protein
SRR348707_TR35148_c0_g1_i3_len=2592	ATP4_IPOBA	Q:470-1865,H:1-200	76,73%|	E:2e-93	ATP synthase subunit delta', mitochondrial	PF02823.13*ATP-synt_DE_N*ATP synthase, Delta/Epsilon chain, beta-sandwich domain*72-143*E:1.9e-17	0,015	-1,206	0,002	-1,724	0,016	-1,559	0	-2,616	0,176	0,443	ATP4_IPOBA	ATP synthase subunit delta', mitochondrial (F-ATPase delta' subunit)		Ipomoea batatas (Sweet potato) (Convolvulus batatas)		ATP synthesis; CF(1); Direct protein sequencing; Hydrogen ion transport; Ion transport; Membrane; Mitochondrion; Mitochondrion inner membrane; Transit peptide; Transport
SRR924147_TR21330_c0_g1_i1_len=866	NA	NA	NA	NA	NA		0,294	-0,581	0,095	-0,859	0,003	-1,076	0	-1,518	0,516	-0,246						
SRR924147_TR34783_c0_g1_i5_len=1155	RL74_ARATH	Q:1045-308,H:1-244	82,52%|	E:7e-136	60S ribosomal protein L7-4	PF00679.9*Ribosomal_L30_N*Ribosomal L30 N-terminal domain*12-83*E:1.1e-25 PF03027.17*Ribosomal_L30*Ribosomal protein L30p/L7e*88-138*E:5e-22	0,402	-1,034	1	0,121	0,002	-2,719	0	-7,175	0,381	-1,876	RL74_ARATH	60S ribosomal protein L7-4	RPL7D At3g13580 K20M4.2	Arabidopsis thaliana (Mouse-ear cress)		Complete proteome; Reference proteome; Ribonucleoprotein; Ribosomal protein
SRR924148_TR11409_c0_g1_i1_len=561	NLTP_VIGUN	Q:146-385,H:20-99	52,5%|	E:1e-22	Probable non-specific lipid-transfer protein AKCS9	PF14368.3*LTP_2*Probable lipid transfer*48-126*E:3.3e-07	0,183	-0,278	0,021	-0,526	1	-0,001	0,001	-0,774	0,003	0,613	NLTP_VIGUN	Probable non-specific lipid-transfer protein AKCS9 (LTP)	Vigna unguiculata (Cowpea)			Disulfide bond; Lipid-binding; Signal; Transport
SRR924148_TR15159_c0_g1_i1_len=1721	PGLR_VITVI	Q:207-1553,H:41-489	81,51%|	E:0	Probable polygalacturonase	PF00295.14*Glyco_hydro_28*Glycosyl hydrolases family 28*187-467*E:2.2e-38	0,204	-0,563	0,003	-2,608	0,002	-1,169	0	-2,387	0,056	0,517	PGLR_VITVI	Probable polygalacturonase (PG) (EC 3.2.1.15) (Pectinase)	GSVIVT00026920001 LOC100243180	Vitis vinifera (Grape)		Direct protein sequencing; Glycoprotein; Glycosidase; Hydrolase; Membrane; Repeat; Transmembrane; Transmembrane helix
SRR924148_TR20412_c0_g1_i1_len=2557	AFC2_ARATH	Q:2417-1575,H:1-206	61,57%|	E:7e-102	Serine/threonine-protein kinase AFC2	PF00069.22*Pkinase*Protein kinase domain*106-161*E:2.1e-07	0	2,767	0	2,754	0,016	-1,313	0	-2,853	1	0	AFC2_ARATH	Serine/threonine-protein kinase AFC2 (EC 2.7.12.1)	AFC2 At4g24740 F22K18.60	Arabidopsis thaliana (Mouse-ear cress)		ATP-binding; Alternative splicing; Complete proteome; Kinase; Nucleotide-binding; Reference proteome; Serine/threonine-protein kinase; Transferase
SRR924148_TR41117_c0_g1_i1_len=641	NA	NA	NA	NA	NA		0,848	0,195	1	0,014	0,129	-0,878	0	-2,517	0,502	0,321						

Supplemental Table S3

Most represented Uniprot keywords in transcripts modulated upon challenge with M. sexta. Enrichment tests were performed by comparison with a hypergeometric distribution.

