

Supplemental table 1: list of the proteins identified from the total protein fraction of *Amborella trichopoda* isolated embryo by shotgun

Proteins have been analyzed by mono-dimensional electrophoresis and identified by mass spectrometry LC/MS-MS. The protein spots were analysed by LC-MS/MS on the PAPPISO platform (Benoit Valot, Thierry Balliau, Michel Zivy, INRA Moulon, France; <http://pappiso.inra.fr>). Based on the spectrum generated, proteins were identified using the X-Tandem software. "NCBI accession number" is the accession number in NCBI database. "Protein name", "Organism" relates to the organism from which the identified protein comes from for functional analysis - efforts were focus on *Arabidopsis thaliana* as a plant model. "AGI", "Function category" and "Function description" relate to the functional categories defined according to the ontological classification of Bevan *et al.* [Bevan *et al.* (1998) Nature 391:485-488]. "log(Evalue) identification" reflects the statistical power of the identification by BLAST (performed on TAIR or BLAST). "Identity" indicates in % the recovery of the *Amborella* protein sequence against the identified protein. "Compartment" indicates if the identification is found in the embryo (emb.), the endosperm (end.) or both (emb./end.). "Description" was taken from the Amborella EVM 27 Predicted Proteins (<http://www.amborella.org>). The "log (E value)" is a statistical parameter that represents the number of peptides present at random in the database. It was calculated by the product of the Evalue of unique peptides identified in the protein spot (Valot *et al.*, 2011). "Coverage" refers to the recovery rate of the protein by the identified peptides, expressed in %. "MW" relates to the molecular weight expressed in kDa. "Spectra" corresponds to the number of spectra which allowed the protein identification from 2DE protein single spot. "Specifics" corresponds to the number of specific spectrum corresponding to the identification among the other identifications of the group. "Uniques" refers to the number of unique peptides (different sequences) that led to the protein identification. "PAI" is the protein abundance index in the spot. "Peptide sequences" displays identified peptides for each protein spot. "Relative abundance" relates to the number of spectra identifying the description among all the spectra.

Functional analysis									Mass spec data									
NCBI accession number	protein name	Organism	AGI	Function category	Function description	log (E-value) identification	Identity	Compartment	Description	log (Evalue)	Coverage	MW	Spectra	Specifics	Uniques	PAI	Peptide sequences	Relative abundance
A1L4Y4	NADPH:quinone reductase	<i>Arabidopsis thaliana</i>	AT5G61510	11 Disease/defence	11.06 Detoxification	e-136	82	emb.	evm_27.model.AmTr_v1.0_scaffold00111.28	-26,24484	27	40,1	11	-	7	0,785714	GMTAQVLVQK TYPLSQAAQA HTDLESR	0,003138
B9DG66	p3 (stress inducible protein)	<i>Arabidopsis thaliana</i>	AT4G12400	06 Protein destination and storage	06.01 Folding and stability	0	79	emb.	evm_27.model.AmTr_v1.0_scaffold00011.153	-21,0117	11	65	4	3	4	0,210526	TATPEEMER GELSPEELKE R	0,001141
B9DHQ0	Tubulin	<i>Arabidopsis thaliana</i>	AT5G19780	09 Cell structure	09.04 Cytoskeleton	0,00E+00	92	emb.	evm_27.model.AmTr_v1.0_scaffold00068.45	-17,26013	9	49,5	3	-	3	0,166667	AVCMISNNTAV AEVFSR IHEFMLSSYAPV	0,000856
C0Z2J1	Adenine nucleotide alpha hydrolases-like protein (similar to)	<i>Arabidopsis thaliana</i>	AT1G11360	11 Disease/defence	11.05 Stress responses	3,00E-59	63	emb.	evm_27.model.AmTr_v1.0_scaffold00072.7	-10,81531	4	26,3	2	-	2	0,068966	LGLSAVIMGSR ATDLAQPLVEA QIPFK	0,000571
F4HQD4	HSP70	<i>Arabidopsis thaliana</i>	AT1G79920	06 Protein destination and storage	06.01 Folding and stability	0,00E+00	85	emb.	evm_27.model.AmTr_v1.0_scaffold00078.198	-67,40158	28	94,4	5	-	5	0,357143	AVLDAATIAGL HPLR QGDPJEER	0,001427
F4HWF8	Nucleic acid/nucleotide binding protein	<i>Arabidopsis thaliana</i>	AT1G21320	04 Transcription	04.22 mRNA processing	6,00E-41	57	emb.	evm_27.model.AmTr_v1.0_scaffold00041.81	-3,76904	14	27	7	-	7	0,291667	LDEHHRDPSN LR VIRDTESLGAS	0,001997
F4HWR0	Dessication-related protein	<i>Arabidopsis thaliana</i>	AT1G47980	11 Disease/defence	11.05 Stress responses	e-109	82	emb./end.	evm_27.model.AmTr_v1.0_scaffold00016.315	-98,60413	9	33,4	2	-	2	0,222222	IVYSSGNEK GGPPPIGATK TILYEQANK	0,000571
F4ID64	Peroxioredoxin	<i>Arabidopsis thaliana</i>	AT1G65980	11 Disease/defence	11.06 Detoxification	7,00E-31	72	emb.	evm_27.model.AmTr_v1.0_scaffold00109.90	-3,133713	5	15,7	2	-	2	0,090909	VVFGVPGAF TPTCSSK VGDSPDGFES	0,000571
F4IHK9	Glycine-rich RNA-binding protein	<i>Arabidopsis thaliana</i>	AT2G21660	04 Transcription	04.22 mRNA processing	3,00E-36	94	emb.	evm_27.model.AmTr_v1.0_scaffold00030.127	-16,67531	59	15,7	8	-	6	1,333333	NITVNEAQR DAIEGMNGQT LDGR	0,002282
F4IHK9	Glycine-rich RNA-binding protein	<i>Arabidopsis thaliana</i>	AT2G21660	04 Transcription	04.22 mRNA processing	8,00E-36	89	emb.	evm_27.model.AmTr_v1.0_scaffold00030.135	-17,09232	38	15,9	8	-	5	1,333333	DAIEGMNGFT LDGR ASSDVEYR	0,002282
F4IHL4	Uncharacterized protein	<i>Arabidopsis thaliana</i>	AT2G21720	12 Unclear classification	12 Unclear classification	9,00E-95	64	emb.	evm_27.model.AmTr_v1.0_scaffold00004.93	-6,361511	7	59,1	2	-	2	0,333333	QTNLSIHPCSP SILR LKAWWDSIPV	0,000571
F4IQK5	Cupin-like protein	<i>Arabidopsis thaliana</i>	AT2G18540	06 Protein destination and storage	06.20 Storage proteins	8,00E-82	62	emb./end.	evm_27.model.AmTr_v1.0_scaffold00059.64	-112,3561	3	44,1	3	-	3	0,083333	RKPIVSTEFGR DNRKPIVSTEF GR	0,000856
F4J4J3	Metalloprotease M24 domain-containing protein	<i>Arabidopsis thaliana</i>	AT3G51800	06 Protein destination and storage	06.13 Proteolysis	e-143	86	emb.	evm_27.model.AmTr_v1.0_scaffold00007.130	-9,744727	19	35,3	3	-	3	0,375	NITVNSNPETR FPIMPFTAR	0,000856
F4JI63	Uncharacterized protein	<i>Arabidopsis thaliana</i>	AT4G03200	12 Unclear classification	12 Unclear classification	0	75	emb.	evm_27.model.AmTr_v1.0_scaffold00057.216	-10,9393	7	90,4	2	-	2	0,090909	SYDAEYGGFG SAPK FRRPVEIQLEL	0,000571
F4JVN6	Subtilase family protein	<i>Arabidopsis thaliana</i>	AT4G20850	06 Protein destination and storage	06.13 Proteolysis	0	79	emb./end.	evm_27.model.AmTr_v1.0_scaffold00009.258	-78,98093	6	143,8	2	1	2	0,095238	VLNDLIGEDAD PPK YALLLVTOER	0,000571
F4K108	Transducin/WD40 repeat-like superfamily protein	<i>Arabidopsis thaliana</i>	AT5G12920	12 Unclear classification	12 Unclear classification	0,37	53	emb.	evm_27.model.AmTr_v1.0_scaffold00140.41	-38,6634	7	10,3	2	-	2	0,222222	CGCSGIHLK CGCSGIHLK SSLTWAGPG	0,000571
F4K1P9	Protein SKU5 similar	<i>Arabidopsis thaliana</i>	AT5G48450	09 Cell structure	09.01 Cell wall	0	82	emb.	evm_27.model.AmTr_v1.0_scaffold00163.22	-13,32809	10	66,4	3	-	2	0,75	YGGIPVTDVYV LLNR DQIGSFYFPS	0,000856

F4K4A7	Branched-chain-amino-acid aminotransferase-like protein	<i>Arabidopsis thaliana</i>	AT5G27410	01 Metabolism	01.01 Amino Acid	0	81	emb.	evm_27.model.AmTr_v1.0_scaffold00025.115	-25,4947	73	62.2	127	-	38	7.470588	VLTAESGESIP HTE AEKEVEVHS	0,036234
F4K6N3	Amidase family protein	<i>Arabidopsis thaliana</i>	AT5G07360	01 Metabolism	01.02 Nitrogen and sulphur	0	81	emb.	evm_27.model.AmTr_v1.0_scaffold00016.285	-26,44326	46	67.1	26	-	18	0.896552	CGVTAIRPTFG TVAR GAEEI NVP/PAF	0,007418
F4KH28	O-Glycosyl hydrolase	<i>Arabidopsis thaliana</i>	AT5G24318	01 Metabolism	01.05 Sugars and polysaccharides	e-144	69	emb.	evm_27.model.AmTr_v1.0_scaffold00012.142	-14,13921	37	51.6	21	-	14	0.7	ASEPPSSGQF R SLHTALVNR	0,005991
O03042	Ribulose biphosphate carboxylase (large chain)	<i>Arabidopsis thaliana</i>	ATCG00490	02 Energy	02.30 Photosynthesis	0,00E+00	94	emb.	evm_27.model.AmTr_v1.0_scaffold000334.4	-17,66324	27	52.7	9	-	7	0.692308	TFQGPPIHQ VER GGIDFTKDE	0,002568
O03983	Late embryogenesis abundant protein (LEA) (cytosol)	<i>Arabidopsis thaliana</i>	AT1G01470	11 Disease/defence	11.05 Stress responses	5,00E-50	74	emb.	evm_27.model.AmTr_v1.0_scaffold00053.174	-6,188425	3	16.5	2	-	2	0.057143	IPEPGPITAK IPEPGPITAK KGELKLP L T L S D	0,000571
O04005	1-Cys peroxiredoxin	<i>Arabidopsis thaliana</i>	AT1G48130	11 Disease/defence	11.05 Stress responses	1,00E-88	82	emb./end.	evm_27.model.AmTr_v1.0_scaffold00045.37	-148,7976	11	24.2	2	-	2	0.25	DNQGKPLPSR ALHIVGPKR ALHIVGPKD	0,000571
O04331	Prohibitin (mitochondrial)	<i>Arabidopsis thaliana</i>	AT5G40770	06 Protein destination and storage	06.01 Folding and stability	e-111	83	emb.	evm_27.model.AmTr_v1.0_scaffold00079.74	-18,10965	18	30.6	5	-	3	0.714286	TRPHTFSSISG TK GSOAAVSFLT	0,001427
O04450	T-complex protein (Chaperonin)	<i>Arabidopsis thaliana</i>	AT1G24510	06 Protein destination and storage	06.01 Folding and stability	0	93	emb.	evm_27.model.AmTr_v1.0_scaffold00049.162	-6,79588	26	67.8	4	-	3	0.5	LLECGIPIR MLYIEQCANS R	0,001141
O04486	Ras-related protein	<i>Arabidopsis thaliana</i>	AT1G09630	08 Intracellular traffic	08.07 Vesicular	2,00E-94	91	emb.	evm_27.model.AmTr_v1.0_scaffold00068.101	-13,02541	12	23.7	3	-	3	0.3	VVLIGDSGVGK	0,000856
O04486	Ras-related protein	<i>Arabidopsis thaliana</i>	AT1G09630	08 Intracellular traffic	08.07 Vesicular	3,00E-99	85	emb.	evm_27.model.AmTr_v1.0_scaffold00071.220	-10,74398	15	24.4	3	-	2	0.6	IVLIGDSGVGK IVLIGDSGVGK	0,000856
O04487	Elongation factor 1-beta gamma	<i>Arabidopsis thaliana</i>	AT1G09640	05 Protein synthesis	05.04 Translation factors	7,00E-78	93	emb.	evm_27.model.AmTr_v1.0_scaffold00019.442	-24,19019	15	49.1	5	-	4	0.277778	GPIFESNAIAR VDINDETQKE R	0,001427
O04834	GTP-binding protein	<i>Arabidopsis thaliana</i>	AT4G02080	08 Intracellular traffic	08.07 Vesicular	1,00E-85	83	emb./end.	evm_27.model.AmTr_v1.0_scaffold00003.24	-26,25288	9	21.8	3	-	3	0.142857	ILFLGLDNAGK LVQHPTQYP TSEELSIGK	0,000856
O22126	Fasciclin-like arabinogalactan protein	<i>Arabidopsis thaliana</i>	AT2G45470	09 Cell structure	09.01 Cell wall	e-101	79	emb.	evm_27.model.AmTr_v1.0_scaffold00069.206	-41,82212	13	43.3	3	-	3	0.166667	VATSGDEVTL DTGVDK AATGPVSTLAS	0,000856
O22263	Thioredoxin family protein	<i>Arabidopsis thaliana</i>	AT2G47470	06 Protein destination and storage	06.01 Folding and stability	e-150	86	emb.	evm_27.model.AmTr_v1.0_scaffold00057.44	-19,31785	27	39.8	5	-	4	1	DVTVLTDNFE QEVGKDR TAFALFEVNT	0,001427
O22588	Aquaporin	<i>Arabidopsis thaliana</i>	AT1G17810	09 Cell structure	09.25 Vacuole	4,00E-85	73	emb.	evm_27.model.AmTr_v1.0_scaffold00171.28	-36,82234	5	26.8	2	-	2	0.083333	RIPIGRPEEAR IPIGRPEEAR AFGPALVGWR	0,000571
O22607	Transducin/WD40 repeat-like superfamily protein	<i>Arabidopsis thaliana</i>	AT2G19520	12 Unclear classification	12 Unclear classification	0,00E+00	82	emb.	evm_27.model.AmTr_v1.0_scaffold00136.8	-25,25825	6	51.8	2	-	2	0.105263	AGGPSVDER VAAAHEHSQFN FEAR	0,000571
O23029	AWPM-19-like family protein	<i>Arabidopsis thaliana</i>	AT1G04560	06 Protein destination and storage	06.01 Folding and stability	5,00E-50	77	emb./end.	evm_27.model.AmTr_v1.0_scaffold00039.123	-45,07803	4	18.6	5	-	5	0.102041	EIDVGGHR DPDYGAGAAA DPAAPK	0,001427
O23254	Serine hydroxymethyltransferase	<i>Arabidopsis thaliana</i>	AT4G13930	01 Metabolism	01.01 Amino Acid	0	91	emb.	evm_27.model.AmTr_v1.0_scaffold00013.279	-8,739928	67	51.6	35	14	20	2.1875	LCDLCNITVNK TPLEAVDTEIY DLIEKEK	0,009986
O23255	Adenosylhomocysteine hydrolase	<i>Arabidopsis thaliana</i>	AT4G13940	01 Metabolism	01.01 Amino Acid	0	92	emb.	evm_27.model.AmTr_v1.0_scaffold00013.277	-44,47913	72	53	361	-	57	12.89286	LVGVSEETTT GVKR LVGVSEETTT	0,102996
O23404	Pyruvate, phosphate dikinase (chloroplastic)	<i>Arabidopsis thaliana</i>	AT4G15530	02 Energy	02.30 Photosynthesis	0	90	emb.	evm_27.model.AmTr_v1.0_scaffold00025.163	-8,065744	20	103.9	10	-	10	0.333333	NNGAQGIGLC R LSEVNPMLGF	0,002853
O23708	proteasome (alpha subunit)	<i>Arabidopsis thaliana</i>	AT1G16470	06 Protein destination and storage	06.13 Proteolysis	1,00E-25	81	emb.	evm_27.model.AmTr_v1.0_scaffold00029.50	-10,37551	6	8.2	4	-	4	0.121212	EGFEGQISGK NIEIGIPEPD PK	0,001141
O23708	proteasome (alpha subunit)	<i>Arabidopsis thaliana</i>	AT1G16470	06 Protein destination and storage	06.13 Proteolysis	1,00E-54	95	emb.	evm_27.model.AmTr_v1.0_scaffold00029.51	-5,476306	12	17.7	4	-	4	0.222222	QAQQYYR AADGVVIATEK KLPSILVDESS	0,001141
O23714	20S proteasome (beta subunit D-1)	<i>Arabidopsis thaliana</i>	AT3G22630	06 Protein destination and storage	06.13 Proteolysis	e-99	93	emb.	evm_27.model.AmTr_v1.0_scaffold00002.60	-16,9567	11	22.8	4	-	4	0.173913	NGIPLTTAATA NFR LIMGASGESGD	0,001141
O23715	20S proteasome (alpha subunit G-1)	<i>Arabidopsis thaliana</i>	AT2G27020	06 Protein destination and storage	06.13 Proteolysis	e-123	96	emb.	evm_27.model.AmTr_v1.0_scaffold00095.85	-34,44231	7	27.1	2	1	2	0.1	HSGMAVAGLA ADGR AVDNSGTVIGI L AAL QGLDAR VIVHPLVLLSIV DNYNR	0,000571
O24412	26S proteasome (regulatory subunit rpn8)	<i>Arabidopsis thaliana</i>	AT5G05780	06 Protein destination and storage	06.13 Proteolysis	e-162	95	emb.	evm_27.model.AmTr_v1.0_scaffold00029.346	-12,74473	9	34.7	2	1	2	0.222222		0,000571