upregulated

downregulated

upregulated

	Counts	-log10 pvalue	Keyword
Core	63	7,31	Oxidoreductase
	28	8,17	Lyase
	25	3,76	Lipid metabolism
	24	4,47	NADP
	22	4,52	Stress response
	16	3,12	Heme
	15	3,11	Lipid biosynthesis
	14	3,78	Amino-acid biosynthesis
	14	5,12	Fatty acid metabolism
	13	3,59	Monooxygenase
	13	4,38	Pyridoxal phosphate
	10	4,56	Fatty acid biosynthesis
	8	5,38	Aromatic amino acid biosynthesis
	7	7,02	Alkaloid metabolism
	7	6,60	Oxylipin biosynthesis
	6	3,48	Aminotransferase
	6	3,07	Decarboxylase
	6	6,64	Tryptophan biosynthesis
	3	4,29	Annexin
	3	3,96	Calcium/phospholipid-binding
MsIntact24h	14	6,15	Plant defense
	9	3,70	Lipid biosynthesis
	7	4,51	Fatty acid metabolism
	6	4,96	Fatty acid biosynthesis
	5	3,60	Dioxygenase
	3	4,92	Glyoxysome
	3	3,13	Hypersensitive response
MsDamaged24h	28	3,85	Signal
	20	4,04	Disulfide bond
	11	3,11	Protease
	11	10,63

	3	3,02	Elongation factor
MsIntact24h	4	3,02	Monooxygenase
	4	6,73	Photorespiration
	3	4,70	One-carbon metabolism
MsDamaged24h	55	16,56	Plastid
	35	13,70	Transit peptide
	34	15,73	Chloroplast
	10	7,00	Thylakoid
	9	9,73	Photosynthesis
	5	7,13	Photosystem I
	3	4,38	Chlorophyll biosynthesis
	3	4,56	Isoprene biosynthesis
Ms6h	27	15,27	Ribonucleoprotein
	23	15,48	Ribosomal protein
	6	4,02	DNA replication
	6	4,02	rRNA-binding
	4	5,35	Nucleosome core
Ms8h	109	23,84	Plastid
	107	23,01	Chloroplast
	107	15,79	Transit peptide
	35	4,03	Disulfide bond
	31	12,07	Thylakoid
	25	4,60	Ribonucleoprotein
	21	5,53	Ribosomal protein
	12	5,15	Photosynthesis
	10	4,05	rRNA-binding
	8	4,86	Photosystem II
	7	3,85	Chromophore
	7	4,83	Photosystem I
	5	3,33	Chlorophyll
Ms1wk	14	3,56	Ribonucleoprotein
	5	3,39	Glycolysis
	4	3,27	Proteasome
	3	3,16	Aspartyl protease
	3	3,84	Threonine protease
MsDamaged24h;MsIntact24h	42	14,07	Chloroplast
	42	13,93	Plastid
	42	10,83	Transit peptide
	21	4,32	Oxidoreductase
	13	7,51	Thylakoid
	12	3,07	Iron
	12	11,41	Photosynthesis
	9	3,94	Lyase
	7	3,47	Electron transport
	6	6,54	Photosystem II
	5	6,26	Chlorophyll
	5	5,16	Chromophore
	5	5,93	Photosystem I
	3	4,13	Calvin cycle
	3	5,71	Carbon dioxide fixation
	3	4,79	Schiff base

Supplemental Table S4

Most represented PFAM domains Uniprot keywords in transcripts modulated upon challenge with M. sexta. Enrichment tests were performed by comparison with a hypergeometric distribution.