O24496	Glyoxalase II (Hydroxyacylglutathione hydrolase)	<i>Arabidopsis thaliana</i>	AT3G10850	11 Disease/defence	11.06 Detoxification	e-114	86	emb.	evm_27.model.AmTr_v1.0_scaffold00077.1_52	-15,60412	4	28.8	2	-	2	0.090909	VYCGHEYTVK VDLPQLQAH GYSSPVEALT	0,000571
O24616	20S proteasome (alpha subunit D-2)	<i>Arabidopsis thaliana</i>	AT5G66140	06 Protein destination and storage	06.13 Proteolysis	e-121	90	emb.	evm_27.model.AmTr_v1.0_scaffold00062.7_1	-11,72308	19	27	3	-	2	0.75	ALLEVVESGG K AITVFPDGH	0,000856
O24653	Rab GDP dissociation inhibitor	<i>Arabidopsis thaliana</i>	AT3G59920	08 Intracellular traffic	08.99 Others	0	92	emb.	evm_27.model.AmTr_v1.0_scaffold00066.7_7	-18,24642	9	49.8	3	-	2	0.5	VSGVTSEGET AR VVCDSYLPN	0,000856
O48646	Glutathione peroxidase	<i>Arabidopsis thaliana</i>	AT4G11600	11 Disease/defence	11.06 Detoxification	2,00E-77	89	emb.	evm_27.model.AmTr_v1.0_scaffold00009.2_76	-22,40532	5	18.6	2	-	2	0.125	FLVDKEGHVV DR ASGSDQTSVH	0,000571
O49006	Pectinesterase inhibitor	<i>Arabidopsis thaliana</i>	AT3G14310	09 Cell structure	09.01 Cell wall	0	78	emb.	evm_27.model.AmTr_v1.0_scaffold00129.2_0	-5,966576	9	61.2	3	-	2	0.2	TVAAVAAPK K DITFONTAGPS	0,000856
O49299	Phosphoglucosyltransferase	<i>Arabidopsis thaliana</i>	AT1G23190	02 Energy	02.01 Glycolysis	0	89	emb./end.	evm_27.model.AmTr_v1.0_scaffold00010.1_23	-81,34531	48	63.7	15	-	7	1.875	LSGTGSEGAT R KETSPIDSQPK	0,004280
O49447	ADP/ATP translocase (mitochondria)	<i>Arabidopsis thaliana</i>	AT4G28390	07 Transporters	07.16 Purine/pyrimidines	e-152	78	emb.	evm_27.model.AmTr_v1.0_scaffold00183.4	-5,522879	10	42.4	3	-	3	0.130435	TAAAPIER MMMTSGEAVK LIGNQDEMIK	0,000856
O49460	Prohibitin (mitochondrial)	<i>Arabidopsis thaliana</i>	AT4G28510	06 Protein destination and storage	06.01 Folding and stability	e-101	89	emb.	evm_27.model.AmTr_v1.0_scaffold00071.1_26	-9,029188	17	30	5	-	5	0.416667	ARPHLVESTS GSR QIAAQEAER	0,001427
O49485	Phosphoglycerate dehydrogenase	<i>Arabidopsis thaliana</i>	AT4G34200	01 Metabolism	01.01 Amino Acid	0	82	emb.	evm_27.model.AmTr_v1.0_scaffold00051.5_9	-6,086186	32	65.2	32	6	7	4.571429	LAVQLVAGGS GVK LGEAGLELR	0,009130
O49543	Cysteine desulfurase	<i>Arabidopsis thaliana</i>	AT5G65720	01 Metabolism	01.01 Amino Acid	0	84	emb.	evm_27.model.AmTr_v1.0_scaffold00078.1_41	-7,89449	82	50.4	65	-	20	16.25	VEPQMSGGG QER ALGVDEDMAH	0,018545
O49595	Nucleosome/chromatin assembly factor	<i>Arabidopsis thaliana</i>	AT3G51880	04 Transcription	04.1904 Specific TFs	2,00E-34	67	emb.	evm_27.model.AmTr_v1.0_scaffold00029.4_12	-8,841638	17	18.9	8	-	8	0.266667	RPPSAFFVFL EFR RPPSAFFVFL	0,002282
O50008	5-methyltetrahydropteroyl tripartite	<i>Arabidopsis thaliana</i>	AT5G17920	01 Metabolism	01.01 Amino Acid	0	92	emb./end.	evm_27.model.AmTr_v1.0_scaffold00004.9_9	-20,86621	76	84.5	81	-	22	7.363637	YGAGIGPGVY DIHSPR GISGFGFDLVR	0,023110
O64586	Pollen Ole e 1 (Putative proline-rich glycoprotein)	<i>Arabidopsis thaliana</i>	AT2G34700	12 Unclear classification	12 Unclear classification	4,00E-29	61	emb./end.	evm_27.model.AmTr_v1.0_scaffold00068.1_22	-30,91422	7	18.6	2	-	2	0.095238	ATDLHGGITGS PLR VFLASSPLATC	0,000571
O64644	Histone deacetylase	<i>Arabidopsis thaliana</i>	AT2G45640	04 Transcription	04.1907 Chromatin modification	9,00E-49	86	emb.	evm_27.model.AmTr_v1.0_scaffold00001.1_93	-7,443698	10	17.6	8	-	7	0.222222	AAVAEQQSR LSFAFVYDPKN GR	0,002282
O64866	Calcium-binding EF-hand-containing protein	<i>Arabidopsis thaliana</i>	AT2G44310	10 Signal transduction	10.99 Others	2,00E-47	83	emb.	evm_27.model.AmTr_v1.0_scaffold00024.1_61	-41,13548	7	15.3	2	-	2	0.105263	TAFESMR DSSGSVDGME FR	0,000571
O65154	RNA polymerase II transcriptional coactivator KIWI	<i>Arabidopsis thaliana</i>	AT5G09250	04 Transcription	04.1901 General TFs	2,00E-26	75	emb.	evm_27.model.AmTr_v1.0_scaffold00017.2_38	-7,903785	20	12	8	-	8	0.444444	QTDEDHAGSE GDSEGVAPPA R	0,002282
O65282	Chaperonin (20 kDa, Cpn21)	<i>Arabidopsis thaliana</i>	AT5G20720	06 Protein destination and storage	06.01 Folding and stability	e-102	83	emb.	evm_27.model.AmTr_v1.0_scaffold00007.3_83	-8,239577	18	26.4	4	-	4	0.363636	AGAQVYVSK TGGGILLPTTA GSKPQGGVEV	0,001141
O65390	Aspartic proteinase	<i>Arabidopsis thaliana</i>	AT1G11910	06 Protein destination and storage	06.13 Proteolysis	0	80	emb./end.	evm_27.model.AmTr_v1.0_scaffold00106.4_8	-30,43041	21	55	4	-	4	0.571429	LSSMPNVAFTI GKK VGEGAAQCI	0,001141
O65390	Aspartic proteinase	<i>Arabidopsis thaliana</i>	AT1G11910	06 Protein destination and storage	06.13 Proteolysis	0	79	emb.	evm_27.model.AmTr_v1.0_scaffold00045.11_9	-12,92203	12	55.2	4	-	4	0.222222	DQAFIATR TQILEYANQLC ER	0,001141
O65398	Lactoylglutathione lyase-like protein	<i>Arabidopsis thaliana</i>	AT1G11840	11 Disease/defence	11.06 Detoxification	e-130	87	emb./end.	evm_27.model.AmTr_v1.0_scaffold00037.1_06	-44,35327	6	37.2	2	-	2	0.142857	ITSFLDPDGW K LVTQELGKK	0,000571
O65660	Lipase	<i>Arabidopsis thaliana</i>	AT4G39730	01 Metabolism	01.06 Lipid and sterol	4,00E-46	72	emb.	evm_27.model.AmTr_v1.0_scaffold00010.1_52	-7,410274	57	19.8	15	8	10	2.5	GNLDIFSGR GNLDIFSGR DAYPYELTAIR	0,004280
O78310	Superoxide dismutase (Cu/Zn)	<i>Arabidopsis thaliana</i>	AT2G28190	11 Disease/defence	11.06 Detoxification	6,00E-70	76	emb.	evm_27.model.AmTr_v1.0_scaffold00102.3_3	-19,01323	11	22.4	2	-	2	0.125	AFVVELEDD LGK AFVVELEDD	0,000571
O80576	Late embryogenesis abundant protein (LEA)	<i>Arabidopsis thaliana</i>	AT2G44060	11 Disease/defence	11.05 Stress responses	e-118	86	emb.	evm_27.model.AmTr_v1.0_scaffold00066.8_0	-10,29912	9	36.2	2	-	2	0.166667	LVSGLIPDAGT R IKVDLIVDVPVE	0,000571
O80763	Nucleoredoxin	<i>Arabidopsis thaliana</i>	AT1G60420	10 Signal transduction	10.99 Others	e-169	64	emb.	evm_27.model.AmTr_v1.0_scaffold00131.8_5	-15,86646	9	68.4	2	-	2	0.181818	RLFELQGFPTL TVIGPDGK MPWLAIPESD	0,000571
O81147	20S proteasome (subunit alpha A-2)	<i>Arabidopsis thaliana</i>	AT2G05840	06 Protein destination and storage	06.13 Proteolysis	e-131	96	emb.	evm_27.model.AmTr_v1.0_scaffold00147.4_7	-29,90146	18	27.4	4	-	3	0.444444	ATEIEVGVVR HITIFSPGR LQVYEYAFK	0,001141

O81148	Proteasome subunit similaire 20S	<i>Arabidopsis thaliana</i>	AT3G22110	06 Protein destination and storage	06.13 Proteolysis	e-118	87	emb.	evm_27.model.AmTr_1.0_scaffold00010.4_31	-10,14503	11	27,5	4	-	4	0,173913	TTIFSPPEGR AAAGANNQA AQSMLK	0,001141
O81148	Proteasome subunit similaire 20S	<i>Arabidopsis thaliana</i>	AT3G22110	06 Protein destination and storage	06.13 Proteolysis	e-105	83	emb.	evm_27.model.AmTr_1.0_scaffold00045.1_99	-10,14503	16	33,7	4	-	2	0,5	TTIFSPPEGR AAAGANNQA AQSMLK	0,001141
O81235	Superoxide dismutase (Mn)	<i>Arabidopsis thaliana</i>	AT3G10920	11 Disease/defence	11.06 Detoxification	8,00E-76	79	emb./end.	evm_27.model.AmTr_1.0_scaffold00077.2_6	-47,63932	3	22,4	2	-	2	0,068966	NLAPVNEGGG EPPK GDASSTVQLQ	0,000571
O81826	Histone H2A.3	<i>Arabidopsis thaliana</i>	AT4G27230	09 Cell structure	09.13 Chromosomes	2,00E-40	80	emb.	evm_27.model.AmTr_1.0_scaffold00115.21_31	-12,21113	14	13,7	2	-	2	0,25	VGAGAPVYLA	0,000571
O82204	60S ribosomal protein (L28-1)	<i>Arabidopsis thaliana</i>	AT2G19730	05 Protein synthesis	05.01 Ribosomal proteins	9,00E-52	82	emb.	evm_27.model.AmTr_1.0_scaffold00036.1_31	-8,182699	43	23	6	-	2	2	AVVSQVADNY YRPDLK QEGNGSAMV	0,001712
O82240	Adenine nucleotide alpha hydrolases-like protein	<i>Arabidopsis thaliana</i>	AT2G47710	11 Disease/defence	11.05 Stress responses	3,00E-50	77	emb.	evm_27.model.AmTr_1.0_scaffold00045.3_18	-21,21112	6	17,4	2	-	2	0,117647	NVLCFAVEK HQATMLAVGS HGYGAIK	0,000571
O82662	Succinyl-CoA ligase	<i>Arabidopsis thaliana</i>	AT2G20420	02 Energy	02.10 TCA pathway	e-178	92	emb.	evm_27.model.AmTr_1.0_scaffold00067.9_8	-5,845272	31	40,6	10	6	9	0,588235	LNFDNNAAYR TTAGPLIACR	0,002853
P06525	Alcohol dehydrogenase	<i>Arabidopsis thaliana</i>	AT1G77120	02 Energy	02.16 Fermentation	e-162	80	emb./end.	evm_27.model.AmTr_1.0_scaffold00071.6_5	-110,6495	35	41,1	10	-	6	1,111111	THPMNFLNER THPMNFLNER THPMNFLNER	0,002853
P06525	Alcohol dehydrogenase	<i>Arabidopsis thaliana</i>	AT1G77120	02 Energy	02.16 Fermentation	e-168	81	emb.	evm_27.model.AmTr_1.0_scaffold00071.6_4	-42,55006	48	41,1	10	-	8	1	FITHSVPFSEIN K DYDKPVQVEI	0,002853
P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	1,00E-70	52	emb./end.	evm_27.model.AmTr_1.0_scaffold00067.1_2	-271,8854	8	53	3	-	3	0,2	VGEGGQQQQ GIKDR RGQEEGQQE	0,000856
P17094	60S ribosomal protein (L3-1)	<i>Arabidopsis thaliana</i>	AT1G43170	05 Protein synthesis	05.01 Ribosomal proteins	0	91	emb.	evm_27.model.AmTr_1.0_scaffold00060.11_2	-14,02393	26	44,3	6	-	5	0,6	AGQESHAIITE FDRTEK TLNTVWAQHL	0,001712
P17745	Elongation factor Tu (chloroplatic)	<i>Arabidopsis thaliana</i>	AT4G20360	05 Protein synthesis	05.04 Translation factors	0	88	emb.	evm_27.model.AmTr_1.0_scaffold00049.2_75	-23,50897	18	52,1	4	1	3	0,444444	NMITGAAQMD GAILVSGADG PMPQTK	0,001141
P19036	HSP17.4 (class I small heat shock protein)	<i>Arabidopsis thaliana</i>	AT3G46230	06 Protein destination and storage	06.01 Folding and stability	2,00E-48	76	emb./end.	evm_27.model.AmTr_1.0_scaffold00165.3_6	-136,3294	7	18,1	2	-	2	0,125	ETDNAHIK LPENKGVDEV K	0,000571
P19037	HSP18.1 (small heat shock protein family)	<i>Arabidopsis thaliana</i>	AT5G59720	06 Protein destination and storage	06.01 Folding and stability	1,00E-46	77	emb./end.	evm_27.model.AmTr_1.0_scaffold00136.4_6	-119,2814	18	17,8	5	-	4	0,384615	ETDDAHMFK KDEVKVELED GR	0,001427
P19366	ATP synthase, chloroplatic	<i>Arabidopsis thaliana</i>	ATCG00480	02 Energy	02.13 Respiration	0	98	emb.	evm_27.model.AmTr_1.0_scaffold00334.5_6	-27,45648	33	49,6	11	-	6	1,1	MPSAVGYQPT LSTEMGSLQE R	0,003138
P20115	Citrate synthase (mitochondrial)	<i>Arabidopsis thaliana</i>	AT2G44350	02 Energy	02.10 TCA pathway	0	88	emb.	evm_27.model.AmTr_1.0_scaffold00131.1_9	-13,96738	16	53,4	5	2	5	0,416667	YYTVLVFVSR VHLGNITVDM VIGGMR	0,001427
P21240	Chaperonin (Chaperonin-60kD, ch60, CPN60)	<i>Arabidopsis thaliana</i>	AT1G55490	06 Protein destination and storage	06.01 Folding and stability	0	92	emb.	evm_27.model.AmTr_1.0_scaffold00106.9_1	-8,055517	14	65	5	-	5	0,227273	NAGVNGSVVT EK VVAAGANPVOI	0,001427
P25696	Enolase	<i>Arabidopsis thaliana</i>	AT2G36530	02 Energy	02.01 Glycolysis	0	93	emb./end.	evm_27.model.AmTr_1.0_scaffold00041.3_4	-148,7665	32	47,9	11	3	10	0,647059	AAVPSGASTG VYEALELR AAVPSGASTG	0,003138
P25819	Catalase 2	<i>Arabidopsis thaliana</i>	AT4G35090	11 Disease/defence	11.06 Detoxification	0	91	emb./end.	evm_27.model.AmTr_1.0_scaffold00001.7_3	-76,36057	3	56,7	2	-	2	0,060606	ENNFKQPQDR SHIQENWR TFAYGDTQR	0,000571
P25819	Catalase 2	<i>Arabidopsis thaliana</i>	AT4G35090	11 Disease/defence	11.06 Detoxification	0	94	emb.	evm_27.model.AmTr_1.0_scaffold00001.8_4	-44,40526	4	56,8	2	-	2	0,055556	GPILLEDYHLV EK GPILLEDYHLV	0,000571
P25858	Glyceraldehyde-3- phosphate dehydrogenase	<i>Arabidopsis thaliana</i>	AT3G04120	02 Energy	02.01 Glycolysis	5,00E-48	87	emb./end.	evm_27.model.AmTr_1.0_scaffold00177.2_2	-51,87639	70	11,8	16	-	7	2	AGIALNDNFM K VDLICHMASV	0,004565
P25858	Glyceraldehyde-3- phosphate dehydrogenase	<i>Arabidopsis thaliana</i>	AT3G04120	02 Energy	02.01 Glycolysis	5,00E-26	98	emb.	evm_27.model.AmTr_1.0_scaffold00177.2_3	-14,09152	43	8,1	13	-	5	2,6	AGIALNDHFM K GILGYTEDDVV	0,003709
P27323	HSP90	<i>Arabidopsis thaliana</i>	AT5G52640	06 Protein destination and storage	06.01 Folding and stability	0	84	emb./end.	evm_27.model.AmTr_1.0_scaffold00001.8_7	-97,96773	8	81	4	3	4	0,235294	ADLVNNLGTIA R GVVDSDDLPL	0,001141
P28188	Ras-related protein	<i>Arabidopsis thaliana</i>	AT1G02130	08 Intracellular traffic	08.07 Vesicular	e-105	95	emb.	evm_27.model.AmTr_1.0_scaffold00111.12_7	-5,08831	33	22,2	3	-	3	0,5	NATNVEQAFM	0,000856
P29197	Chaperonin (Chaperonin-60kD, ch60, CPN60)	<i>Arabidopsis thaliana</i>	AT3G23990	06 Protein destination and storage	06.01 Folding and stability	0	93	emb./end.	evm_27.model.AmTr_1.0_scaffold00003.2_61	-94,10696	6	61,2	2	1	2	0,125	LLEQDNPDLG YDAAK AAVEGIVPG	0,000571

P29448	Thioredoxin	<i>Arabidopsis thaliana</i>	AT3G51030	06 Protein destination and storage	06.01 Folding and stability	9,00E-37	78	emb.	evm_27.model.AmTr_v1.0_scaffold00002.333	-38,81908	13	13,4	5	-	4	0,277778	MEQVGIIPCHTK MEQVGIIPCH	0,001427
P29514	Tubulin	<i>Arabidopsis thaliana</i>	AT5G12250	09 Cell structure	09.04 Cytoskeleton	0	96	emb.	evm_27.model.AmTr_v1.0_scaffold00010.73	-22,96072	11	50,1	3	-	3	0,1875	NSSYFVEWIPN	0,000856
P29516	Tubulin	<i>Arabidopsis thaliana</i>	AT5G23860	09 Cell structure	09.04 Cytoskeleton	0	96	emb.	evm_27.model.AmTr_v1.0_scaffold00009.283	-22,96072	8	50	3	-	3	0,166667	NSSYFVEWIPN	0,000856
P29516	Tubulin	<i>Arabidopsis thaliana</i>	AT5G23860	09 Cell structure	09.04 Cytoskeleton	0	94	emb.	evm_27.model.AmTr_v1.0_scaffold00032.35	-25,37089	9	49,8	3	-	3	0,142857	INVYYNEASGG	0,000856
P29525	Oleosin type 1	<i>Arabidopsis thaliana</i>	AT4G25140	09 Cell structure	09.99 Others	1,00E-25	82	emb.	evm_27.model.AmTr_v1.0_scaffold00056.169	-19,34313	4	15,4	2	-	2	0,08	AEQPKPVTQK LEAEEKPPTS HQAVK	0,000571
P29525	Oleosin type 1	<i>Arabidopsis thaliana</i>	AT4G25140	09 Cell structure	09.99 Others	4,00E-18	67	emb.	evm_27.model.AmTr_v1.0_scaffold00111.94	-9,730487	4	14	2	-	2	0,095238	RSQLALSR AQDLKEQYAS HTQSQ	0,000571
P29830	HSP17.6 (class II heat shock protein) (cytoplasm)	<i>Arabidopsis thaliana</i>	AT5G12020	06 Protein destination and storage	06.01 Folding and stability	2,00E-42	71	emb.	evm_27.model.AmTr_v1.0_scaffold00146.15	-37,11984	29	16,8	5	-	4	0,384615	AMAATPADIK AMAATPADIKE YPNYSVFIIDM	0,001427
P29830	HSP17.6 (class II heat shock protein)	<i>Arabidopsis thaliana</i>	AT5G12020	06 Protein destination and storage	06.01 Folding and stability	1,00E-39	80	emb.	evm_27.model.AmTr_v1.0_scaffold00146.16	-32,79142	15	17,2	5	-	4	0,333333	FNLPEANVE AISAVYHDGVL TVTVQK	0,001427
P30184	Leucine aminopeptidase	<i>Arabidopsis thaliana</i>	AT2G24200	06 Protein destination and storage	06.13 Proteolysis	0	78	emb./end.	evm_27.model.AmTr_v1.0_scaffold00065.204	-112,4282	11	54,8	4	-	4	0,235294	TIEVNTDAEGR GFGEVAASSA	0,001141
P31168	Dehydrin	<i>Arabidopsis thaliana</i>	AT1G20440	11 Disease/defence	11.05 Stress responses	2,00E-06	52	emb.	evm_27.model.AmTr_v1.0_scaffold00001.295	-12,76548	8	23,3	2	-	2	0,133333	GLFGHHHPET PEOK ADEHTTSVVP	0,000571
P31170	HSP25.3 (chloroplast)	<i>Arabidopsis thaliana</i>	AT4G27670	06 Protein destination and storage	06.01 Folding and stability	9,00E-34	56	emb.	evm_27.model.AmTr_v1.0_scaffold00049.61	-22,6356	5	26,2	2	1	2	0,117647	IALPENVEIK TPWDIQETDE EFR	0,000571
P31265	Translationally-controlled tumor protein homolog	<i>Arabidopsis thaliana</i>	AT3G16640	03 Cell growth/division	03.26 Growth regulators	9,00E-75	88	emb.	evm_27.model.AmTr_v1.0_scaffold00045.319	-12,27278	30	19	8	-	6	0,470588	VVDIVDFR EGATDPFTLYF AYGLK	0,002282
P34066	20S proteasome (alpha subunit F-1)	<i>Arabidopsis thaliana</i>	AT5G42790	06 Protein destination and storage	06.13 Proteolysis	e-119	90	emb.	evm_27.model.AmTr_v1.0_scaffold00003.138	-19,08291	17	29,3	4	-	3	0,307692	HVVLASVNK NQYTDVTTW SPAGR	0,001141
P34788	40S ribosomal protein (S18)	<i>Arabidopsis thaliana</i>	AT4G09800	05 Protein synthesis	05.01 Ribosomal proteins	3,00E-64	90	emb.	evm_27.model.AmTr_v1.0_scaffold00078.175	-25,97266	37	17,5	7	-	7	0,5	VLNTNVDGR IMFALTSIK IPDWELNR	0,001997
P34795	Phosphoglucose isomerase	<i>Arabidopsis thaliana</i>	AT5G42740	02 Energy	02.01 Glycolysis	0	90	emb./end.	evm_27.model.AmTr_v1.0_scaffold00111.63	-52,01955	44	63	14	-	6	2,333333	DSVINCDGK FSPHIQQVSM FSNGK	0,003994
P39207	Nucleoside diphosphate kinase.	<i>Arabidopsis thaliana</i>	AT4G09320	10 Signal transduction	10.0404 Kinases	4,00E-63	83	emb.	evm_27.model.AmTr_v1.0_scaffold00002.226	-30,88658	6	16,1	2	-	2	0,125	NVIHGSDSVE SAK NVIHGSDSVE	0,000571
P40283	Histone H2B.11	<i>Arabidopsis thaliana</i>	AT5G59910	09 Cell structure	09.13 Chromosomes	5,00E-48	86	emb.	evm_27.model.AmTr_v1.0_scaffold00010.258	-13,77436	18	16,5	3	-	3	0,1875	YNKKTITSR AMGMINSFIND IFEK	0,000856
P40283	Histone H2B.11	<i>Arabidopsis thaliana</i>	AT5G59910	09 Cell structure	09.13 Chromosomes	5,00E-48	86	emb.	evm_27.model.AmTr_v1.0_scaffold00012.26	-13,77436	5	16,4	3	-	3	0,103448	YNKKTITSR AMGMINSFIND IFEK	0,000856
P40283	Histone H2B.11	<i>Arabidopsis thaliana</i>	AT5G59910	09 Cell structure	09.13 Chromosomes	5,00E-48	86	emb.	evm_27.model.AmTr_v1.0_scaffold00012.38	-13,77436	8	15,3	3	-	2	0,75	YNKKTITSR AMGMINSFIND IFEK	0,000856
P40283	Histone H2B.11	<i>Arabidopsis thaliana</i>	AT5G59910	09 Cell structure	09.13 Chromosomes	5,00E-48	86	emb.	evm_27.model.AmTr_v1.0_scaffold00012.39	-13,77436	8	16,4	2	-	2	0,166667	YNKKTITSR AMGMINSFIND IFEK	0,000571
P41127	60S ribosomal protein (L13-1)	<i>Arabidopsis thaliana</i>	AT3G49010	05 Protein synthesis	05.01 Ribosomal proteins	3,00E-78	89	emb.	evm_27.model.AmTr_v1.0_scaffold00022.339	-3,829152	13	23,8	4	1	3	0,285714	ANLNVFPR	0,001141
P41127	60S ribosomal protein (L13-1)	<i>Arabidopsis thaliana</i>	AT3G49010	05 Protein synthesis	05.01 Ribosomal proteins	1,00E-72	84	emb.	evm_27.model.AmTr_v1.0_scaffold00029.120	-7,488251	13	23,8	4	1	3	0,333333	SLEGLQTNVQR	0,001141
P41376	Eukaryotic initiation factor	<i>Arabidopsis thaliana</i>	AT3G13920	05 Protein synthesis	05.04 Translation factors	0	96	emb.	evm_27.model.AmTr_v1.0_scaffold00036.91	-47,45055	13	46,7	6	-	6	0,230769	SRDHTVSATH GDMDQNTNR DHTVSATHGD	0,001712
P41916	GTP-binding nuclear protein	<i>Arabidopsis thaliana</i>	AT5G20010	08 Intracellular traffic	08.01 Nuclear	e-112	98	emb.	evm_27.model.AmTr_v1.0_scaffold00009.135	-25,94122	14	25,1	3	-	3	0,375	HITGEFEK LVVGDGGTG K	0,000856
P42730	Chaperone protein ClpB1 (HSP 101)	<i>Arabidopsis thaliana</i>	AT1G74310	06 Protein destination and storage	06.01 Folding and stability	0	91	emb.	evm_27.model.AmTr_v1.0_scaffold00086.64	-63,38146	24	101	5	-	5	0,384615	VILFIDEHLVL GAGR TAVVEGLAQR	0,001427

P42742	20S proteasome (beta subunit F-1)	<i>Arabidopsis thaliana</i>	AT3G60820	06 Protein destination and storage	06.13 Proteolysis	e-109	92	emb.	evm_27.model.AmTr.v1.0_scaffold00055.168	-19,45213	15	24,9	4	-	4	0,153846	SIMASSGFQA DVK MSTGYSLTR	0,001141
P42798	40S ribosomal protein (S15a-1)	<i>Arabidopsis thaliana</i>	AT5G59850	05 Protein synthesis	05.01 Ribosomal proteins	1,00E-68	97	emb.	evm_27.model.AmTr.v1.0_scaffold00010.173	-9,665868	26	14,7	7	-	3	1,4	HGYIGEFEYVD	0,001997
P42798	40S ribosomal protein (S15a-1)	<i>Arabidopsis thaliana</i>	AT5G59850	05 Protein synthesis	05.01 Ribosomal proteins	2,00E-69	99	emb.	evm_27.model.AmTr.v1.0_scaffold00168.6	-10,7537	18	18,9	6	1	6	0,333333	HGYIGEFEYVD	0,001712
P43297	Cysteine proteinase	<i>Arabidopsis thaliana</i>	AT1G47128	06 Protein destination and storage	06.13 Proteolysis	e-168	78	emb.	evm_27.model.AmTr.v1.0_scaffold00051.91	-17,5397	6	59,1	4	-	3	0,166667	AVAHQPVSVAI EAAGR AVAHQPVSVAI	0,001141
P46644	Aspartate aminotransferase (chloroplastic)	<i>Arabidopsis thaliana</i>	AT5G11520	01 Metabolism	01.01 Amino acid	0,00E+00	88	emb.	evm_27.model.AmTr.v1.0_scaffold00109.53	-17,11962	52	49	29	-	14	2,230769	VATVQGLSGT GSLR QAFQLLINDGS	0,008274
P47998	Cysteine synthase	<i>Arabidopsis thaliana</i>	AT4G14880	01 Metabolism	01.02 Nitrogen and sulphur	e-129	82	emb.	evm_27.model.AmTr.v1.0_scaffold00004.37	-11,63078	58	34,8	26	-	20	1	LEGMEPCSSV K AFGAEVLTD	0,007418
P48491	Triosephosphate isomerase	<i>Arabidopsis thaliana</i>	AT3G55440	02 Energy	02.01 Glycolysis	e-114	87	emb./end.	evm_27.model.AmTr.v1.0_scaffold00012.164	-71,36359	36	27,3	14	-	6	4,666667	VATPAQAQEV HFELR SLLNTEFEV	0,003994
P49206	40S ribosomal protein (S26)	<i>Arabidopsis thaliana</i>	AT2G40590	05 Protein synthesis	05.01 Ribosomal proteins	3,00E-31	79	emb.	evm_27.model.AmTr.v1.0_scaffold00077.25	-7,511449	13	14,1	4	1	3	0,333333	NIVEQAAVR NIVEQAAVR DVQEAQVYDG	0,001141
P49209	60S ribosomal protein (L9-1)	<i>Arabidopsis thaliana</i>	AT1G33140	05 Protein synthesis	05.01 Ribosomal proteins	3,00E-86	89	emb.	evm_27.model.AmTr.v1.0_scaffold00018.62	-8,736127	39	21,4	6	-	6	0,4	VDAWFGSR TAISHVGNLIT GVTK	0,001712
P49690	60S ribosomal protein (L23)	<i>Arabidopsis thaliana</i>	AT3G04400	05 Protein synthesis	05.01 Ribosomal proteins	3,00E-67	99	emb.	evm_27.model.AmTr.v1.0_scaffold00067.229	-11,52288	13	13,4	4	1	3	0,363636	VMPAIVR VMPAIVR MSLGLPVAAT	0,001141
P50883	60S ribosomal protein (L12-1)	<i>Arabidopsis thaliana</i>	AT2G37190	05 Protein synthesis	05.01 Ribosomal proteins	4,00E-82	96	emb.	evm_27.model.AmTr.v1.0_scaffold00105.23	-14,46781	26	17,7	7	-	3	1,4	HSGNISLDDVI EIAR HSGNISLDDVI	0,001997
P50883	60S ribosomal protein (L12-1)	<i>Arabidopsis thaliana</i>	AT2G37190	05 Protein synthesis	05.01 Ribosomal proteins	1,00E-81	96	emb.	evm_27.model.AmTr.v1.0_scaffold00148.11	-13,85599	27	17,7	7	-	3	1,4	HSGNISLDDVI	0,001997
P51413	60S ribosomal protein (L17-2)	<i>Arabidopsis thaliana</i>	AT1G67430	05 Protein synthesis	05.01 Ribosomal proteins	2,00E-85	91	emb.	evm_27.model.AmTr.v1.0_scaffold00013.147	-7,632458	22	20,6	5	1	3	0,714286	INPYMSSPCHI ELILSEK GLDVRTLFISH	0,001427
P51413	60S ribosomal protein (L17-2)	<i>Arabidopsis thaliana</i>	AT1G67430	05 Protein synthesis	05.01 Ribosomal proteins	1,00E-85	91	emb.	evm_27.model.AmTr.v1.0_scaffold00013.159	-7,632458	22	20,6	4	1	3	0,571429	INPYMSSPCHI ELILSEK GLDVRTLFISH	0,001141
P51413	60S ribosomal protein (L17-2)	<i>Arabidopsis thaliana</i>	AT1G67430	05 Protein synthesis	05.01 Ribosomal proteins	9,00E-74	91	emb.	evm_27.model.AmTr.v1.0_scaffold00013.162	-7,632458	11	20,6	6	-	6	0,4	INPYMSSPCHI ELILSEK GLDVRTLFISH	0,001712
P51413	60S ribosomal protein (L17-2)	<i>Arabidopsis thaliana</i>	AT1G67430	05 Protein synthesis	05.01 Ribosomal proteins	7,00E-86	92	emb.	evm_27.model.AmTr.v1.0_scaffold00013.166	-7,632458	8	20,6	6	-	5	0,176471	INPYMSSPCHI ELILSEK GLDVRTLFISH	0,001712
P53492	Actin 7	<i>Arabidopsis thaliana</i>	AT5G09810	09 Cell structure	09.04 Cytoskeleton	0	99	emb./end.	evm_27.model.AmTr.v1.0_scaffold00018.104	-77,59848	18	41,6	3	-	3	0,214286	AGFAGDDAPR AEYEEGSPSIV HR	0,000856
P54904	Pyroglutamate-5-carboxylate reductase	<i>Arabidopsis thaliana</i>	AT5G14800	01 Metabolism	01.01 Amino Acid	3,00E-92	75	emb.	evm_27.model.AmTr.v1.0_scaffold00053.25	-4,422508	80	28,8	40	-	19	2,352941	LLVSIAGIR EVLSELKPFSL K	0,011412
P57106	Malate dehydrogenase	<i>Arabidopsis thaliana</i>	AT5G43330	02 Energy	02.10 TCA pathway	6,00E-49	84	emb.	evm_27.model.AmTr.v1.0_scaffold01428.1	-28,50888	11	12,3	11	-	10	0,255814	KKLDATADELS EEK KLDATADELS	0,003138
P57681	Farnesylcysteine lyase	<i>Arabidopsis thaliana</i>	AT5G63910	06 Protein destination and storage	06.13 Proteolysis	e-149	73	emb.	evm_27.model.AmTr.v1.0_scaffold00186.16	-15,94746	8	53,6	4	-	4	0,129032	LQHTHATFVR YGFLLR GVLNPGYFGL	0,001141
P57751	UDP-glucose pyrophosphorylase	<i>Arabidopsis thaliana</i>	AT5G17310	01 Metabolism	01.05 Sugars and polysaccharides	0	87	emb./end.	evm_27.model.AmTr.v1.0_scaffold00044.42	-123,1749	26	52,2	12	5	9	0,571429	ANPANPSIELG PEFK FFDQAIGNVP	0,003424
P59233	Ubiquitin-40S ribosomal protein	<i>Arabidopsis thaliana</i>	AT3G62250	05 Protein synthesis	05.01 Ribosomal proteins	3,00E-68	82	emb.	evm_27.model.AmTr.v1.0_scaffold00017.35	-20,29835	10	17,7	6	-	4	0,315789	IQDKEGIPPDQ QR TLADYNIQK	0,001712
P59259	Histone H4	<i>Arabidopsis thaliana</i>	AT5G59970	09 Cell structure	09.13 Chromosomes	3,00E-41	100	emb.	evm_27.model.AmTr.v1.0_scaffold00001.489	-22,56048	13	11,3	2	1	2	0,166667	DAVYTEHAR DNIQGITKPAIR ISGLIYEETR	0,000571
P59259	Histone H4	<i>Arabidopsis thaliana</i>	AT5G59970	09 Cell structure	09.13 Chromosomes	3,00E-41	100	emb.	evm_27.model.AmTr.v1.0_scaffold00003.187	-22,56048	17	11,3	3	-	3	0,6	DAVYTEHAR DNIQGITKPAIR ISGLIYEETR	0,000856
P59259	Histone H4	<i>Arabidopsis thaliana</i>	AT5G59970	09 Cell structure	09.13 Chromosomes	3,00E-41	100	emb.	evm_27.model.AmTr.v1.0_scaffold00003.316	-22,56048	22	11,3	3	-	2	0,5	DAVYTEHAR DNIQGITKPAIR ISGLIYEETR	0,000856

P59259	Histone H4	<i>Arabidopsis thaliana</i>	AT5G59970	09 Cell structure	09.13 Chromosomes	3,00E-41	100	emb.	evm_27.model.AmTr_v1.0_scaffold00007.1_51	-22,56048	11	11,3	3	-	2	0,230769	DAVYTEHAR DNIQGITKPAIR ISGLIYEETR	0,000856
P59259	Histone H4	<i>Arabidopsis thaliana</i>	AT5G59970	09 Cell structure	09.13 Chromosomes	3,00E-41	100	emb.	evm_27.model.AmTr_v1.0_scaffold00019.2_76	-22,56048	40	11,3	3	-	3	0,75	DAVYTEHAR DNIQGITKPAIR ISGLIYEETR	0,000856
P59259	Histone H4	<i>Arabidopsis thaliana</i>	AT5G59970	09 Cell structure	09.13 Chromosomes	3,00E-41	100	emb.	evm_27.model.AmTr_v1.0_scaffold00019.2_78	-22,56048	15	11,3	3	-	3	0,3	DAVYTEHAR DNIQGITKPAIR ISGLIYEETR	0,000856
P59259	Histone H4	<i>Arabidopsis thaliana</i>	AT5G59970	09 Cell structure	09.13 Chromosomes	3,00E-41	100	emb.	evm_27.model.AmTr_v1.0_scaffold00019.2_80	-22,56048	14	11,3	3	-	3	0,333333	DAVYTEHAR DNIQGITKPAIR ISGLIYEETR	0,000856
P59259	Histone H4	<i>Arabidopsis thaliana</i>	AT5G59970	09 Cell structure	09.13 Chromosomes	3,00E-41	100	emb.	evm_27.model.AmTr_v1.0_scaffold00032.4_9	-22,56048	16	11,3	3	-	3	0,375	DAVYTEHAR DNIQGITKPAIR ISGLIYEETR	0,000856
P59259	Histone H4	<i>Arabidopsis thaliana</i>	AT5G59970	09 Cell structure	09.13 Chromosomes	3,00E-41	100	emb.	evm_27.model.AmTr_v1.0_scaffold00059.1_70	-22,56048	16	11,3	3	-	3	0,3	DAVYTEHAR DNIQGITKPAIR ISGLIYEETR	0,000856
P60040	60S ribosomal protein (L7-2)	<i>Arabidopsis thaliana</i>	AT2G01250	05 Protein synthesis	05.01 Ribosomal proteins	6,00E-96	78	emb.	evm_27.model.AmTr_v1.0_scaffold00061.2_12	-22,10278	18	28,5	6	1	6	0,3	NHYVEGGDAG NR EYQEQELELV	0,001712
P83483	ATP synthase, mitochondrial	<i>Arabidopsis thaliana</i>	AT5G08690	02 Energy	02.13 Respiration	0	88	emb.	evm_27.model.AmTr_v1.0_scaffold00006.1_7	-85,84645	18	59,9	11	-	9	0,392857	VGLTGLTVAEH FR MLSPHILGQD	0,003138
P92963	Ras-related protein	<i>Arabidopsis thaliana</i>	AT4G17170	08 Intracellular traffic	08.07 Vesicular	e-108	91	emb.	evm_27.model.AmTr_v1.0_scaffold00061.11_5	-23,66726	8	23,1	3	-	3	0,130435	YIIIGDTEGVGK LQIWDTAGQE SFR	0,000856
P93047	Nucleosome/chromatin assembly factor	<i>Arabidopsis thaliana</i>	AT1G20696	04 Transcription	04.1907 Chromatin modification	2,00E-32	75	emb.	evm_27.model.AmTr_v1.0_scaffold00044.1_70	-13,16115	35	17,5	8	-	6	0,8	RPASAFFVFM EERFK RPASAFFVFM	0,002282
P94078	Alpha-mannosidase	<i>Arabidopsis thaliana</i>	AT3G26720	01 Metabolism	01.05 Sugars and polysaccharides	0	81	emb.	evm_27.model.AmTr_v1.0_scaffold00016.6_8	-48,99678	80	114,9	24	-	7	4	TFYTDNSGR ITEMSLSANQE R	0,006847
Q02973	Em-like protein GEA6	<i>Arabidopsis thaliana</i>	AT2G40170	11 Disease/defence	11.05 Stress responses	2,00E-33	92	emb.	evm_27.model.AmTr_v1.0_scaffold00007.1_24	-43,95663	3	10,2	2	-	2	0,057143	QGETVPPGGT GGK REQLGTGEYO	0,000571
Q04980	Desiccation-responsive protein rd29B (Low-temperature-induced 65	<i>Arabidopsis thaliana</i>	AT5G52300	11 Disease/defence	11.05 Stress responses	1,00E-22	42	emb.	evm_27.model.AmTr_v1.0_scaffold00009.2_90	-14,32239	14	51	2	-	2	0,222222	SLGESENLSA ESDKR NDQAAHPOPO	0,000571
Q05212	DNA-damage-repair/tolerance protein	<i>Arabidopsis thaliana</i>	AT3G04880	03 Cell growth/division	03.19 Recombination/repair	e-115	75	emb.	evm_27.model.AmTr_v1.0_scaffold00007.1_60	-20,50897	30	34	9	-	9	0,5625	ADANGSQAKP IK SINDCNVIALG	0,002568
Q08770	S ribosomal protein(L10	<i>Arabidopsis thaliana</i>	AT1G26910	05 Protein synthesis	05.01 Ribosomal proteins	e-109	93	emb.	evm_27.model.AmTr_v1.0_scaffold00077.1_55	-21,52743	25	25,1	7	-	3	1,4	ENVSSEALEA AR VSIQOVLLSVR	0,001997
Q0WNX3	RNA-binding KH domain-containing protein	<i>Arabidopsis thaliana</i>	AT5G15270	12 Unclear classification	12 Unclear classification	e-120	64	emb.	evm_27.model.AmTr_v1.0_scaffold00010.5_13	-19,13608	8	58,5	2	-	2	0,133333	IGETIHGCEER LLADETPGEE GDDTNSQNVV	0,000571
Q1PER6	Ascorbate peroxidase	<i>Arabidopsis thaliana</i>	AT3G09640	11 Disease/defence	11.06 Detoxification	3,00E-99	79	emb./end.	evm_27.model.AmTr_v1.0_scaffold00023.2_36	-75,35624	5	27,8	2	-	2	0,133333	TEPPVEGR YAAEDAFFA DYAEHLK	0,000571
Q1WIQ6	Glyceraldehyde-3-phosphate dehydrogenase	<i>Arabidopsis thaliana</i>	AT2G24270	02 Energy	02.01 Glycolysis	0	94	emb.	evm_27.model.AmTr_v1.0_scaffold00065.1_46	-23,84917	43	54,2	13	-	5	2,6	VQACTGEEVN K TVSIINPTTR	0,003709
Q2V3C1	Non-specific lipid-transfer protein	<i>Arabidopsis thaliana</i>	AT4G33355	09 Cell structure	09.99 Others	1,00E-18	58	emb.	evm_27.model.AmTr_v1.0_scaffold00032.7	-17,54814	12	16,5	3	-	2	0,333333	KGICFCCLK GAYNQFPQIK GAYNOFPQIK	0,000856
Q38798	Calnexin homolog	<i>Arabidopsis thaliana</i>	AT5G07340	06 Protein destination and storage	06.10 Complex assembly	e-172	71	emb.	evm_27.model.AmTr_v1.0_scaffold00016.2_79	-10,08197	11	60,4	4	-	3	0,8	EAVPESDGNQ GTSANEDEN EKEDAAAPR	0,001141
Q38867	Cyclophilin	<i>Arabidopsis thaliana</i>	AT3G56070	06 Protein destination and storage	06.01 Folding and stability	2,00E-72	82	emb.	evm_27.model.AmTr_v1.0_scaffold00009.1_09	-5,364516	17	18,6	4	-	4	0,363636	VVMELFSDITP K VFFDILIGK	0,001141
Q38882	Phospholipase D (alpha 1)	<i>Arabidopsis thaliana</i>	AT3G15730	10 Signal transduction	10.99 Others	0,00E+00	87	emb.	evm_27.model.AmTr_v1.0_scaffold00078.2_5	-31,05755	25	92	2	-	2	0,666667	ILTNESVNP SGEYAPQEQP EPDTPYER	0,000571
Q38900	Rotamase cyclophilin-3	<i>Arabidopsis thaliana</i>	AT2G16600	06 Protein destination and storage	06.01 Folding and stability	4,00E-74	83	emb./end.	evm_27.model.AmTr_v1.0_scaffold00041.1_79	-47,90715	25	18,1	5	-	4	0,5	NTNGSOFFICT AK VFFDMEIGGV	0,001427
Q38900	Rotamase cyclophilin-3	<i>Arabidopsis thaliana</i>	AT2G16600	06 Protein destination and storage	06.01 Folding and stability	8,00E-55	74	emb.	evm_27.model.AmTr_v1.0_scaffold00041.1_82	-23,29116	21	26,8	4	1	2	1,333333	VFCSSGDCTG GESIYGK VFFDITIGGVK	0,001141
Q39044	Vacuolar-processing enzyme	<i>Arabidopsis thaliana</i>	AT1G62710	06 Protein destination and storage	06.13 Proteolysis	e-179	79	emb.	evm_27.model.AmTr_v1.0_scaffold00002.2_62	-9,66254	9	50,3	3	-	3	0,2	GIIINHQPQED VYAGVPK HQADVCHAYQ	0,000856