upregulated
downregulated

upregulated

	Counts	-log10pvalue	PFAM domain
Core	145		No domain
	32	7,38	PF00067.19 p450 Cytochrome P450
	19	3,58	PF12697.4 Abhydrolase_6 Alpha/beta hydrolase family
	18	2,13	PF00561.17 Abhydrolase_1 alpha/beta hydrolase fold
	18	1,37	PF01535.17 PPR PPR repeat
	17	0,60	PF00407.16 Bet_v_1 Pathogenesis-related protein Bet v I family
	15	0,82	PF01554.15 MatE MatE
	15	0,45	PF03171.17 2OG-Fe(II) Oxy 2OG-Fe(II) oxygenase superfamily
	15	-0,13	PF12146.5 Hydrolase_4 Serine aminopeptidase
	14	-0,35	PF00191.17 Annexin Annexin
MsIntact24h	45	2,59	No domain
	14	0,72	PF01535.17 PPR PPR repeat
	10	0,20	PF00069.22 Pkinase Protein kinase domain
	9	0,00	PF07714.14 Pkinase_Tyr Protein tyrosine kinase
	7	0,17	PF00400.29 WD40 WD domain
	5	-0,21	PF00168.27 C2 C2 domain
	5	-0,19	PF13041.3 PPR_2 PPR repeat family
MsDamaged24h	61	2,04	No domain
	7	3,60	PF00230.17 MIP Major intrinsic protein
	6	1,36	PF00407.16 Bet_v_1 Pathogenesis-related protein Bet v I family
	5	1,11	PF00005.24 ABC_tran ABC transporter
	5	0,83	PF00026.20 Asp Eukaryotic aspartyl protease
	5	0,42	PF00067.19 p450 Cytochrome P450
	5	0,38	PF00112.20 Peptidase_C1 Papain family cysteine protease
	5	0,23	PF00234.19 Tryp_alpha_amyl Protease inhibitor/seed storage/LTP family
	5	-0,08	PF00892.17 EamA EamA-like transporter family
	5	-0,26	PF04969.13 CS CS domain
Ms6h	35	-0,45	No domain
Ms8h	105	#N/D	No domain
	24	7,81	PF08240.9 ADH_N Alcohol dehydrogenase GroES-like domain
	23	1,57	PF00240.20 ubiquitin Ubiquitin family
	22	0,78	PF11976.5 Rad60-SLD Ubiquitin-2 like Rad60 SUMO-like
	21	0,48	PF00107.23 ADH_zinc_N Zinc-binding dehydrogenase
	19	0,10	PF00067.19 p450 Cytochrome P450
	19	0,07	PF14560.3 Ubiquitin_2 Ubiquitin-like domain
	17	0,01	PF13202.3 EF-hand_5 EF hand
	16	-0,35	PF00036.29 EF-hand_1 EF hand
	14	-0,46	PF13881.3 Rad60-SLD_2 Ubiquitin-2 like Rad60 SUMO-like
Ms1wk	67	4,50	No domain
	15	2,20	PF01535.17 PPR PPR repeat
	7	1,77	PF00098.20 zf-CCHC Zinc knuckle
	7	1,10	PF07727.11 RVT_2 Reverse transcriptase (RNA-dependent DNA polymerase)
	6	1,01	PF13976.3 gag_pre-integrs GAG-pre-integrase domain
	5	0,73	PF00009.24 GTP_EFTU Elongation factor Tu GTP binding domain
	5	0,70	PF00067.19 p450 Cytochrome P450
	5	0,48	PF00076.19 RRM_1 RNA recognition motif. (a.k.a. RRM
	5	0,09	PF00091.22 Tubulin Tubulin/FtsZ family
	5	-0,13	PF00578.18 AhpC-TSA AhpC/TSA family
MsDamaged24h;MsIntact24h	79	2,34	No domain
	7	5,49	PF00407.16 Bet_v_1 Pathogenesis-related protein Bet v I family
	6	2,14	PF00067.19 p450 Cytochrome P450
	5	1,71	PF00011.18 HSP20 Hsp20/alpha crystallin family
	5	1,30	PF00854.18 PTR2 POT family
	5	0,74	PF01554.15 MatE MatE
	5	0,71	PF13855.3 LRR_8 Leucine rich repeat