Q39044	Vacuolar-processing enzyme	<i>Arabidopsis thaliana</i>	AT1G62710	06 Protein destination and storage	06.13 Proteolysis	e-100	81	emb.	evm_27.model.AmTr_v1.0_scaffold00002.2_63	-9,66254	29	30,1	3	-	2	0,6	GIINHPPQGED VYAGVPK HQADVCHAYO	0,000856
Q39165	Oleosin type 2	<i>Arabidopsis thaliana</i>	AT5G40420	09 Cell structure	09.99 Others	1,00E-22	63	emb./end.	evm_27.model.AmTr_v1.0_scaffold00014.1_32	-47,09798	4	15,5	2	-	2	0,076923	KMHESGGHM GQQVVGOR MHESGGHMG	0,000571
Q3E902	40S ribosomal protein (S21-2)	<i>Arabidopsis thaliana</i>	AT5G27700	05 Protein synthesis	05.01 Ribosomal proteins	3,00E-37	91	emb.	evm_27.model.AmTr_v1.0_scaffold00016.3_41	-10,47289	22	9,1	6	-	4	0,461538	MQNEEGNM DLYIPR GQFTTFALCG	0,001712
Q3EDG6	Uncharacterized protein	<i>Arabidopsis thaliana</i>	AT1G07985	13 Unclassified	13 Unclassified	0,003	55	emb.	evm_27.model.AmTr_v1.0_scaffold00103.11_5	-31,87922	3	15	2	-	2	0,068966	CRPLDTVSVE TQVK CRPLDTVSVE	0,000571
Q42112	60S acidic ribosomal protein	<i>Arabidopsis thaliana</i>	AT3G09200	05 Protein synthesis	05.01 Ribosomal proteins	e-140	94	emb.	evm_27.model.AmTr_v1.0_scaffold00029.3_68	-10,72308	13	34,3	6	-	5	0,230769	VGSSEAALLA K FAVAAAPVASE	0,001712
Q42134	20S proteasome (alpha subunit E-2)	<i>Arabidopsis thaliana</i>	AT3G14290	06 Protein destination and storage	06.13 Proteolysis	e-134	98	emb.	evm_27.model.AmTr_v1.0_scaffold00129.5_8	-22,03186	10	25,9	4	-	4	0,210526	GVNTFSPEGR VTPNNVDIAK GVNTFSPEGR	0,001141
Q42521	Glutamate decarboxylase	<i>Arabidopsis thaliana</i>	AT5G17330	01 Metabolism	01.01 Amino Acid	0	88	emb.	evm_27.model.AmTr_v1.0_scaffold00024.1_04	-10,32188	66	56,2	80	17	23	4,210527	ETQEEITR GASQIIAQYQ FIR	0,022825
Q42539	Protein-L-isoaspartate O-methyltransferase	<i>Arabidopsis thaliana</i>	AT3G48330	11 Disease/defence	11.06 Detoxification	4,00E-94	85	emb.	evm_27.model.AmTr_v1.0_scaffold00166.1_4	-15,80341	26	29	8	2	8	0,533333	VAEVMETIDR MVIPIVGNIFQD LK	0,002282
Q42605	UDP-glucose epimerase	<i>Arabidopsis thaliana</i>	AT1G12780	01 Metabolism	01.05 Sugars and polysaccharides	e-164	82	emb.	evm_27.model.AmTr_v1.0_scaffold00069.4_9	-4,040958	18	42,4	6	5	6	0,25	YFNPVGAHES GQIGEDPK FDAVIHFAGLK	0,001712
Q494P3	Dihydroxyacetone kinase	<i>Arabidopsis thaliana</i>	AT3G17770	01 Metabolism	01.05 Sugars and polysaccharides	0	86	emb.	evm_27.model.AmTr_v1.0_scaffold00024.3_9	-6,540608	32	61,2	14	11	12	0,482759	ADVSSGSYEK QILSTEAHVYP ITR	0,003994
Q56WD9	Acetyl-CoA acyltransferase	<i>Arabidopsis thaliana</i>	AT2G33150	01 Metabolism	01.06 Lipid and sterol	0	80	emb.	evm_27.model.AmTr_v1.0_scaffold00039.1_61	-17,74242	62	48	18	-	7	2,571429	FKDEIIPVDTC ASTNTQAQDC LLPMGITSENV	0,005136
Q56XG6	DEAD-box ATP-dependent RNA helicase	<i>Arabidopsis thaliana</i>	AT5G11170	04 Transcription	04.1901 General TFs	0	93	emb.	evm_27.model.AmTr_v1.0_scaffold00036.1_65	-12,7131	15	48,2	8	-	8	0,2	ILVATDLVGR VNVINVDMP E SADTYLHR	0,002282
Q56YU0	Aldehyde dehydrogenase	<i>Arabidopsis thaliana</i>	AT3G24503	20 Secondary metabolism	20.1 Phenylpropanoids/phenolics	e-146	79	emb.	evm_27.model.AmTr_v1.0_scaffold00078.1_94	-28,07077	2	42,3	2	-	2	0,05	VAFTGSTVEVGR MGGELOQYTL	0,000571
Q680A5	Ribose-phosphate pyrophosphokinase	<i>Arabidopsis thaliana</i>	AT2G42910	03 Cell growth/division	03.16 DNA synth/replication	e-154	89	emb.	evm_27.model.AmTr_v1.0_scaffold00066.1_60	-15,99068	28	35,6	9	-	9	0,5	SFDDGFPNLF NNAAHDIR LGELPADNII	0,002568
Q6DBN4	Reticulon-like protein	<i>Arabidopsis thaliana</i>	AT3G61560	09 Cell structure	09.07 ER/Golgi	4,00E-18	52	emb.	evm_27.model.AmTr_v1.0_scaffold00033.2_65	-14,70997	10	17,3	2	1	2	0,2	EQWTAEMASV LSER WWHFMGTR	0,000571
Q7DLR9	20S proteasome (beta subunit G-1)	<i>Arabidopsis thaliana</i>	AT1G56450	06 Protein destination and storage	06.13 Proteolysis	e-113	90	emb.	evm_27.model.AmTr_v1.0_scaffold00041.1_07	-13,67531	9	27,7	4	-	4	0,137931	CMLVLLYR HSLLGASGEIS DFOEILR	0,001141
Q7DLS1	20S proteasome (beta subunit B-2)	<i>Arabidopsis thaliana</i>	AT5G40580	06 Protein destination and storage	06.13 Proteolysis	e-135	93	emb.	evm_27.model.AmTr_v1.0_scaffold00088.1_26	-15,27737	11	29,4	4	-	4	0,16	ATEGPIVCDKN CEK ATEGPIVCDK	0,001141
Q84J81	HSP70 (predicted) (cytoplasm, nucleus)	<i>Arabidopsis thaliana</i>	AT3G09350	06 Protein destination and storage	06.01 Folding and stability	e-142	80	emb.	evm_27.model.AmTr_v1.0_scaffold00012.2_53	-19,68881	5	44,4	2	1	2	0,117647	IIMHLASSEDPEVR AAEVVTIVQNV	0,000571
Q84MC0	GPI-anchored protein (uncharacterized)	<i>Arabidopsis thaliana</i>	AT3G06035	12 Unclear classification	12 Unclear classification	9,00E-40	75	emb.	evm_27.model.AmTr_v1.0_scaffold00025.1_5	-26,5189	13	22,3	2	-	2	0,2	SSSNLPALSSN ENAAACLADK QLFNSLSYR	0,000571
Q84WM9	Elongation factor 1	<i>Arabidopsis thaliana</i>	AT5G12110	05 Protein synthesis	05.04 Translation factors	7,00E-60	63	emb.	evm_27.model.AmTr_v1.0_scaffold00038.7_6	-4,38934	23	24,5	4	1	3	0,571429	NLEMPGLFWG	0,001141
Q84WV1	Chaperonin (Chaperonin-60KD, ch60, CPN60)	<i>Arabidopsis thaliana</i>	AT5G26360	06 Protein destination and storage	06.01 Folding and stability	0	94	emb.	evm_27.model.AmTr_v1.0_scaffold00058.1_66	-9,998699	13	60,1	3	2	3	0,333333	TLAQNCGVNVR IAVPIDVNDR	0,000856
Q8GTY0	Translation elongation factor 1	<i>Arabidopsis thaliana</i>	AT5G60390	05 Protein synthesis	05.04 Translation factors	0	97	emb.	evm_27.model.AmTr_v1.0_scaffold00012.2_00	-60,82369	14	49,2	6	-	5	0,5	YEIITKEVSSYK VETGVLKPGM	0,001712
Q8GTY0	Translation elongation factor 1	<i>Arabidopsis thaliana</i>	AT5G60390	05 Protein synthesis	05.04 Translation factors	0	98	emb.	evm_27.model.AmTr_v1.0_scaffold00066.5_0	-59,68082	14	49,3	6	-	6	0,352941	FHINIVIGHVD SGK FHALLAFTLVG	0,001712
Q8GWR2	Uncharacterized protein	<i>Arabidopsis thaliana</i>	AT2G31985	13 Unclassified	13 Unclassified	2,00E-50	86	emb./end.	evm_27.model.AmTr_v1.0_scaffold00071.1_99	-47,08577	26	21,4	2	-	2	0,285714	QCCLYDSPDAD AR SGTLEMPGVLP	0,000571
Q8GYL5	40S ribosomal protein (S25-3)	<i>Arabidopsis thaliana</i>	AT4G34555	05 Protein synthesis	05.01 Ribosomal proteins	3,00E-25	98	emb.	evm_27.model.AmTr_v1.0_scaffold00011.65	-6,154902	13	12	5	1	3	0,416667	LITPSILSDR MISSHASQIYI TR	0,001427

Q8H0X6	Cysteine proteinase inhibitor	<i>Arabidopsis thaliana</i>	AT3G12490	11 Disease/defence	11.02 Defence-related	2,00E-75	82	emb./end.	evm_27.model.AmTr_v1.0_scaffold00101.7	-51,52199	11	23.2	2	-	2	0,25	AEVIEESAK EFNHVGDSSL TSSDLGAK	0,000571
Q8H103	Phosphoglucose isomerase	<i>Arabidopsis thaliana</i>	AT4G24620	02 Energy	02.01 Glycolysis	0	92	emb./end.	evm_27.model.AmTr_v1.0_scaffold00135.2	-40,67403	43	68,4	13	-	5	2,6	IVAHMAANDR GAIANPEGR GSTDQHAYIQ	0,003709
Q8H107	2-oxoglutarate dehydrogenase	<i>Arabidopsis thaliana</i>	AT4G26910	02 Energy	02.10 TCA pathway	e-162	76	emb.	evm_27.model.AmTr_v1.0_scaffold00165.2	-13,43797	55	49	12	-	9	1	GLVVPVIR EGD TVVPGTI AVISR	0,003424
Q8H173	40S ribosomal protein (Sa-2)	<i>Arabidopsis thaliana</i>	AT3G04770	05 Protein synthesis	05.01 Ribosomal proteins	e-114	78	emb.	evm_27.model.AmTr_v1.0_scaffold00010.3	-14,84207	15	32,8	7	-	7	0,241379	HTPGTFTNQL QTSYSEPR HTPGTFTNQL	0,001997
Q8H173	40S ribosomal protein (Sa-2)	<i>Arabidopsis thaliana</i>	AT3G04770	05 Protein synthesis	05.01 Ribosomal proteins	e-110	76	emb.	evm_27.model.AmTr_v1.0_scaffold00041.5	-17,22228	42	34	7	-	7	0,7	FAHYIGAHPIA GR HTPGTFTNQL	0,001997
Q8L742	Amine oxidase	<i>Arabidopsis thaliana</i>	AT4G12290	20 Secondary metabolism	20.5 Amines	0	76	emb.	evm_27.model.AmTr_v1.0_scaffold00069.6	-40,99756	9	82,5	2	-	2	0,666667	VGLSGILMIK HTECPITGMQI R	0,000571
Q8L831	MutT/nudix family protein	<i>Arabidopsis thaliana</i>	AT1G79690	20 Secondary metabolism	20.2 Terpenoids	0	79	emb./end.	evm_27.model.AmTr_v1.0_scaffold00019.5	-57,37792	10	86	2	-	2	0,333333	VEGAVESLSR EILTQAQGDK PAAASLLDK	0,000571
Q8LD27	20S proteasome (beta subunit A-1)	<i>Arabidopsis thaliana</i>	AT4G31300	06 Protein destination and storage	06.13 Proteolysis	e-106	88	emb.	evm_27.model.AmTr_v1.0_scaffold00025.2	-19,16342	10	24,7	4	-	4	0,2	TSTGMYVANR SGSAADSOVV SDYVR	0,001141
Q8LDH6	Thaumatococcus putative	<i>Arabidopsis thaliana</i>	AT2G28790	11 Disease/defence	11.01 Resistance genes	5,00E-57	61	emb.	evm_27.model.AmTr_v1.0_scaffold00124.2	-5,912219	3	26,4	2	-	2	0,076923	SACEAFQND YCCR TCPAQLVVR	0,000571
Q8LFH1	Aldose 1-epimerase-like protein	<i>Arabidopsis thaliana</i>	AT3G47800	01 Metabolism	01.05 Sugars and polysaccharides	e-105	71	emb.	evm_27.model.AmTr_v1.0_scaffold00010.3	-19,20723	25	40,6	19	-	16	1,266667	FVLNGQAYR VLELWTDNVG LOFYTGNNMLN	0,005421
Q8RUF8	Omega-amidase	<i>Arabidopsis thaliana</i>	AT5G12040	01 Metabolism	01.01 Amino Acid	e-140	84	emb.	evm_27.model.AmTr_v1.0_scaffold00024.1	-26,6164	70	33,7	179	37	43	8,523809	ATAYKPEEAR AVDNIQVYATC SPAR	0,051070
Q8VXZ9	Polyadenylate-binding protein	<i>Arabidopsis thaliana</i>	AT5G19350	04 Transcription	04.22 mRNA processing	3,00E-96	59	emb.	evm_27.model.AmTr_v1.0_scaffold00062.1	-20,48149	17	55	7	-	4	0,636364	FGDNEQLR IIQTVNGTTPM NTEQFSR	0,001997
Q8VYK6	40S ribosomal protein (S4-3)	<i>Arabidopsis thaliana</i>	AT5G58420	05 Protein synthesis	05.01 Ribosomal proteins	e-134	96	emb.	evm_27.model.AmTr_v1.0_scaffold00041.3	-16,74127	14	30,2	6	-	4	0,75	LGNVFTIGK EVISILMQR TDKTYPAGFM	0,001712
Q8VYS0	Cysteine protease (papain)	<i>Arabidopsis thaliana</i>	AT3G54940	06 Protein destination and storage	06.13 Proteolysis	e-130	77	emb./end.	evm_27.model.AmTr_v1.0_scaffold00022.3	-35,96054	18	38,4	4	-	3	0,363636	HVNHGVLVVG YGAK FAGGLEDFENS	0,001141
Q8VZC3	Aldehyde dehydrogenase	<i>Arabidopsis thaliana</i>	AT5G62530	11 Disease/defence	11.06 Detoxification	0	85	emb.	evm_27.model.AmTr_v1.0_scaffold00078.9	-9,050611	8	61,3	2	-	2	0,153846	SVNGTTYAQIR FLENFSGDQV R	0,000571
Q8W034	Heterogeneous nuclear ribonucleoprotein	<i>Arabidopsis thaliana</i>	AT4G14300	04 Transcription	04.22 mRNA processing	5,00E-81	76	emb.	evm_27.model.AmTr_v1.0_scaffold00067.1	-14,73993	23	47,2	5	2	5	0,416667	NFGAGSGAAA GSNVR GFGFVVFVTD	0,001427
Q8W112	Beta-D-glucan exohydrolase-like protein	<i>Arabidopsis thaliana</i>	AT5G20950	01 Metabolism	01.05 Sugars and polysaccharides	0	81	emb.	evm_27.model.AmTr_v1.0_scaffold00004.1	-14,29757	25	65,8	22	-	15	0,709677	FQMGLFENPL ADLSLADQLG SQEHR	0,006277
Q8W112	Beta-D-glucan exohydrolase-like protein	<i>Arabidopsis thaliana</i>	AT5G20950	01 Metabolism	01.05 Sugars and polysaccharides	0	79	emb.	evm_27.model.AmTr_v1.0_scaffold00004.1	-15,51617	56	68,3	23	-	10	2,3	IGQMTQIDR STVDPHTEVV YQENPDPSL	0,006562
Q8W4L0	Calmodulin-like protein	<i>Arabidopsis thaliana</i>	AT3G10300	10 Signal transduction	10.04 Mediators	2,00E-29	92	emb.	evm_27.model.AmTr_v1.0_scaffold00053.1	-12,38216	17	15,8	2	-	2	0,333333	ALSSYNQSF LR TVHLLMFLFTN	0,000571
Q93VB8	40S ribosomal protein (S2-2)	<i>Arabidopsis thaliana</i>	AT1G58684	05 Protein synthesis	05.01 Ribosomal proteins	e-111	92	emb.	evm_27.model.AmTr_v1.0_scaffold00002.2	-30,86073	28	30,3	6	-	4	1	VLGFAGIEDVF TSSR SPFQEFDFL	0,001712
Q93VH5	Rossmann-fold NAD(P) binding domain-containing protein	<i>Arabidopsis thaliana</i>	AT5G10730	12 Unclear classification	12 Unclear classification	e-106	80	emb.	evm_27.model.AmTr_v1.0_scaffold00006.2	-12,00349	14	32	2	-	2	0,285714	INGTANINAIR LVLGGNGFV GSHVCR	0,000571
Q93W30	SWIB/MDM2 domain-containing protein	<i>Arabidopsis thaliana</i>	AT2G35605	04 Transcription	04.1904 Specific TFs	4,00E-30	66	emb.	evm_27.model.AmTr_v1.0_scaffold00011.19	-12,83003	19	13,7	6	1	3	0,75	ANNLQNPADR STANPSLLKPS QPK	0,001712
Q93WN0	Selenium-binding protein (Protein EMBRYO SAC	<i>Arabidopsis thaliana</i>	AT4G14040	03 Cell growth/division	03.99 Other	0,00E+00	89	emb.	evm_27.model.AmTr_v1.0_scaffold00021.4	-23,07199	29	54,8	6	3	4	0,666667	IVVVDTQSPR ATGLTEPLSSD HK	0,001712
Q93Y35	26S proteasome (regulatory subunit RPN7)	<i>Arabidopsis thaliana</i>	AT4G24820	06 Protein destination and storage	06.13 Proteolysis	e-163	96	emb.	evm_27.model.AmTr_v1.0_scaffold00007.2	-14,50585	21	35,3	3	-	2	1	IADAEENLGES EVR SFFSAFAGLTE	0,000856
Q93Y35	26S proteasome (regulatory subunit RPN7)	<i>Arabidopsis thaliana</i>	AT4G24820	06 Protein destination and storage	06.13 Proteolysis	0	91	emb.	evm_27.model.AmTr_v1.0_scaffold00049.4	-14,50585	10	44,4	2	1	2	0,25	IADAEENLGES EVR SFFSAFAGLTE	0,000571

Q93Z51	Isochorismatase family protein	<i>Arabidopsis thaliana</i>	AT3G16190	20 Secondary metabolism	20.3 Alkaloids	2,00E-65	75	emb.	evm_27.model.AmTr_v1.0_scaffold00067.1_82	-4,311225	5	21,1	3	-	2	0,1875	ERGALIVVVV R GALIVVVVV	0,000856
Q940P8	T-complex protein (cpn60 chaperonin family protein)	<i>Arabidopsis thaliana</i>	AT5G20890	06 Protein destination and storage	06.01 Folding and stability	0	94	emb.	evm_27.model.AmTr_v1.0_scaffold00149.8	-20,81264	51	57,2	5	-	4	1,25	VAGIEAAEKEK ILSQDKEHFAK GASSHVLDFA	0,001427
Q941A4	Uncharacterized protein	<i>Arabidopsis thaliana</i>	AT5G45690	13 Unclassified	13 Unclassified	1,00E-74	70	emb./end.	evm_27.model.AmTr_v1.0_scaffold00162.9	-122,382	12	28,9	2	-	2	0,222222	QIQQHVCVSFR IFESLPDEEK TGLWVNPR	0,000571
Q944A2	Alba DNA/RNA-binding protein	<i>Arabidopsis thaliana</i>	AT1G20220	04 Transcription	04.1907 Chromatin modification	6,00E-51	78	emb.	evm_27.model.AmTr_v1.0_scaffold00017.1_96	-6,754488	52	28,4	8	-	5	2	VEKPRPDTPIN ENEIR TVMIAELIK	0,002282
Q944G9	Fructose-bisphosphate aldolase (chloroplastic)	<i>Arabidopsis thaliana</i>	AT4G38970	02 Energy	02.01 Glycolysis	0	90	emb.	evm_27.model.AmTr_v1.0_scaffold00017.6_0	-10,25181	43	42,4	13	-	5	2,6	GILAMDESNA T CGK LASIGLENTEA	0,003709
Q945P1	Hydroxyproline-rich glycoprotein-like protein	<i>Arabidopsis thaliana</i>	AT2G39050	09 Cell structure	09.01 Cell wall	4,00E-45	79	emb.	evm_27.model.AmTr_v1.0_scaffold00119.23	-8,134256	7	37,8	3	-	3	0,176471	SRLPQGGDVR LNLDFAFNK K	0,000856
Q94AM1	Zinc-like metalloproteases family protein	<i>Arabidopsis thaliana</i>	AT5G65620	06 Protein destination and storage	06.13 Proteolysis	0	90	emb.	evm_27.model.AmTr_v1.0_scaffold00046.1_60	-10,62893	16	79,2	3	-	2	1,5	GREPSPDALL R AIQESSWQA	0,000856
Q94CC6	Serine carboxypeptidase	<i>Arabidopsis thaliana</i>	AT4G36195	06 Protein destination and storage	06.13 Proteolysis	0	84	emb.	evm_27.model.AmTr_v1.0_scaffold00182.2_9	-25,79096	14	54,3	4	-	2	1	LLDNEIAVK YYINTPGQLET YDR	0,001141
Q94JT5	Cyclase	<i>Arabidopsis thaliana</i>	AT4G35220	12 Unclear classification	12 Unclear classification	2,00E-97	88	emb.	evm_27.model.AmTr_v1.0_scaffold00047.1_74	-10,81275	20	29	2	-	2	0,333333	LIGAEGSPIR DGAQWLVDNT DIK	0,000571
Q94JT5	Cyclase	<i>Arabidopsis thaliana</i>	AT4G35220	12 Unclear classification	12 Unclear classification	4,00E-99	88	emb.	evm_27.model.AmTr_v1.0_scaffold00051.6_0	-10,81275	20	29,4	2	-	2	0,333333	LIGAEGSPIR DGAQWLVDNT DIK	0,000571
Q94K05	Chaperonin (Chaperonin-60kD, ch60, CPN60)	<i>Arabidopsis thaliana</i>	AT3G03960	06 Protein destination and storage	06.01 Folding and stability	0	92	emb.	evm_27.model.AmTr_v1.0_scaffold00004.6_5	-16,30627	28	58,6	3	1	2	0,75	AVDDGVNTYK VAVFSGGVD SATDTK	0,000856
Q94KE3	Pyruvate kinase	<i>Arabidopsis thaliana</i>	AT3G52990	02 Energy	02.01 Glycolysis	0	95	emb.	evm_27.model.AmTr_v1.0_scaffold00040.2_85	-18,85379	43	57,3	13	-	5	2,6	HPAESTSATN ESVLK VVDSDMTDNL	0,003709
Q96251	ATP synthase	<i>Arabidopsis thaliana</i>	AT5G13450	02 Energy	02.13 Respiration	4,00E-53	63	emb.	evm_27.model.AmTr_v1.0_scaffold00022.3_92	-6,068542	10	27,7	11	-	6	0,407407	YATALFSAAK VPLVLFVPG K	0,003138
Q96270	Late embryogenesis abundant protein (LEA)	<i>Arabidopsis thaliana</i>	AT1G52690	11 Disease/defence	11.05 Stress responses	1,00E-11	57	emb.	evm_27.model.AmTr_v1.0_scaffold00039.1_46	-21,87236	14	14,4	2	-	2	0,285714	SEDISHSAGET K SAAQGEVETV	0,000571
Q96300	14-3-3-like protein GF14 nu (General regulatory factor 7)	<i>Arabidopsis thaliana</i>	AT3G02520	04 Transcription	04.1901 General TFs	e-132	94	emb.	evm_27.model.AmTr_v1.0_scaffold00038.2_0	-61,20176	22	29,7	4	2	3	0,4	TVDVEELTVEE R IISSEIQKEFSR	0,001141
Q96321	Importin	<i>Arabidopsis thaliana</i>	AT3G06720	08 Intracellular traffic	08.01 Nuclear	0,00E+00	89	emb.	evm_27.model.AmTr_v1.0_scaffold00147.1_7	-28,7334	22	58,3	3	-	2	0,375	FVQFLTR SPPIEEVIEAG VVPR	0,000856
Q96520	Peroxidase	<i>Arabidopsis thaliana</i>	AT1G71695	11 Disease/defence	11.06 Detoxification	e-125	79	emb.	evm_27.model.AmTr_v1.0_scaffold00017.1_81	-39,49575	3	38	2	-	2	0,074074	DLSNFATR CGHTVSCSDIT ALAAAR	0,000571
Q96520	Peroxidase	<i>Arabidopsis thaliana</i>	AT1G71695	11 Disease/defence	11.06 Detoxification	e-126	80	emb.	evm_27.model.AmTr_v1.0_scaffold00017.1_82	-24,47475	5	38,3	2	-	2	0,125	TPNVFDNKYY VDLMNR ESVFLAGGPE	0,000571
Q9ASR1	Translation elongation factor 2	<i>Arabidopsis thaliana</i>	AT1G56070	05 Protein synthesis	05.04 Translation factors	0	93	emb.	evm_27.model.AmTr_v1.0_scaffold00032.9_3	-77,63349	29	93,9	5	-	5	0,416667	NATITNEEVD AHPIR RVIYASQLTAT	0,001427
Q9C4Z6	Guanine nucleotide-binding protein (subunit beta-like protein B)	<i>Arabidopsis thaliana</i>	AT1G48630	10 Signal transduction	10.04 Mediators	e-151	86	emb.	evm_27.model.AmTr_v1.0_scaffold00105.2_6	-33,9679	4	34,7	2	-	2	0,105263	DKSVLLWHLT K GHSMDVMTAIA	0,000571
Q9C550	2-isopropylmalate synthase	<i>Arabidopsis thaliana</i>	AT1G74040	01 Metabolism	01.01 Amino Acid	0	88	emb.	evm_27.model.AmTr_v1.0_scaffold00066.2_1	-7,177178	66	67,9	64	-	20	16	DGEQSPGAS MTSK SDREFLYLVG	0,018260
Q9C5C4	Acetylornithine deacetylase	<i>Arabidopsis thaliana</i>	AT4G17830	01 Metabolism	01.02 Nitrogen and sulphur	0	89	emb.	evm_27.model.AmTr_v1.0_scaffold00149.8_2	-7,394695	41	48,4	19	11	15	0,95	HVSIVVEGR GNVIVYEPGTE PDR	0,005421
Q9C5U3	26S proteasome (AAA-ATPase subunit RPT6a)	<i>Arabidopsis thaliana</i>	AT5G19990	06 Protein destination and storage	06.13 Proteolysis	0	94	emb.	evm_27.model.AmTr_v1.0_scaffold00007.4_05	-10,34199	9	44,7	4	-	4	0,222222	TMLELLNLQD	0,001141
Q9C5U3	26S proteasome (AAA-ATPase subunit RPT6a)	<i>Arabidopsis thaliana</i>	AT5G19990	06 Protein destination and storage	06.13 Proteolysis	0	94	emb.	evm_27.model.AmTr_v1.0_scaffold00045.3_07	-10,34199	8	44,6	4	-	4	0,285714	TMLELLNLQD	0,001141
Q9C5W6	General regulatory factor	<i>Arabidopsis thaliana</i>	AT1G26480	04 Transcription	04.1901 General TFs	e-120	94	emb.	evm_27.model.AmTr_v1.0_scaffold00110.99	-3,259637	21	29,5	8	-	7	0,444444	AYQAASNTAN TDLASTHPIR QKVEELSK	0,002282

Q9C6D2	Methylthioribose kinase	<i>Arabidopsis thaliana</i>	AT1G49820	01 Metabolism	01.01 Amino Acid	e-171	81	emb.	evm_27.model.AmTr_v1.0_scaffold00015.4_2	-5,053057	29	48,4	28	5	6	4	QALPYIR TLFYTSLLYLS TTDHK	0,007989
Q9C6D2	Methylthioribose kinase	<i>Arabidopsis thaliana</i>	AT1G49820	01 Metabolism	01.01 Amino Acid	8,00E-61	77	emb.	evm_27.model.AmTr_v1.0_scaffold00015.4_3	-5,053057	47	18,5	50	-	23	2,941176	QALPYIR TLFYTSLLYLS TTDHK	0,014265
Q9C6E4	Phosphate-induced protein (Phi-1)	<i>Arabidopsis thaliana</i>	AT1G35140	12 Unclear classification	12 Unclear classification	1,00E-99	73	emb.	evm_27.model.AmTr_v1.0_scaffold00038.2_37	-56,55116	13	32,6	2	-	2	0,153846	VSGASYNANG VNGR ALVQOPPLVLN	0,000571
Q9C7F4	Putative uncharacterized protein F13K9	<i>Arabidopsis thaliana</i>	AT1G27990	12 Unclear classification	12 Unclear classification	4,00E-93	79	emb.	evm_27.model.AmTr_v1.0_scaffold00086.6_3	-15,42822	8	29,7	2	-	2	0,166667	TDSGRPEAPD PAAK SGLSLAVAPR	0,000571
Q9C7F5	Nuclear transport factor 2	<i>Arabidopsis thaliana</i>	AT1G27970	08 Intracellular traffic	08.01 Nuclear	1,00E-53	86	emb.	evm_27.model.AmTr_v1.0_scaffold00013.3_5	-21,09196	8	13,8	3	-	3	0,214286	AGLASLYQDN SMLTFEGQK ESQMFHLLQ	0,000856
Q9C7F7	GPI-anchored protein (uncharacterized)	<i>Arabidopsis thaliana</i>	AT1G27950	12 Unclear classification	12 Unclear classification	3,00E-18	54	emb.	evm_27.model.AmTr_v1.0_scaffold00013.6_7	-7,868895	20	19,6	2	-	2	0,333333	LTDVEER TLQLPTVCK SVLCLCYLLR	0,000571
Q9C820	Ras-related protein	<i>Arabidopsis thaliana</i>	AT1G52280	08 Intracellular traffic	08.07 Vesicular	e-111	97	emb.	evm_27.model.AmTr_v1.0_scaffold00109.2_7	-6,806876	12	23	3	-	3	0,375	VILGDSGVGK TSLMNYVNR VILGDSGVGK	0,000856
Q9C9C5	60S ribosomal protein (L6-3)	<i>Arabidopsis thaliana</i>	AT1G74050	05 Protein synthesis	05.01 Ribosomal proteins	2,00E-74	75	emb.	evm_27.model.AmTr_v1.0_scaffold00022.2_63	-17,73745	7	25,9	6	-	6	0,157895	KPAAPKPEEK PPK AIEAVPDLKPY	0,001712
Q9C9U9	Thaumatococcus putative	<i>Arabidopsis thaliana</i>	AT1G73620	11 Disease/defence	11.01 Resistance genes	3,00E-92	82	emb.	evm_27.model.AmTr_v1.0_scaffold00010.6_4	-15,65896	3	25,3	2	-	2	0,076923	AYSYAYDDPTS IVTCK ILPNQJESLK	0,000571
Q9CA83	Malate dehydrogenase	<i>Arabidopsis thaliana</i>	AT1G79750	02 Energy	02.10 TCA pathway	0	87	emb.	evm_27.model.AmTr_v1.0_scaffold00056.8_7	-23,95607	18	71,9	11	-	10	0,314286	QYQVPLQK LPRPENLVAYA EFCMYSPPYR	0,003138
Q9CAR3	Cystathionine beta-synthase (CBS) protein	<i>Arabidopsis thaliana</i>	AT1G47271	01 Metabolism	01.01 Amino acid	e-124	64	emb.	evm_27.model.AmTr_v1.0_scaffold00078.9_8	-15,08009	68	55,1	26	-	19	1,625	VIEIAPHTSIAD TVR NFITQSAVIHG	0,007418
Q9CAV0	40S ribosomal protein (S3a-1)	<i>Arabidopsis thaliana</i>	AT3G04840	05 Protein synthesis	05.01 Ribosomal proteins	e-112	89	emb.	evm_27.model.AmTr_v1.0_scaffold00002.6_35	-16,10855	18	30,3	6	1	6	0,3	APSFNVNR TCYAQTQIR EIMVNOATSC	0,001712
Q9FF39	Lipid transfer protein	<i>Arabidopsis thaliana</i>	AT5G38170	07 Transporters	07.13 Lipids	2,00E-12	54	emb.	evm_27.model.AmTr_v1.0_scaffold00044.2_25	-11,30309	9	9,9	3	-	3	0,15	YSGIINSPNGK LLDQQSCYQK YLKDPR	0,000856
Q9FF40	2S albumin	<i>Arabidopsis thaliana</i>	AT5G38160	06 Protein destination and storage	06.20 Storage proteins	2,7	36	emb./end.	evm_27.model.AmTr_v1.0_scaffold00005.2_12	-49,01415	6	16,8	3	-	3	0,130435	RCCEKENLR LENIREECR SLMSEAGQGE	0,000856
Q9FG31	Late embryogenesis abundant protein (LEA)	<i>Arabidopsis thaliana</i>	AT5G06760	11 Disease/defence	11.05 Stress responses	4,00E-09	48	emb./end.	evm_27.model.AmTr_v1.0_scaffold00022.1_82	-80,4304	4	14,8	2	-	2	0,064516	TAGSHPIGHNT GTGGTTTR ETAGNVAASA	0,000571
Q9FH31	2S albumin	<i>Arabidopsis thaliana</i>	AT5G54740	06 Protein destination and storage	06.20 Storage proteins	0,045	55	emb./end.	evm_27.model.AmTr_v1.0_scaffold00005.2_15	-44,63863	6	17,2	3	-	3	0,115385	CCEQLENMRE ECR RCCEQLENMR	0,000856
Q9FIF3	40S ribosomal protein (S8-2)	<i>Arabidopsis thaliana</i>	AT5G59240	05 Protein synthesis	05.01 Ribosomal proteins	8,00E-76	72	emb.	evm_27.model.AmTr_v1.0_scaffold00055.7_2	-11,57193	22	24,5	6	-	4	2	EGEEAEAGATE EVKK EGEEAEAGATE	0,001712
Q9FIF3	40S ribosomal protein (S8-2)	<i>Arabidopsis thaliana</i>	AT5G59240	05 Protein synthesis	05.01 Ribosomal proteins	3,00E-73	70	emb.	evm_27.model.AmTr_v1.0_scaffold00109.1_8	-17,61618	12	24,6	6	-	5	0,428571	LDTGNYSWGS	0,001712
Q9FIK0	Phosphofructokinase	<i>Arabidopsis thaliana</i>	AT5G47810	02 Energy	02.01 Glycolysis	0	84	emb.	evm_27.model.AmTr_v1.0_scaffold00061.1_34	-5,517127	43	51,4	13	-	5	2,6	TVDNDVGIHQR GGLFEFLDQR	0,003709
Q9FJA6	40S ribosomal protein (S3-3)	<i>Arabidopsis thaliana</i>	AT5G35530	05 Protein synthesis	05.01 Ribosomal proteins	e-119	94	emb.	evm_27.model.AmTr_v1.0_scaffold00024.21_1	-17,99697	11	26	6	-	5	0,272727	ELAEDGYSGV EVR KFVADGVFFA	0,001712
Q9FJA6	40S ribosomal protein (S3-3)	<i>Arabidopsis thaliana</i>	AT5G35530	05 Protein synthesis	05.01 Ribosomal proteins	e-118	94	emb.	evm_27.model.AmTr_v1.0_scaffold00030.9_8	-17,99697	20	26	6	-	6	0,285714	ELAEDGYSGV EVR KFVADGVFFA	0,001712
Q9FJE8	Histone H2A.7	<i>Arabidopsis thaliana</i>	AT5G59870	09 Cell structure	09.13 Chromosomes	2,00E-34	78	emb.	evm_27.model.AmTr_v1.0_scaffold00057.2_72	-6,414088	4	15,5	2	-	2	0,125	LLAGVITIASGG VLPNIHSVLLP K	0,000571
Q9FJF1	Ras-related protein	<i>Arabidopsis thaliana</i>	AT5G59840	08 Intracellular traffic	08.07 Vesicular	9,00E-87	83	emb.	evm_27.model.AmTr_v1.0_scaffold00168.1_2	-6,164944	12	24	3	-	3	0,375	GQALADEYGIK	0,000856
Q9FJH0	Ras-related protein	<i>Arabidopsis thaliana</i>	AT5G60860	08 Intracellular traffic	08.07 Vesicular	e-118	97	emb.	evm_27.model.AmTr_v1.0_scaffold00021.1_50	-13,02541	12	24,2	3	-	3	0,3	VVLIGDSGVGK	0,000856
Q9FJH0	Ras-related protein	<i>Arabidopsis thaliana</i>	AT5G60860	08 Intracellular traffic	08.07 Vesicular	e-113	95	emb.	evm_27.model.AmTr_v1.0_scaffold00108.3_9	-13,02541	7	24,2	3	-	2	0,176471	VVLIGDSGVGK	0,000856

Q9FJ5	Glucose-6-phosphate dehydrogenase, cytoplasmic	<i>Arabidopsis thaliana</i>	AT5G40760	02 Energy	02.07 Pentose phosphate	0	92	emb.	evm_27.model.AmTr_v1.0_scaffold00049.6_8	-41,1825	31	59,8	11	2	11	0,578947	SDSFSETSSLK GNEASSSEFS AVSK	0,003138
Q9FJW0	RuvB DNA helicase-like protein	<i>Arabidopsis thaliana</i>	AT5G67630	03 Cell growth/division	03.16 DNA synth/replication	0	90	emb.	evm_27.model.AmTr_v1.0_scaffold00049.5_0	-7,517698	19	51,4	9	-	7	0,529412	AVLIAGOPGTG K VYQLFLDVKR	0,002568
Q9FKH1	Transcriptional regulator STERILE APETALA	<i>Arabidopsis thaliana</i>	AT5G35770	04 Transcription	04.1904 Specific TFs	7,00E-90	57	emb.	evm_27.model.AmTr_v1.0_scaffold00028.2_4	-14,78728	19	48,5	7	1	3	0,875	VGAGGLVAC TESR YLALGFLDGS	0,001997
Q9FKK7	Xylose isomerase	<i>Arabidopsis thaliana</i>	AT5G57655	01 Metabolism	01.05 Sugars and polysaccharides	0	89	emb.	evm_27.model.AmTr_v1.0_scaffold00019.2_26	-11,80041	70	53	19	-	9	3,166667	YGLAGEFK FFQAAYEYK ESTDVEDIFLA	0,005421
Q9FL61	Uncharacterized protein	<i>Arabidopsis thaliana</i>	AT5G24130	12 Unclear classification	12 Unclear classification	9,00E-10	61	emb.	evm_27.model.AmTr_v1.0_scaffold00015.11_8	-9,829152	5	13,3	2	-	2	0,105263	EGRLPLLLDE QR EGRLPLLLDE	0,000571
Q9FLH2	2-oxoglutarate dehydrogenase	<i>Arabidopsis thaliana</i>	AT5G65750	02 Energy	02.10 TCA pathway	0	90	emb.	evm_27.model.AmTr_v1.0_scaffold00168.1_9	-5,137868	24	115,7	11	-	5	5,5	SADLGVESIVI GMSHR LIWSTQFENFL	0,003138
Q9FL4	Subtilisin serine protease	<i>Arabidopsis thaliana</i>	AT5G51750	06 Protein destination and storage	06.13 Proteolysis	0	70	emb.	evm_27.model.AmTr_v1.0_scaffold00069.1_75	-36,24484	7	84,1	2	1	2	0,1	CEASPDFTPE VNCNKK TVTNVGSFVS	0,000571
Q9FM19	Hypersensitive-induced response protein	<i>Arabidopsis thaliana</i>	AT5G62740	11 Disease/defence	11.01 Resistance genes	e-150	95	emb.	evm_27.model.AmTr_v1.0_scaffold00078.6_9	-26,21967	6	31,2	2	-	2	0,125	SSSVFIPHGPG AVR QAMNEINAAS	0,000571
Q9FM19	Hypersensitive-induced response protein	<i>Arabidopsis thaliana</i>	AT5G62740	11 Disease/defence	11.01 Resistance genes	e-132	97	emb.	evm_27.model.AmTr_v1.0_scaffold00078.7_0	-26,51907	4	27,9	2	-	2	0,08	TQIQAYVFDVI R AMNEINAASR	0,000571
Q9FMR9	TATA box-binding protein-interacting protein	<i>Arabidopsis thaliana</i>	AT5G22330	11 Disease/defence	11.02 Defence-related	0	90	emb.	evm_27.model.AmTr_v1.0_scaffold00175.2_7	-16,71688	3	49,5	2	-	2	0,064516	ALLLAGAPGT GK HAVQLI SPASI	0,000571
Q9FN21	FAD-dependent oxidoreductase-like protein	<i>Arabidopsis thaliana</i>	AT5G67290	13 Unclassified	13 Unclassified	e-108	71	emb.	evm_27.model.AmTr_v1.0_scaffold00092.1_42	-14,58436	4	40,6	2	-	2	0,066667	VVAGGVSPWI DGPVR ASIVDLEFPNP	0,000571
Q9FNN1	Pyruvate kinase	<i>Arabidopsis thaliana</i>	AT5G08570	02 Energy	02.01 Glycolysis	0	95	emb.	evm_27.model.AmTr_v1.0_scaffold00171.3_0	-8,26865	43	55,1	13	-	5	2,6	ATLIVLTR STPLPMSPLE SLASSAVR	0,003709
Q9FNP8	40S ribosomal protein (S19-3)	<i>Arabidopsis thaliana</i>	AT5G61170	05 Protein synthesis	05.01 Ribosomal proteins	1,00E-63	92	emb.	evm_27.model.AmTr_v1.0_scaffold00045.2_80	-7,619789	11	15,8	6	-	6	0,1875	HILQOLEK ELAPYDWDY FIR	0,001712
Q9FNR1	Glycine-rich RNA-binding protein	<i>Arabidopsis thaliana</i>	AT5G61030	04 Transcription	04.22 mRNA processing	3,00E-41	83	emb.	evm_27.model.AmTr_v1.0_scaffold00154.7_0	-17,20761	21	30,2	7	-	7	0,388889	VNYATDR EAFASYGEVIE AR	0,001997
Q9FWA3	6-Phosphogluconate dehydrogenase	<i>Arabidopsis thaliana</i>	AT3G02360	02 Energy	02.07 Pentose phosphate	0	94	emb.	evm_27.model.AmTr_v1.0_scaffold00061.2_03	-15,6382	64	53,8	13	-	8	1,3	LPANLVQAQR VAAQVPDSGP CVTYIGK	0,003709
Q9FX54	Glyceraldehyde-3-phosphate dehydrogenase	<i>Arabidopsis thaliana</i>	AT1G13440	02 Energy	02.01 Glycolysis	3,00E-51	82	emb./end.	evm_27.model.AmTr_v1.0_scaffold00177.2_1	-22,35972	41	15,5	4	2	4	1	TLFGDKPVTV FGVR NPEEIPWGET	0,001141
Q9FX54	Glyceraldehyde-3-phosphate dehydrogenase	<i>Arabidopsis thaliana</i>	AT1G13440	02 Energy	02.01 Glycolysis	8,00E-95	86	emb./end.	evm_27.model.AmTr_v1.0_scaffold00177.2_4	-56,13214	42	24,7	13	5	7	1,857143	AAGFNIIPSS T TLLFGDKPVTV	0,003709
Q9FY64	40S ribosomal protein (S15-4)	<i>Arabidopsis thaliana</i>	AT5G09510	05 Protein synthesis	05.01 Ribosomal proteins	6,00E-68	88	emb.	evm_27.model.AmTr_v1.0_scaffold00022.5_7	-12,79697	13	17,2	5	1	3	0,333333	EAPPGEKPEP VR EAPPGEKPEP	0,001427
Q9FZE0	Beta-glucosidase	<i>Arabidopsis thaliana</i>	AT1G26560	01 Metabolism	01.05 Sugars and polysaccharides	e-129	86	emb.	evm_27.model.AmTr_v1.0_scaffold00110.65_0	-4,910095	15	35	18	-	16	0,295082	CSVLLHLFCR ASSIWLIVPH GIR	0,005136
Q9LDZ0	HSP70 (Heat shock cognate 70 kDa protein)	<i>Arabidopsis thaliana</i>	AT5G09590	06 Protein destination and storage	06.01 Folding and stability	0	92	emb.	evm_27.model.AmTr_v1.0_scaffold00046.1_70	-18,13021	5	71,9	2	1	2	0,125	TTPSVVAFNPK ATRSKYESLVNHLI ER	0,000571
Q9LEV3	Cystathionine beta-synthase (CBS) protein	<i>Arabidopsis thaliana</i>	AT1G47271	01 Metabolism	01.01 Amino acid	2,00E-89	85	emb.	evm_27.model.AmTr_v1.0_scaffold00045.2_2	-11,36091	62	27,6	31	-	19	1,47619	AMQLMTDNR LEEHGFESTTI SDVLK	0,008845
Q9LF88	Late embryogenesis abundant protein (LEA)	<i>Arabidopsis thaliana</i>	AT3G53040	11 Disease/defence	11.05 Stress responses	4,00E-29	56	emb.	evm_27.model.AmTr_v1.0_scaffold00002.3_88	-18,01729	4	33,9	2	-	2	0,086957	AGEANDSAAD ATR AGEANDSAAD	0,000571
Q9LFA3	Monodehydroascorbate reductase	<i>Arabidopsis thaliana</i>	AT3G52880	11 Disease/defence	11.06 Detoxification	e-175	84	emb./end.	evm_27.model.AmTr_v1.0_scaffold00069.1_93	-70,47884	10	47,1	2	-	2	0,285714	EAVAPYERPAL SK EAVAPYERPAL	0,000571
Q9LHL7	Aha1 domain-containing protein (HSP90 co-activator)	<i>Arabidopsis thaliana</i>	AT3G12050	06 Protein destination and storage	06.01 Folding and stability	e-137	79	emb.	evm_27.model.AmTr_v1.0_scaffold00024.1_27	-10,88306	13	39,1	2	1	2	0,222222	LTQTDVPEED RYGNATVVEN TER	0,000571
Q9LHT0	Short chain alcohol dehydrogenase	<i>Arabidopsis thaliana</i>	AT5G06060	02 Energy	02.16 Fermentation	9,00E-99	82	emb./end.	evm_27.model.AmTr_v1.0_scaffold00012.3_18	-16,529	20	28,9	11	-	11	0,305556	TNSVTPWFIR TPLAELLIGNE EHYK	0,003138