downregulated

	Counts	-log10pvalue	PFAM domain
Core	96	1,71	No domain
	24	1,04	PF00504.18 Chloroa_b-bind Chlorophyll A-B binding protein
	19	0,07	PF00125.21 Histone Core histone H2A/H2B/H3/H4
	13	0,31	PF01535.17 PPR PPR repeat
	10	0,46	PF13041.3 PPR_2 PPR repeat family
	9	0,20	PF12854.4 PPR_1 PPR repeat
	9	0,17	PF13812.3 PPR_3 Pentatricopeptide repeat domain
	6	0,44	PF00560.30 LRR_1 Leucine Rich Repeat
	6	0,04	PF02969.14 TAF TATA box binding protein associated factor (TAF)
	6	-0,19	PF15511.3 CENP-T_C Centromere kinetochore component CENP-T histone fold
MsIntact24h	24	1,47	No domain
	5	1,09	PF00067.19 p450 Cytochrome P450
MsDamaged24h	22	1,58	No domain
	7	0,53	PF01535.17 PPR PPR repeat
	6	0,02	PF00153.24 Mito_carr Mitochondrial carrier protein
	5	0,00	PF13540.3 RCC1_2 Regulator of chromosome condensation (RCC1) repeat
Ms6h	34	6,79	No domain
	8	2,41	PF00076.19 RRM_1 RNA recognition motif. (a.k.a. RRM
	7	0,85	PF00400.29 WD40 WD domain
	7	0,43	PF01248.23 Ribosomal_L7Ae Ribosomal protein L7Ae/L30e/S12e/Gad45 family
	6	0,41	PF00125.21 Histone Core histone H2A/H2B/H3/H4
	5	0,27	PF00428.16 Ribosomal_60s 60s Acidic ribosomal protein
Ms8h	204	0,01	No domain
	35	2,22	PF01535.17 PPR PPR repeat
	24	0,71	PF13041.3 PPR_2 PPR repeat family
	22	0,32	PF00560.30 LRR_1 Leucine Rich Repeat
	20	0,20	PF13812.3 PPR_3 Pentatricopeptide repeat domain
	17	0,01	PF13855.3 LRR_8 Leucine rich repeat
	13	0,39	PF12854.4 PPR_1 PPR repeat
	12	0,26	PF07714.14 Pkinase_Tyr Protein tyrosine kinase
	10	0,00	PF00069.22 Pkinase Protein kinase domain
	10	-0,28	PF13516.3 LRR_6 Leucine Rich repeat

Ms1wk	92	0,53	No domain
	5	6,27	PF00025.18 Arf ADP-ribosylation factor family
	5	2,34	PF00071.19 Ras Ras family
	5	1,56	PF00400.29 WD40 WD domain
	5	1,18	PF00505.16 HMG_box HMG (high mobility group) box
	5	0,66	PF02469.19 Fasciclin Fasciclin domain
	5	0,63	PF08477.10 Roc Ras of Complex
	5	0,43	PF09011.7 HMG_box_2 HMG-box domain
	5	0,05	PF13417.3 GST_N_3 Glutathione S-transferase
MsDamaged24h:MsIntact24h	44	1,81	No domain
	10	1,21	PF00400.29 WD40 WD domain
	5	0,98	PF00067.19 p450 Cytochrome P450
	5	0,60	PF00201.15 UDPGT UDP-glucoronosyl and UDP-glucosyl transferase
	5	0,41	PF00504.18 Chloroa_b-bind Chlorophyll A-B binding protein

Supplemental Table S5

Primers used in this study.

qPCR Target	Primer Name	Sequence (5'-3')
SLS1	150116-SLS1-F	GGTCCATGTCAGTAAAACTCCAGTA
	150116-SLS1-R	AACAAGGATCCCATGAAGTTGA
STR	qSTR-for	CATAGCTCTGTGGGTATATTAGTGT
	qSTR-rev	ACCTTCAAAAAGCCATAGAATTTGCA
SGD	qSGD-for	CTTCGACAACTTCGAATGGAA
	qSGD-rev	CTTCTTGACTAACTCAACTAGT
40S ribosomal	Rps9-up	TTACAAGTCCCTTCGGTGGT
protein 9	Rps9-down	TGCTTATTCTTCATCCTCTTCATC
16OMT	qDL-16OMT-F	GTGGATTCTCCATGACTGGAACGA
	qDL-16OMT-R	GATTATCACCTTTCGACCCTTCGC
16T3O	CYP6_141119_a_F	ACCCTCCTGCTCCATTGTTG
	CYP6_141119_a_R	GCCCAGACATTGATGAACGC
ORCA3	qORCA3bis-for	TGTCAGGAGGATTCTGTTGTGGGA
	qORCA3bis-rev	CGCATATTAAACGCGGCTGCATCA
HDS	qHDS-up	GTCCCTTACTGAACCTCCAGAG
	qHDS-down	AATCACCTGTCCTGCGTTGG
G10H	qG10H-up	ATCAGTTCCAAACGCCTCC
	qG10H-down	TTCTCCATCGTGAGGTACC