Q9LI2	Oleoin / glycine-rich protein	<i>Arabidopsis thaliana</i>	AT3G18570	09 Cell structure	09.99 Others	1,00E-23	61	emb.	evm_27.model.AmTr_v1.0_scaffold00147.3_0	-39,18943	5	17,7	2	-	2	0,111111	HPVGSDRVYAR LLTASOMKDK	0,000571
Q9LIP2	20S proteasome (beta subunit E-2)	<i>Arabidopsis thaliana</i>	AT3G26340	06 Protein destination and storage	06.13 Proteolysis	e-131	88	emb.	evm_27.model.AmTr_v1.0_scaffold00078.5_6	-35,00134	17	29,8	4	-	3	0,333333	LLANILYSYR ASMGYISSQ SVK	0,001141
Q9LJ97	Late embryogenesis abundant protein (LEA) (Seed maturation)	<i>Arabidopsis thaliana</i>	AT3G22490	11 Disease/defence	11.05 Stress responses	2,00E-30	48	emb.	evm_27.model.AmTr_v1.0_scaffold00004.2_2	-28,4304	5	24,2	2	-	2	0,117647	SQGGPQRPIK TGQVQGGGEL R	0,000571
Q9LJH8	RNA binding protein nucleolysin	<i>Arabidopsis thaliana</i>	AT3G14100	04 Transcription	04.22 mRNA processing	e-150	76	emb.	evm_27.model.AmTr_v1.0_scaffold00007.4_03	-7,932557	25	45,4	7	-	3	1,4	NQDDAQNAIN EQNGK GFGVFSFR	0,001997
Q9LKA4	RNA-binding protein putative	<i>Arabidopsis thaliana</i>	AT3G15010	12 Unclear classification	12 Unclear classification	9,00E-91	78	emb.	evm_27.model.AmTr_v1.0_scaffold00021.5_9	-13,06783	20	42,6	2	-	2	0,285714	HIDGALNALKE PSK HPPDVL DLVR	0,000571
Q9LKA5	Uncharacterized mitochondrial protein	<i>Arabidopsis thaliana</i>	AT3G15000	12 Unclear classification	12 Unclear classification	2,00E-74	67	emb.	evm_27.model.AmTr_v1.0_scaffold00021.5_3	-15,46852	30	47,1	2	-	2	0,333333	TLAQVVGSE EAR WVLPDSYLDV	0,000571
Q9LKR3	HSP70 (Luminal binding protein 1)	<i>Arabidopsis thaliana</i>	AT5G28540	06 Protein destination and storage	06.01 Folding and stability	0	90	emb./end.	evm_27.model.AmTr_v1.0_scaffold00002.5_4	-40,35821	14	74,2	5	-	5	0,25	IINEPTAAAIY GLDKK IINEPTAAAIY	0,001427
Q9LNJ3	Aspartyl protease-like protein	<i>Arabidopsis thaliana</i>	AT1G01300	06 Protein destination and storage	06.13 Proteolysis	e-125	64	emb.	evm_27.model.AmTr_v1.0_scaffold00021.2_34	-66,43501	5	52,4	2	1	2	0,1	LVSSAYDVVR LDPTNGGGVI VDSGTSVTR	0,000571
Q9LNU4	26S proteasome (regulatory subunit RPN3a)	<i>Arabidopsis thaliana</i>	AT1G20200	06 Protein destination and storage	06.13 Proteolysis	0	80	emb.	evm_27.model.AmTr_v1.0_scaffold00057.2_46	-10,85636	12	55,1	3	-	3	0,375	IGDLELFR HDELGGTLL NLLLR	0,000856
Q9LNW1	Ras-related protein	<i>Arabidopsis thaliana</i>	AT1G07410	08 Intracellular traffic	08.07 Vesicular	e-100	89	emb.	evm_27.model.AmTr_v1.0_scaffold00165.3_9	-10,74398	17	23,7	3	-	3	0,166667	IVLIGDSGVGK IVLIGDSGVGK	0,000856
Q9LPT6	OTU-containing deubiquitinating enzyme	<i>Arabidopsis thaliana</i>	AT1G50670	06 Protein destination and storage	06.13 Proteolysis	2,00E-94	88	emb.	evm_27.model.AmTr_v1.0_scaffold00037.2_2	-7,374173	19	24	4	-	3	0,4	QVIAATVADP TR EIAAYDIQTR GYDIMSTVDA	0,001141
Q9LSV0	Glyoxylate/succinic semialdehyde reductase	<i>Arabidopsis thaliana</i>	AT3G25530	11 Disease/defence	11.05 Stress responses	e-125	84	emb.	evm_27.model.AmTr_v1.0_scaffold00024.31_1	-12,59414	6	30,7	2	-	2	0,142857	STTSK LAIALGDAQNV	0,000571
Q9LUF1	Hydroxysteroid dehydrogenase (Steroleosin-B)	<i>Arabidopsis thaliana</i>	AT5G50700	01 Metabolism	01.06 Lipid and sterol	e-106	71	emb.	evm_27.model.AmTr_v1.0_scaffold00016.2_15	-47,61949	26	39	16	-	6	8	REGSLQEVAE K EGEMVNVTE	0,004565
Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	4,00E-53	48	emb./end.	evm_27.model.AmTr_v1.0_scaffold00002.6_57	-407,8164	15	59,8	3	-	3	0,272727	ERESESEGE R KGGDTATIPAGK	0,000856
Q9LV09	Late embryogenesis abundant protein (small LEA) Protein BOBBER	<i>Arabidopsis thaliana</i>	AT5G53400	06 Protein destination and storage	06.01 Folding and stability	3,00E-77	68	emb.	evm_27.model.AmTr_v1.0_scaffold00017.1_84	-8,309981	13	35,1	5	-	4	0,294118	SPNSNGLDL EK LSDLPETR	0,001427
Q9LV33	Beta-glucosidase	<i>Arabidopsis thaliana</i>	AT3G18080	09 Cell structure	09.01 Cell wall	0,00E+00	82	emb.	evm_27.model.AmTr_v1.0_scaffold00005.2_26	-11,45284	38	55,1	3	-	3	0,5	VIAALGYDNF	0,000856
Q9LV33	Beta-glucosidase	<i>Arabidopsis thaliana</i>	AT3G18080	09 Cell structure	09.01 Cell wall	0	81	emb.	evm_27.model.AmTr_v1.0_scaffold00005.2_27	-11,45284	21	55,1	3	-	3	0,214286	VIAALGYDNF	0,000856
Q9LV33	Beta-glucosidase	<i>Arabidopsis thaliana</i>	AT3G18080	09 Cell structure	09.01 Cell wall	0	82	emb.	evm_27.model.AmTr_v1.0_scaffold00005.2_28	-11,45284	12	55,1	3	-	3	0,214286	VIAALGYDNF	0,000856
Q9LV33	Beta-glucosidase	<i>Arabidopsis thaliana</i>	AT3G18080	09 Cell structure	09.01 Cell wall	0,00E+00	83	emb.	evm_27.model.AmTr_v1.0_scaffold00095.2_7	-14,55105	7	57,9	3	-	3	0,12	LIDYLLER AYSPGLMVP WGIYK	0,000856
Q9LVA0	BAG7 (molecular chaperone regulator)	<i>Arabidopsis thaliana</i>	AT5G62390	06 Protein destination and storage	06.01 Folding and stability	5,00E-32	67	emb.	evm_27.model.AmTr_v1.0_scaffold00086.7_2	-37,88794	22	48,9	5	-	4	0,416667	LASDPEER GGSGSADASH YTFK	0,001427
Q9LVH4	GTPase activating protein-like	<i>Arabidopsis thaliana</i>	AT3G17980	10 Signal transduction	10.0410 G proteins	9,00E-55	79	emb.	evm_27.model.AmTr_v1.0_scaffold00007.2_80	-33,52149	14	18,4	2	-	2	0,153846	LNLEGVPSPA VIR SSNPYVLLTM	0,000571
Q9LW57	Fibrillin	<i>Arabidopsis thaliana</i>	AT3G23400	09 Cell structure	09.99 Others	1,00E-77	84	emb.	evm_27.model.AmTr_v1.0_scaffold00016.2_86	-8,931814	3	28,8	2	-	2	0,054054	WKLIVSSAFSA R LLPITLQVFO	0,000571
Q9LY84	GDGL esterase/lipase	<i>Arabidopsis thaliana</i>	AT5G14450	01 Metabolism	01.06 Lipid and sterol	e-121	75	emb.	evm_27.model.AmTr_v1.0_scaffold00049.2_80	-38,97112	17	41,7	2	-	2	0,5	ALYTFDIGND LVAGFR NIDKYGCVYT	0,000571
Q9LYG2	Putative uncharacterized protein	<i>Arabidopsis thaliana</i>	AT5G11680	12 Unclear classification	12 Unclear classification	2,00E-87	83	emb.	evm_27.model.AmTr_v1.0_scaffold00016.3_70	-21,5284	34	23,5	2	-	2	0,5	HAYVDPSPDT R IYLQQPNLDSQ	0,000571
Q9LYJ2	Universal stress protein	<i>Arabidopsis thaliana</i>	AT5G14680	11 Disease/defence	11.05 Stress responses	1,00E-73	84	emb.	evm_27.model.AmTr_v1.0_scaffold00058.2_06	-4,650528	7	20,3	2	-	2	0,133333	NVRPDLVGC R VFGVTSEFC	0,000571

Q9LYR4	Transaldolase	<i>Arabidopsis thaliana</i>	AT5G13420	02 Energy	02.07 Pentose phosphate	e-163	87	emb.	evm_27.model.AmTr_v1.0_scaffold00016.4_0	-20,91982	20	47.3	13	-	12	0,382353	TIDSNVEQAK ALQAFDLHGV VSR	0,003709
Q9LZC3	Malate synthase	<i>Arabidopsis thaliana</i>	AT5G03860	02 Energy	02.10 TCA pathway	0	85	emb.	evm_27.model.AmTr_v1.0_scaffold00049.8_6	-7,540608	31	64,8	13	-	5	13	VLDEEMIR EAAIWNVAFER	0,003709
Q9LZF6	Cell division control protein 48 homolog E	<i>Arabidopsis thaliana</i>	AT5G03340	03 Cell growth/division	03.22 Cell cycle	0	93	emb.	evm_27.model.AmTr_v1.0_scaffold00085.2_2	-6,226214	30	90	9	-	8	0,5625	GSSVGDAGGA ADR GILLYPPGSG	0,002568
Q9M040	Pyruvate decarboxylase-like protein	<i>Arabidopsis thaliana</i>	AT5G01320	02 Energy	02.16 Fermentation	0	88	emb./end.	evm_27.model.AmTr_v1.0_scaffold00007.1_42	-75,78744	53	65,3	11	-	5	2,75	EPVPFCIAPK NWNVYALVEAI HNGEGK	0,003138
Q9M084	Aspartyl-tRNA synthetase	<i>Arabidopsis thaliana</i>	AT4G31180	01 Metabolism	01.01 Amino Acid	0	80	emb.	evm_27.model.AmTr_v1.0_scaffold00025.2_84	-9,07263	38	63	37	-	15	2,055556	GSSQQVEVQ GR AIPTL PFNLED	0,010556
Q9M088	Glucan endo-1,3-beta-glucosidase	<i>Arabidopsis thaliana</i>	AT4G31140	01 Metabolism	01.05 Sugars and polysaccharides	e-174	81	emb.	evm_27.model.AmTr_v1.0_scaffold00025.3_07	-17,09657	67	53,4	21	-	7	7	YQLGVGNSQL IGAK VKPTVPLNAD	0,005991
Q9M5J9	Polygalacturonase inhibitor	<i>Arabidopsis thaliana</i>	AT5G06860	11 Disease/defence	11.01 Resistance genes	3,00E-98	70	emb.	evm_27.model.AmTr_v1.0_scaffold00022.2_71	-17,6891	8	36,2	2	-	2	0,090909	LCGAIPQGGG MK NLLEGDVSHL	0,000571
Q9M5K2	Dihydropyrimidine dehydrogenase	<i>Arabidopsis thaliana</i>	AT3G17240	02 Energy	02.10 TCA pathway	0	86	emb.	evm_27.model.AmTr_v1.0_scaffold00014.11_4	-11,77222	68	53,9	12	-	6	4	HIITATGSDVK GVYAGDVVP GPMIAHK	0,003424
Q9M5K3	Dihydropyrimidine dehydrogenase	<i>Arabidopsis thaliana</i>	AT1G48030	02 Energy	02.10 TCA pathway	0	87	emb.	evm_27.model.AmTr_v1.0_scaffold00064.4_9	-11,77222	48	53,8	17	-	6	2,428572	HIITATGSDVK GVYAGDVVP GPMIAHK	0,004850
Q9M7Q7	Proliferating cellular nuclear antigen	<i>Arabidopsis thaliana</i>	AT1G07370	03 Cell growth/division	03.16 DNA synth/replication	e-114	82	emb.	evm_27.model.AmTr_v1.0_scaffold00009.3_15	-3,211125	19	29	9	-	7	0,75	IADMGYLR LMDISSEQLGI PESEYQSIVR	0,002568
Q9M7T0	Peroxioredoxin (mitochondrial)	<i>Arabidopsis thaliana</i>	AT3G06050	11 Disease/defence	11.06 Detoxification	5,00E-62	75	emb.	evm_27.model.AmTr_v1.0_scaffold00025.2_5	-15,39358	8	21,6	2	-	2	0,153846	SLDLGLDLSA LLGHR SWDEGVSSK	0,000571
Q9M885	40S ribosomal protein (S7-2)	<i>Arabidopsis thaliana</i>	AT3G02560	05 Protein synthesis	05.01 Ribosomal proteins	2,00E-78	90	emb.	evm_27.model.AmTr_v1.0_scaffold00017.2_90	-8,791827	41	22,1	6	-	5	1	FSGKDVIVIAT R NNTYEKLETFS	0,001712
Q9M888	Chaperonin (Chaperonin-60kD, ch60, CPN60)	<i>Arabidopsis thaliana</i>	AT3G02530	06 Protein destination and storage	06.01 Folding and stability	e-135	97	emb.	evm_27.model.AmTr_v1.0_scaffold00002.7_1	-4,705975	25	27,5	4	-	3	0,8	LVEGLVLDHG SR VLVDGFIEAKR	0,001141
Q9M888	Chaperonin (Chaperonin-60kD, ch60, CPN60)	<i>Arabidopsis thaliana</i>	AT3G02530	06 Protein destination and storage	06.01 Folding and stability	0	95	emb.	evm_27.model.AmTr_v1.0_scaffold00010.5_5	-4,705975	10	59	4	-	3	0,285714	LVEGLVLDHG SR VLVDGFIEAKR	0,001141
Q9M8R4	Glyoxalase	<i>Arabidopsis thaliana</i>	AT3G02720	11 Disease/defence	11.06 Detoxification	e-173	85	emb.	evm_27.model.AmTr_v1.0_scaffold00029.2_15	-23,01314	8	41,7	3	2	3	0,230769	AGEACTTAVH ER APEYLSMNS	0,000856
Q9MAH0	Phosphoenolpyruvate carboxylase	<i>Arabidopsis thaliana</i>	AT1G53310	02 Energy	02.10 TCA pathway	0	89	emb.	evm_27.model.AmTr_v1.0_scaffold00021.2_8	-12,87228	20	110	9	-	9	0,310345	TPPTPQDEMR EIQAAFR VVPLFEK	0,002568
Q9MAH3	4-Methyl-5-(B-hydroxyethyl)-thiazole monophosphate	<i>Arabidopsis thaliana</i>	AT1G53280	01 Metabolism	01.07 Cofactors	e-142	79	emb.	evm_27.model.AmTr_v1.0_scaffold00021.4_3	-7,279841	27	45,5	8	5	6	0,533333	LTDQSAVVNR VVVDGNLITSR	0,002282
Q9MAK9	26S proteasome (AAA-ATPase subunit RPT4b)	<i>Arabidopsis thaliana</i>	AT1G45000	06 Protein destination and storage	06.13 Proteolysis	0	96	emb.	evm_27.model.AmTr_v1.0_scaffold00083.2_3	-6,496891	8	44,4	4	-	4	0,181818	HGEIDEYAVVK	0,001141
Q9S7E4	Formate dehydrogenase (mitochondrial)	<i>Arabidopsis thaliana</i>	AT5G14780	01 Metabolism	01.07 Cofactors	e-174	86	emb.	evm_27.model.AmTr_v1.0_scaffold00058.1_64	-17,65412	31	41,5	13	3	10	0,764706	LKPFNCNLLYH DR GEVNSWAESE TK	0,003709
Q9S7T8 (Serpiln-ZX (Serine protease inhibitor)	<i>Arabidopsis thaliana</i>	AT1G47710	06 Protein destination and storage	06.13 Proteolysis	e-116	69	emb.	evm_27.model.AmTr_v1.0_scaffold00169.8_8	-5,473661	29	42,7	3	-	3	1,5	AGFLNTVNSIY	0,000856
Q9S9K7	Histone H2AXb	<i>Arabidopsis thaliana</i>	AT1G54690	09 Cell structure	09.13 Chromosomes	5,00E-42	76	emb.	evm_27.model.AmTr_v1.0_scaffold00055.1_71	-12,21113	11	13,8	2	-	2	0,166667	VGAGAPVYLA	0,000571
Q9S9K7	Histone H2AXb	<i>Arabidopsis thaliana</i>	AT1G54690	09 Cell structure	09.13 Chromosomes	8,00E-40	70	emb.	evm_27.model.AmTr_v1.0_scaffold00197.1_0	-12,21113	10	14,5	2	-	2	0,333333	VGAGAPVYLA	0,000571
Q9SAJ4	Phosphoglycerate kinase	<i>Arabidopsis thaliana</i>	AT1G79550	02 Energy	02.01 Glycolysis	0	93	emb./end.	evm_27.model.AmTr_v1.0_scaffold00062.1_99	-116,7405	44	42,4	16	-	10	1,777778	RPFAAIVGGSK VDLNVPLDDN QK	0,004565
Q9SAK4	Succinate-semialdehyde dehydrogenase	<i>Arabidopsis thaliana</i>	AT1G79440	01 Metabolism	01.01 Amino Acid	0	83	emb.	evm_27.model.AmTr_v1.0_scaffold00004.21_1	-12,52923	39	52,9	36	-	9	9	KITFTGSTAVG K IYGDIIPTTSAD	0,010271
Q9SCN8	Cell division control protein 48 homolog D	<i>Arabidopsis thaliana</i>	AT3G53230	03 Cell growth/division	03.22 Cell cycle	0	92	emb.	evm_27.model.AmTr_v1.0_scaffold00072.5_9	-6,226214	16	89,9	9	-	9	0,236842	GSSVGDAGGA ADR GILLYPPGSG	0,002568

Q9SEE5	Galactokinase	<i>Arabidopsis thaliana</i>	AT3G06580	01 Metabolism	01.05 Sugars and polysaccharides	0	83	emb.	evm_27.model.AmTr_v1.0_scaffold00003.234	-8,468905	37	54,1	18	-	17	0,62069	AVTAATNYNNR LAAIVLGIK	0,005136
Q9SEI2	26S proteasome (AAA-ATPase subunit RPT5a)	<i>Arabidopsis thaliana</i>	AT3G05530	06 Protein destination and storage	06.13 Proteolysis	0	93	emb.	evm_27.model.AmTr_v1.0_scaffold00022.94	-8,547447	9	47,3	2	1	2	0,181818	RFDSQVSGDR	0,000571
Q9SF16	Chaperonin (Chaperonin-60kD, ch60, CPN60)	<i>Arabidopsis thaliana</i>	AT3G11830	06 Protein destination and storage	06.01 Folding and stability	0	91	emb.	evm_27.model.AmTr_v1.0_scaffold00001.74	-12,97021	28	60,8	3	1	2	0,75	VTEEDLQR GGADQFIEEA ER	0,000856
Q9SF20	MD-2-related lipid recognition domain-containing protein	<i>Arabidopsis thaliana</i>	AT3G11780	11 Disease/defence	11.02 Defence-related	4,00E-46	74	emb./end.	evm_27.model.AmTr_v1.0_scaffold00004.191	-14,61979	10	16,4	2	-	2	0,117647	VSGMEVDPDP VER	0,000571
Q9SF40	60S ribosomal protein (L4-1)	<i>Arabidopsis thaliana</i>	AT3G09630	05 Protein synthesis	05.01 Ribosomal proteins	e-172	81	emb.	evm_27.model.AmTr_v1.0_scaffold00105.4	-39,17127	35	44,7	7	-	4	2,333333	KEPPKENAAAI K RQPYAVSTK	0,001997
Q9SFB1	Uncharacterized protein	<i>Arabidopsis thaliana</i>	AT3G08030	12 Unclear classification	12 Unclear classification	e-140	79	emb.	evm_27.model.AmTr_v1.0_scaffold00141.27	-6,241088	9	39,5	2	-	2	0,133333	FMALQPR KVYTLSFIVGD AK	0,000571
Q9SGA6	S ribosomal protein (S19)	<i>Arabidopsis thaliana</i>	AT3G02080	05 Protein synthesis	05.01 Ribosomal proteins	4,00E-61	88	emb.	evm_27.model.AmTr_v1.0_scaffold00110.33	-7,619789	33	18,7	6	-	6	0,545455	HILQOLEK ELAPYDPDWY FIR	0,001712
Q9SHE7	Ubiquitin-NEDD8-like protein	<i>Arabidopsis thaliana</i>	AT1G31340	06 Protein destination and storage	06.13 Proteolysis	4,00E-38	95	emb.	evm_27.model.AmTr_v1.0_scaffold00101.25	-8,287351	25	10,2	4	-	3	0,4	EGIPPVQQR EVEIDIEPTDI ER	0,001141
Q9SI20	Elongation factor 1	<i>Arabidopsis thaliana</i>	AT2G18110	05 Protein synthesis	05.04 Translation factors	3,00E-77	72	emb.	evm_27.model.AmTr_v1.0_scaffold00029.307	-7,221849	21	27,4	5	-	4	0,5	WYNNHIDALLK R WYNNHIDALLK	0,001427
Q9SIB9	Aconitase	<i>Arabidopsis thaliana</i>	AT2G05710	02 Energy	02.10 TCA pathway	0	91	emb.	evm_27.model.AmTr_v1.0_scaffold00001.143	-32,89288	29	107	12	-	9	0,8	TSLAPGSGVV TK MEVDYNEPQT	0,003424
Q9SIV2	26S proteasome (non-ATPase regulatory subunit 2 1A)	<i>Arabidopsis thaliana</i>	AT2G20580	06 Protein destination and storage	06.13 Proteolysis	0	83	emb.	evm_27.model.AmTr_v1.0_scaffold00057.266	-6,211125	7	73,3	3	-	3	0,230769	ANSMEQLIER GLLTLAPYHSD R	0,000856
Q9SIZ2	Eukaryotic translation initiation factor	<i>Arabidopsis thaliana</i>	AT2G40290	05 Protein synthesis	05.04 Translation factors	e-144	89	emb.	evm_27.model.AmTr_v1.0_scaffold00109.126	-13,37366	18	38,7	5	-	4	0,384615	EIGPDGQEVTR VSEEDIQACEE	0,001427
Q9SJQ9	Fructose-bisphosphate aldolase	<i>Arabidopsis thaliana</i>	AT2G36460	02 Energy	02.01 Glycolysis	e-178	91	emb./end.	evm_27.model.AmTr_v1.0_scaffold00040.204	-156,2496	43	38,2	13	-	5	2,6	LSSINVENVES NRR EENIPAAQK	0,003709
Q9SK09	Cupin family protein (Vicilin)	<i>Arabidopsis thaliana</i>	AT2G28490	06 Protein destination and storage	06.20 Storage proteins	e-118	66	emb./end.	evm_27.model.AmTr_v1.0_scaffold00080.82	-82,5947	10	50,4	3	-	2	0,25	HTTDSYNLYK IGWINRDDLVE K	0,000856
Q9SK22	40S ribosomal protein (S16-1)	<i>Arabidopsis thaliana</i>	AT2G09990	05 Protein synthesis	05.01 Ribosomal proteins	9,00E-69	92	emb.	evm_27.model.AmTr_v1.0_scaffold00046.31	-20,89915	39	16,8	6	-	6	0,75	AYEPILVLR ATEAVQAVESV QCFGR	0,001712
Q9SK39	Steroid-binding protein	<i>Arabidopsis thaliana</i>	AT2G24940	10 Signal transduction	10.01 Receptors	8,00E-39	83	emb.	evm_27.model.AmTr_v1.0_scaffold00019.45	-18,78824	3	12,9	2	-	2	0,057143	NEEDISPSIND LSEK MELTEQGLR	0,000571
Q9SN35	Ras-related protein	<i>Arabidopsis thaliana</i>	AT4G18800	08 Intracellular traffic	08.07 Vesicular	e-108	92	emb.	evm_27.model.AmTr_v1.0_scaffold00130.15	-13,02541	8	24,3	3	-	3	0,125	VVLIGDSGVGK	0,000856
Q9SN86	Malate dehydrogenase	<i>Arabidopsis thaliana</i>	AT3G47520	02 Energy	02.10 TCA pathway	e-151	82	emb.	evm_27.model.AmTr_v1.0_scaffold00010.472	-12,38038	39	43,7	12	-	9	0,857143	VAILGAAGGIG QPLSLLIK VAILGAAGGIG	0,003424
Q9SN96	Uncharacterized protein	<i>Arabidopsis thaliana</i>	AT5G59613	12 Unclear classification	12 Unclear classification	2,00E-18	81	emb.	evm_27.model.AmTr_v1.0_scaffold00016.318	-6,38426	6	12,6	2	-	2	0,125	ARFDPWPVFF R FDPWPVFFR	0,000571
Q9SR13	RNA-binding KH domain-containing protein	<i>Arabidopsis thaliana</i>	AT3G04610	12 Unclear classification	12 Unclear classification	e-109	77	emb.	evm_27.model.AmTr_v1.0_scaffold00002.479	-13,90434	5	50,9	2	-	2	0,4	SIQEGSNCTV R VIDGDOEYGH	0,000571
Q9SRH5	Mitochondrial outer membrane protein porin	<i>Arabidopsis thaliana</i>	AT3G01280	11 Disease/defence	11.06 Detoxification	e-108	82	emb.	evm_27.model.AmTr_v1.0_scaffold00078.71	-58,69769	5	29,3	2	-	2	0,111111	ASALIQHEWR PK GNLTLSASYHT	0,000571
Q9SRL5	Ferritin, chloroplastic	<i>Arabidopsis thaliana</i>	AT3G11050	11 Disease/defence	11.02 Defence-related	2,00E-88	84	emb.	evm_27.model.AmTr_v1.0_scaffold00007.7	-34,92614	5	28,1	2	-	2	0,222222	SNDPQMLDFI ESEYLAECVD SIK	0,000571
Q9SRT9	UDP-L-arabinose mutase	<i>Arabidopsis thaliana</i>	AT3G02230	09 Cell structure	09.01 Cell wall	0	95	emb./end.	evm_27.model.AmTr_v1.0_scaffold00047.149	-6,537902	14	40,9	3	-	2	0,428571	GYPFSLR ATSATPHLKDE LDVIPTIR	0,000856
Q9SRY5	Glutathione S-transferase	<i>Arabidopsis thaliana</i>	AT1G02920	11 Disease/defence	11.06 Detoxification	2,00E-37	67	emb.	evm_27.model.AmTr_v1.0_scaffold00057.265	-13,45075	6	19,4	2	-	2	0,133333	FSLVDLHHLPN IR AMILGIPVDETV	0,000571
Q9SRZ4	Peroxioredoxin	<i>Arabidopsis thaliana</i>	AT1G65970	11 Disease/defence	11.06 Detoxification	2,00E-34	88	emb.	evm_27.model.AmTr_v1.0_scaffold00109.91	-21,60504	3	9,5	2	-	2	0,054054	AWAESYPENK VANLEEGGAF SVSSADEIK	0,000571

Q9SRZ6	Isocitrate dehydrogenase	<i>Arabidopsis thaliana</i>	AT1G65930	02 Energy	02.10 TCA pathway	0	92	emb.	evm_27.model.AmTr_v1.0_scaffold00071.1_47	-19,81776	36	46,7	11	-	10	0,578947	LEAACVGTVE SGK FEAAGIWIYEH	0,003138
Q9SS98	Oleoin	<i>Arabidopsis thaliana</i>	AT3G01570	09 Cell structure	09.99 Others	8,00E-13	79	emb.	evm_27.model.AmTr_v1.0_scaffold00061.1_05	-20,00506	6	14,7	2	-	2	0,133333	ELGAHLQOR IPAQVVDTAQK VOIPIENK	0,000571
Q9SSB5	26S proteasome (AAA-ATPase subunit RPT1a)	<i>Arabidopsis thaliana</i>	AT1G53750	06 Protein destination and storage	06.13 Proteolysis	0	98	emb.	evm_27.model.AmTr_v1.0_scaffold00131.5_6	-10,77469	15	47,5	4	-	3	0,5	FDDGVGGDNE VQR ELFQMAR	0,001141
Q9SSB5	26S proteasome (AAA-ATPase subunit RPT1a)	<i>Arabidopsis thaliana</i>	AT1G53750	06 Protein destination and storage	06.13 Proteolysis	e-170	98	emb.	evm_27.model.AmTr_v1.0_scaffold00131.5_9	-10,77469	16	32,6	3	-	2	0,6	FDDGVGGDNE VQR ELFQMAR	0,000856
Q9SSQ8	HSP26.5 (chloroplast, mitochondrion)	<i>Arabidopsis thaliana</i>	AT1G52560	06 Protein destination and storage	06.01 Folding and stability	2,00E-29	64	emb.	evm_27.model.AmTr_v1.0_scaffold00078.2_3	-20,8514	26	15,5	3	1	2	0,6	YGYNTSLR FEMPGLSKEDI K	0,000856
Q9STS1	Betaine aldehyde dehydrogenase	<i>Arabidopsis thaliana</i>	AT3G48170	11 Disease/defence	11.05 Stress responses	0	89	emb.	evm_27.model.AmTr_v1.0_scaffold00055.1_45	-26,67567	13	54,6	2	-	2	0,222222	VSDPLQDQGR SEGATILCGGD RPQHLEK	0,000571
Q9STW6	HSP70 (chloroplastic)	<i>Arabidopsis thaliana</i>	AT4G24280	06 Protein destination and storage	06.01 Folding and stability	0	82	emb.	evm_27.model.AmTr_v1.0_scaffold00071.9_2	-34,14368	12	75,1	5	-	5	0,217391	SEVFSTAADG QTSVSEINVLQ GER	0,001427
Q9STX2	3-oxo-Delta(4,5)-steroid 5-beta-reductase	<i>Arabidopsis thaliana</i>	AT4G24220	20 Secondary metabolism	20.2 Terpenoids	e-154	81	emb.	evm_27.model.AmTr_v1.0_scaffold00029.8_6	-57,93979	5	43,7	2	-	2	0,125	ISEAENCVDN GHMFR ISEAENCVDN	0,000571
Q9STX5	HSP90	<i>Arabidopsis thaliana</i>	AT4G24190	06 Protein destination and storage	06.01 Folding and stability	0	90	emb.	evm_27.model.AmTr_v1.0_scaffold00041.11_4	-19,162	17	93,6	5	-	5	0,333333	EVTDDEEYSK IMQSGTSDA NK	0,001427
Q9STY6	40S ribosomal protein (S20-2)	<i>Arabidopsis thaliana</i>	AT3G47370	05 Protein synthesis	05.01 Ribosomal proteins	1,00E-53	89	emb.	evm_27.model.AmTr_v1.0_scaffold00024.5_2	-10,79697	18	13,4	6	-	3	0,75	VCADLVR AGLEEPQVPL NR	0,001712
Q9SU13	Fasciclin-like arabinogalactan protein	<i>Arabidopsis thaliana</i>	AT4G12730	10 Signal transduction	10.99 Others	e-103	73	emb.	evm_27.model.AmTr_v1.0_scaffold00006.1_27	-18,89825	8	41,2	2	-	2	0,133333	VSIGADDDGG VLDASYVK ITGTIIDEPLA	0,000571
Q9SU40	Monocopper oxidase-like protein	<i>Arabidopsis thaliana</i>	AT4G12420	09 Cell structure	09.01 Cell wall	0	81	emb.	evm_27.model.AmTr_v1.0_scaffold00085.6_6	-18,91027	56	66,3	3	-	3	0,75	GLYNKWDGVA R VTGVAILHYSN	0,000856
Q9SUB2	Late embryogenesis abundant protein (LEA)	<i>Arabidopsis thaliana</i>	AT4G21020	11 Disease/defence	11.05 Stress responses	1,00E-09	52	emb.	evm_27.model.AmTr_v1.0_scaffold00037.1_58	-16,1536	7	30	2	-	2	0,125	VKDTAESAVD TGKEGASK DSAADMAQR	0,000571
Q9SUT2	Peroxidase	<i>Arabidopsis thaliana</i>	AT4G11290	11 Disease/defence	11.06 Detoxification	e-104	70	emb.	evm_27.model.AmTr_v1.0_scaffold00037.7_7	-26,11464	13	35,5	2	-	2	0,142857	MHFHDCFVR DLVLLSGGHTI GIAR	0,000571
Q9SVM8	Glycine-rich RNA-binding protein (mitochondrial)	<i>Arabidopsis thaliana</i>	AT4G13850	04 Transcription	04.22 mRNA processing	3,00E-41	82	emb.	evm_27.model.AmTr_v1.0_scaffold00013.2_51	-16,30715	19	15	5	1	4	0,416667	LFVGLSFGT DDQSLR GFGFVNFDDN	0,001427
Q9SX53	Oligopeptidase B	<i>Arabidopsis thaliana</i>	AT1G50380	06 Protein destination and storage	06.13 Proteolysis	0	85	emb.	evm_27.model.AmTr_v1.0_scaffold00171.4_7	-11,73993	8	87,1	3	-	3	0,136364	VEGVTDVSH R SAGGLLIGSVL	0,000856
Q9SX53	Oligopeptidase B	<i>Arabidopsis thaliana</i>	AT1G50380	06 Protein destination and storage	06.13 Proteolysis	0	85	emb.	evm_27.model.AmTr_v1.0_scaffold00171.4_8	-11,73993	7	80,9	3	-	3	0,166667	VEGVTDVSH R SAGGLLIGSVL	0,000856
Q9SYG7	Aldehyde dehydrogenase	<i>Arabidopsis thaliana</i>	AT1G54100	11 Disease/defence	11.05 Stress responses	0	85	emb.	evm_27.model.AmTr_v1.0_scaffold00024.3_06	-13,85387	13	54,8	2	-	2	0,333333	SVLFAAVGTAG QR LLLHESIYQNF	0,000571
Q9SYT0	Annexin 1	<i>Arabidopsis thaliana</i>	AT1G35720	10 Signal transduction	10.99 Others	1,00E-92	73	emb.	evm_27.model.AmTr_v1.0_scaffold00060.11_3	-33,47177	11	35,9	2	-	2	0,2	SSEELFFIRR SSEELFFIRR	0,000571
Q9SYT0	Annexin 1	<i>Arabidopsis thaliana</i>	AT1G35720	10 Signal transduction	10.99 Others	e-100	78	emb.	evm_27.model.AmTr_v1.0_scaffold00060.11_4	-30,12498	9	35,5	2	-	2	0,285714	SSEELLIRR SLEEDVAQHT TGDFFR	0,000571
Q9SZE1	3-hydroxyisobuturate dehydrogenase-like	<i>Arabidopsis thaliana</i>	AT4G29120	02 Energy	02.07 Pentose phosphate	6,00E-92	72	emb.	evm_27.model.AmTr_v1.0_scaffold00056.1_06	-39,91016	27	32,3	11	2	11	0,578947	GCVALDCPVS GGDTGAR SQPPSTAAPL	0,003138
Q9SZH4	RNA-binding KH domain-containing protein	<i>Arabidopsis thaliana</i>	AT4G26000	12 Unclear classification	12 Unclear classification	e-118	73	emb.	evm_27.model.AmTr_v1.0_scaffold00002.1_78	-33,30272	13	47,1	2	-	2	0,153846	SVTTSVQER VAGVNEGEDD AAPK	0,000571
Q9T043	60S ribosomal protein (L14-2)	<i>Arabidopsis thaliana</i>	AT4G27090	05 Protein synthesis	05.01 Ribosomal proteins	4,00E-56	90	emb.	evm_27.model.AmTr_v1.0_scaffold00067.7_4	-10,72182	28	15,4	6	-	5	0,428571	SLIAAIEADVY K ASLTDFDRFK	0,001712
Q9T0A7	UDP-glucose 4-epimerase	<i>Arabidopsis thaliana</i>	AT4G23920	01 Metabolism	01.05 Sugars and polysaccharides	e-156	85	emb.	evm_27.model.AmTr_v1.0_scaffold00024.7_8	-9,600673	44	37,9	18	-	12	1,2	RPALTVYGN D YSTK RPALTVYGN D	0,005136
Q9T0G0	Hydroxysteroid dehydrogenase (Steroleosin-B)	<i>Arabidopsis thaliana</i>	AT4G10020	01 Metabolism	01.06 Lipid and sterol	7,00E-88	84	emb./end.	evm_27.model.AmTr_v1.0_scaffold00099.1_3	-32,96927	28	24,8	9	5	6	0,642857	GANLVLVAR AADVVKEDC RR	0,002568

Q9XFK7	protein MOTHER of FT and TF 1	<i>Arabidopsis thaliana</i>	AT1G18100	03 Cell growth/division	03.26 Growth regulators	6,00E-58	76	emb.	evm_27.model.AmTr_v1.0_scaffold00003.4_62	-29,35434	29	24,5	8	-	4	1,142857	QQGPLGSVAR LGLGLPVAAYV FNAQKEPASR	0,002282
Q9XI01	Protein disulfide isomerase	<i>Arabidopsis thaliana</i>	AT1G21750	06 Protein destination and storage	06.01 Folding and stability	e-172	79	emb.	evm_27.model.AmTr_v1.0_scaffold00186.1_4	-30,92249	22	57,4	5	-	5	0,357143	QAGPASAEIK LVEYDGGD NNDPSTLAK	0,001427
Q9XI36	Methyl-CpG-binding domain-containing protein	<i>Arabidopsis thaliana</i>	AT1G15340	04 Transcription	04.1907 Chromatin modification	4,00E-34	86	emb.	evm_27.model.AmTr_v1.0_scaffold00004.1_89	-11,18046	15	39	8	-	7	0,347826	GVTTTEDVGP GDSK RNEIVFVPTG	0,002282
Q9ZP06	Malate dehydrogenase	<i>Arabidopsis thaliana</i>	AT1G53240	02 Energy	02.10 TCA pathway	e-143	90	emb./end.	evm_27.model.AmTr_v1.0_scaffold00021.8_7	-83,35638	30	36,1	11	-	10	0,647059	LNPLVSSLSLY DIAGTPGVAAD VSHINTR	0,003138
Q9ZPE7	Phosphate-responsive 1 family protein	<i>Arabidopsis thaliana</i>	AT4G08950	03 Cell growth/division	03.22 Cell cycle	e-105	75	emb.	evm_27.model.AmTr_v1.0_scaffold00038.2_39	-13,2786	30	32,4	9	-	7	0,529412	TLTNAQLVALA SKGDEK QILDTSYSLGK	0,002568
Q9ZPE7	Phosphate-responsive 1 family protein	<i>Arabidopsis thaliana</i>	AT4G08950	03 Cell growth/division	03.22 Cell cycle	e-105	76	emb.	evm_27.model.AmTr_v1.0_scaffold00038.2_41	-13,2786	27	32,5	8	-	7	1,333333	TLTNAQLVALA SKGDEK QILDTSYSLGK	0,002282
Q9ZPI5	Peroxisomal fatty acid beta-oxidation multifunctional protein	<i>Arabidopsis thaliana</i>	AT3G06860	01 Metabolism	01.06 Lipid and sterol	0	85	emb.	evm_27.model.AmTr_v1.0_scaffold00045.2_39	-7,079877	7	78,1	4	1	3	0,222222	GGVVFWADSF GAK WALDIAEFR	0,001141
Q9ZPW6	Late embryogenesis abundant protein (LEA)	<i>Arabidopsis thaliana</i>	AT2G18340	11 Disease/defence	11.05 Stress responses	0,35	69	emb.	evm_27.model.AmTr_v1.0_scaffold00045.2_8	-27,38684	4	30,1	2	-	2	0,083333	QOEDATEQAG DAMKK AEFHVAEKGE	0,000571
Q9ZQ26	ATPase-related DNA repair protein	<i>Arabidopsis thaliana</i>	AT2G24420	03 Cell growth/division	03.19 Recombination/repair	3,00E-98	61	emb.	evm_27.model.AmTr_v1.0_scaffold00025.2_10	-4,964571	32	49,7	9	-	7	0,9	LQEITQEQQ AQALIKPHVER	0,002568
Q9ZRW8	Glutathione S-transferase	<i>Arabidopsis thaliana</i>	AT1G78380	11 Disease/defence	11.06 Detoxification	4,00E-74	76	emb./end.	evm_27.model.AmTr_v1.0_scaffold00092.8_1	-56,82902	6	24,5	2	-	2	0,222222	IPVLIHGDK EENLANKGEL LTK	0,000571
Q9ZSK1	Tocopherol O-methyltransferase	<i>Arabidopsis thaliana</i>	AT1G64970	20 Secondary metabolism	20.1 Phenylpropanoids/phenolics	1,00E-96	74	emb.	evm_27.model.AmTr_v1.0_scaffold00048.2_05	-6,005243	12	33,6	2	-	2	0,25	SLRPDELHILN R ADDSTLLWR	0,000571
Q9ZST4	Nitrogen regulatory protein P-II	<i>Arabidopsis thaliana</i>	AT4G01900	01 Metabolism	01.02 Nitrogen and sulphur	9,00E-56	87	emb.	evm_27.model.AmTr_v1.0_scaffold00003.1_94	-5,058488	63	16,2	26	-	18	1,181818	VPLVSSALIQM GIR VPLVSSALIQM	0,007418
Q9ZU52	Fructose-bisphosphate aldolase (chloroplastic)	<i>Arabidopsis thaliana</i>	AT2G01140	02 Energy	02.01 Glycolysis	0	89	emb./end.	evm_27.model.AmTr_v1.0_scaffold00001.1_61	-19,78169	43	42,4	13	-	5	2,6	LSSIGLDNTEP NR YSAAGESEEA	0,003709
Q9ZU91	Glucan endo-1,3-beta-glucosidase	<i>Arabidopsis thaliana</i>	AT2G01630	01 Metabolism	01.05 Sugars and polysaccharides	0	83	emb.	evm_27.model.AmTr_v1.0_scaffold00060.1_25	-20,30002	54	56,1	21	-	11	1,75	GVATVTTDPS HSCSFPGSG GK	0,005991
Q9ZUC0	OB-fold nucleic acid binding domain-containing protein	<i>Arabidopsis thaliana</i>	AT1G23750	12 Unclear classification	12 Unclear classification	5,00E-49	90	emb.	evm_27.model.AmTr_v1.0_scaffold00058.1_63	-3,489455	9	15,3	2	-	2	0,153846	AEAKPGMR NDQVDMMKP NSTIILR	0,000571
Q9ZUT9	40S ribosomal protein (S5-1)	<i>Arabidopsis thaliana</i>	AT2G37270	05 Protein synthesis	05.01 Ribosomal proteins	e-102	96	emb.	evm_27.model.AmTr_v1.0_scaffold00068.7_5	-19,15892	26	21,8	7	-	5	0,636364	HATYVPHTAGR	0,001997
Q9ZUT9	40S ribosomal protein (S5-1)	<i>Arabidopsis thaliana</i>	AT2G37270	05 Protein synthesis	05.01 Ribosomal proteins	4,00E-94	97	emb.	evm_27.model.AmTr_v1.0_scaffold00090.1_2	-18,18665	15	21,9	7	-	7	0,225806	AEVATLPEVK AEVATLPEVK	0,001997
Q9ZV34	Thaumatococcus putative	<i>Arabidopsis thaliana</i>	AT2G28790	11 Disease/defence	11.01 Resistance genes	6,00E-91	81	emb./end.	evm_27.model.AmTr_v1.0_scaffold00012.9_4	-81,15208	4	26,5	2	-	2	0,086957	FHCETGDCGR SFAAPHTHWS GR	0,000571
Q9ZV45	Small nuclear ribonucleoprotein	<i>Arabidopsis thaliana</i>	AT2G18740	04 Transcription	04.22 mRNA processing	5,00E-42	98	emb.	evm_27.model.AmTr_v1.0_scaffold00032.4_2	-9,199421	19	10,3	7	-	2	1,166667	ILLKGDNITLM MSTGK JMTQPINLFR	0,001997
Q9ZVD5	Protein argonaute 4	<i>Arabidopsis thaliana</i>	AT2G27040	04 Transcription	04.22 mRNA processing	0,00E+00	76	emb.	evm_27.model.AmTr_v1.0_scaffold00008.1_21	-44,93415	47	87,4	8	-	4	1,6	NYADLGGGVT GCR TAGVSIQONFT	0,002282
Q9ZVQ3	Glutathione S-transferase	<i>Arabidopsis thaliana</i>	AT2G02390	11 Disease/defence	11.06 Detoxification	5,00E-66	71	emb.	evm_27.model.AmTr_v1.0_scaffold00099.1_57	-11,24642	13	26,7	2	-	2	0,181818	FKVDMSQPFL LTR VSTTEEMFSWV	0,000571
Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	2,00E-64	51	emb./end.	evm_27.model.AmTr_v1.0_scaffold00067.11	-177,6197	8	49,1	3	-	3	0,272727	VLIPEEEERE EER YNREEQLMIFP	0,000856
Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	7,00E-70	51	emb./end.	evm_27.model.AmTr_v1.0_scaffold00067.7	-301,4168	7	54,5	3	-	3	0,272727	GRQEGEYGE EQR QEGEYGEFQ	0,000856

Supplemental table 2: list of the proteins identified from the total protein fraction of *Amborella trichopoda* isolated endosperm by *shot gun*

Proteins have been analyzed by mono-dimensional electrophoresis and identified by mass spectrometry LC/MS-MS. The protein spots were analysed by LC-MS/MS on the PAPPSo platform (Benoit Valot, Thierry Balliau, Michel Zivy, INRA Moulon, France; <http://pappso.inra.fr>). Based on the spectrum generated, proteins were identified using the X-Tandem software. "NCBI accession number" is the accession number in NCBI database. "Protein name". "Organism" relates to the organism from which the identified protein comes from for functional analysis - efforts were focus on *Arabidopsis thaliana* as a plant model. "AGI". "Function category" and "Function description" relate to the functional categories defined according to the ontological classification of Bevan *et al.* [Bevan *et al.* (1998) Nature 391:485-488]. "log(Evalue) identification" reflects the statistical power of the identification by BLAST (performed on TAIR or BLAST). "Identity" indicates in % the recovery of the *Amborella* protein sequence against the identified protein. "Compartment" indicates if the identification is found in the embryo (emb.), the endosperm (end.) or both (emb./end.). "Description" was taken from the Amborella EVM 27 Predicted Proteins (<http://www.amborella.org>). The "log (E value)" is a statistical parameter that represents the number of peptides present at random in the database. It was calculated by the product of the Evaluate of unique peptides identified in the protein spot (Valot *et al.*, 2011). "Coverage" refers to the recovery rate of the protein by the identified peptides, expressed in %. "MW" relates to the molecular weight expressed in kDa. "Spectra" corresponds to the number of spectra which allowed the protein identification from 2DE protein single spot. "Specifics" corresponds to the number of specific spectrum corresponding to the identification among the other identifications of the group. "Uniques" refers to the number of unique peptides (different sequences) that led to the protein identification. "PAI" is the protein abundance index in the spot. "Peptide sequences" displays identified peptides for each protein spot. "Relative abundance" relates to the number of spectra identifying the description among all the spectra.

Functional analysis									Mass spec data									
NCBI accession number	protein name	Organism	AGI	Function category	Function description	log (Evalue) identification	Identity	Compartment	Description	log (Evalue)	Coverage	MW	Spectra	Specifics	Uniques	PAI	Peptide sequences	Relative abundance
F4HWR0	Dessication-related protein	<i>Arabidopsis thaliana</i>	AT1G47980	11 Disease/defence	11.05 Stress responses	e-109	82	emb./end.	evm_27.model.AmTr_v1.0_scaffold00016.3_15	-82,63454	30	33,4	18	-	9	1,384615	#####	0,010011123
F4IQK5	Cupin-like protein	<i>Arabidopsis thaliana</i>	AT2G18540	06 Protein destination and storage	06.20 Storage proteins	8,00E-82	62	emb./end.	evm_27.model.AmTr_v1.0_scaffold00059.6_4	-52,20936	24	44,1	13	-	8	0,823529	VESVEV YDGSEK SGSVFY	0,007230256
F4JVN6	Subtilase family protein	<i>Arabidopsis thaliana</i>	AT4G20850	06 Protein destination and storage	06.13 Proteolysis	0	79	emb./end.	evm_27.model.AmTr_v1.0_scaffold00009.2_58	-22,34748	3	143,8	4	-	4	0,065574	VNVTQT GQEAPI TR	0,002224694
O04005	1-Cys peroxiredoxin	<i>Arabidopsis thaliana</i>	AT1G48130	11 Disease/defence	11.05 Stress responses	1,00E-88	82	emb./end.	evm_27.model.AmTr_v1.0_scaffold00045.3_7	-68,92651	47	24,2	15	-	9	1,363636	VVIPPNV SEEEKK	0,008342603
O04834	GTP-binding protein	<i>Arabidopsis thaliana</i>	AT4G02080	08 Intracellular traffic	08.07 Vesicular	1,00E-85	83	emb./end.	evm_27.model.AmTr_v1.0_scaffold00003.2_4	-12,54363	13	21,8	2	-	2	0,153846	VDVVVY LVDAAD KER	0,001112347
O23029	AWPM-19-like family protein	<i>Arabidopsis thaliana</i>	AT1G04560	06 Protein destination and storage	06.01 Folding and stability	5,00E-50	77	emb./end.	evm_27.model.AmTr_v1.0_scaffold00039.1_23	-24,01773	12	18,6	3	-	2	1	DPDYGA GAAADP AAPK	0,001668521
O49299	Phosphoglucosylase	<i>Arabidopsis thaliana</i>	AT1G23190	02 Energy	02.01 Glycolysis	0	89	emb./end.	evm_27.model.AmTr_v1.0_scaffold00010.1_23	-11,51145	4	63,7	2	-	2	0,068966	ETSPIDS QKPGTS GLR	0,001112347
O50008	5-methyltetrahydropteroyl triglutamate-	<i>Arabidopsis thaliana</i>	AT5G17920	01 Metabolism	01.01 Amino Acid	0	92	emb./end.	evm_27.model.AmTr_v1.0_scaffold00004.9_9	-23,59006	7	84,5	4	-	4	0,121212	YGAGIG PGYVDI HSPR	0,002224694
O64586	Pollen Ole e 1 (Putative proline-rich glycoprotein)	<i>Arabidopsis thaliana</i>	AT2G34700	12 Unclear classification	12 Unclear classification	4,00E-29	61	emb./end.	evm_27.model.AmTr_v1.0_scaffold00068.1_22	-32,69975	22	18,6	6	-	4	0,666667	ATLDHKI GITGSPL R	0,003337041
O65390	Aspartic proteinase	<i>Arabidopsis thaliana</i>	AT1G11910	06 Protein destination and storage	06.13 Proteolysis	0	80	emb./end.	evm_27.model.AmTr_v1.0_scaffold00106.4_8	-16,94059	7	55	3	-	3	0,176471	SDEDIIS LK AFELTP	0,001668521
O65398	Lactoylglutathione lyase-like protein	<i>Arabidopsis thaliana</i>	AT1G11840	11 Disease/defence	11.06 Detoxification	e-130	87	emb./end.	evm_27.model.AmTr_v1.0_scaffold00037.1_06	-34,24854	18	37,2	9	-	6	0,6	ITREPG PKPGINT K	0,005005562
O81235	Superoxide dismutase (Mn)	<i>Arabidopsis thaliana</i>	AT3G10920	11 Disease/defence	11.06 Detoxification	8,00E-76	79	emb./end.	evm_27.model.AmTr_v1.0_scaffold00077.2_6	-43,13104	48	22,4	5	-	5	0,625	GDASST VQLQSA IK	0,002780868
O81270	Peroxygenase	<i>Arabidopsis thaliana</i>	AT4G26740	01 Metabolism	01.06 Lipid and sterol	2,00E-91	82	end.	evm_27.model.AmTr_v1.0_scaffold00158.1_7	-20,07572	19	27	3	-	3	0,3	TDLDDKI PKPYVP R	0,001668521
P06525	Alcohol dehydrogenase	<i>Arabidopsis thaliana</i>	AT1G77120	02 Energy	02.16 Fermentation	e-162	80	emb./end.	evm_27.model.AmTr_v1.0_scaffold00071.6_5	-37,99723	22	41,1	7	-	6	0,4375	THPMNF LNER IJVDVN	0,003893215
P13853	HSP17.6 (class 1 heat shock protein)	<i>Arabidopsis thaliana</i>	AT1G53540	06 Protein destination and storage	06.01 Folding and stability	1,00E-52	75	end.	evm_27.model.AmTr_v1.0_scaffold00048.2_2	-7,012334	14	17,4	2	-	2	0,285714	KEEVKV ELEDGR SLIPSIF	0,001112347
P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	1,00E-70	52	emb./end.	evm_27.model.AmTr_v1.0_scaffold00067.1_2	-758,4857	80	53	294	-	84	18,05882	#####	0,163515017

P19036	HSP17.4 (class I small heat shock protein)	<i>Arabidopsis thaliana</i>	AT3G46230	06 Protein destination and storage	06.01 Folding and stability	2,00E-48	76	emb./end.	evm_27.model.AmTr.v1.0_scaffold00165.36	-49,59718	41	18,1	7	-	5	1,75	FRLPEN GKVDEVK	0,003893215
P19037	HSP18.1 (small heat shock protein family)	<i>Arabidopsis thaliana</i>	AT5G59720	06 Protein destination and storage	06.01 Folding and stability	1,00E-46	77	emb./end.	evm_27.model.AmTr.v1.0_scaffold00136.4	-29,60712	39	17,8	8	-	5	2	KDEVKV ELEDGR KDEVKK	0,004449388
P25696	Enolase	<i>Arabidopsis thaliana</i>	AT2G36530	02 Energy	02.01 Glycolysis	0	93	emb./end.	evm_27.model.AmTr.v1.0_scaffold00041.34	-32,83449	19	47,9	6	-	6	0,285714	HAGWGW VMASHR LTAEIGE	0,003337041
P25819	Catalase 2	<i>Arabidopsis thaliana</i>	AT4G35090	11 Disease/defence	11.06 Detoxification	0	91	emb./end.	evm_27.model.AmTr.v1.0_scaffold00001.7	-34,23456	14	56,7	6	-	5	0,3	APGVQT PLIVR GPILLED	0,003337041
P25858	Glyceraldehyde-3-phosphate dehydrogenase	<i>Arabidopsis thaliana</i>	AT3G04120	02 Energy	02.01 Glycolysis	5,00E-48	87	emb./end.	evm_27.model.AmTr.v1.0_scaffold00177.22	-19,82915	25	11,8	3	-	2	0,5	VIDLICH MASVAR VPTVDV	0,001668521
P27323	HSP90	<i>Arabidopsis thaliana</i>	AT5G52640	06 Protein destination and storage	06.01 Folding and stability	0	84	emb./end.	evm_27.model.AmTr.v1.0_scaffold00001.8	-11,81924	4	81	3	-	3	0,096774	AVENSP FLER ADVVNN	0,001668521
P29197	Chaperonin (Chaperonin-60kD, ch60, CPN60)	<i>Arabidopsis thaliana</i>	AT3G23990	06 Protein destination and storage	06.01 Folding and stability	0	93	emb./end.	evm_27.model.AmTr.v1.0_scaffold00003.261	-27,64265	18	61,2	7	-	6	0,266667	IGGASE VEVSEK K	0,003893215
P30184	Leucine aminopeptidase	<i>Arabidopsis thaliana</i>	AT2G24200	06 Protein destination and storage	06.13 Proteolysis	0	78	emb./end.	evm_27.model.AmTr.v1.0_scaffold00065.204	-31,81124	16	54,8	4	-	4	0,137931	VGLIGL GQGSLS TATFK	0,002224694
P34795	Phosphoglucose isomerase	<i>Arabidopsis thaliana</i>	AT5G42740	02 Energy	02.01 Glycolysis	0	90	emb./end.	evm_27.model.AmTr.v1.0_scaffold00111.63	-17,425	6	63	3	-	3	0,107143	FSPHIQ QVSMES NCK	0,001668521
P48491	Triosephosphate isomerase	<i>Arabidopsis thaliana</i>	AT3G55440	02 Energy	02.01 Glycolysis	e-114	87	emb./end.	evm_27.model.AmTr.v1.0_scaffold00012.164	-22,53165	16	27,3	2	-	2	0,25	ESGSTM DVVAAQ TK	0,001112347
P53492	Actin 7	<i>Arabidopsis thaliana</i>	AT5G09810	09 Cell structure	09.04 Cytoskeleton	0	99	emb./end.	evm_27.model.AmTr.v1.0_scaffold00018.104	-21,26761	10	41,6	3	-	3	0,2	EITALAP SSMK AVFPSIV	0,001668521
P53492	Actin 7	<i>Arabidopsis thaliana</i>	AT5G09810	09 Cell structure	09.04 Cytoskeleton	0	99	end.	evm_27.model.AmTr.v1.0_scaffold00030.17	-21,26761	10	41,5	3	-	3	0,2	EITALAP SSMK AVFPSIV	0,001668521
P53496	Actin 11	<i>Arabidopsis thaliana</i>	AT3G12110	09 Cell structure	09.04 Cytoskeleton	0	98	end.	evm_27.model.AmTr.v1.0_scaffold00044.61	-21,26761	9	43,9	3	-	3	0,1875	EITALAP SSMK AVFPSIV	0,001668521
P53496	Actin 11	<i>Arabidopsis thaliana</i>	AT3G12110	09 Cell structure	09.04 Cytoskeleton	0	99	end.	evm_27.model.AmTr.v1.0_scaffold00062.182	-21,26761	10	41,5	3	-	3	0,2	EITALAP SSMK AVFPSIV	0,001668521
P57751	UDP-glucose pyrophosphorylase	<i>Arabidopsis thaliana</i>	AT5G17310	01 Metabolism	01.05 Sugars and polysaccharides	0	87	emb./end.	evm_27.model.AmTr.v1.0_scaffold00044.42	-23,47092	10	52,2	4	-	4	0,153846	KILKQS AVAGL LQSAVA	0,002224694
Q1PER6	Ascorbate peroxidase	<i>Arabidopsis thaliana</i>	AT3G09640	11 Disease/defence	11.06 Detoxification	3,00E-99	79	emb./end.	evm_27.model.AmTr.v1.0_scaffold00023.236	-18,79412	12	27,8	4	-	3	0,333333	ALIEDPA FHPYVE K	0,002224694
Q38900	Rotamase cyclophilin-3	<i>Arabidopsis thaliana</i>	AT2G16600	06 Protein destination and storage	06.01 Folding and stability	4,00E-74	83	emb./end.	evm_27.model.AmTr.v1.0_scaffold00041.179	-21,51145	25	18,1	4	-	3	0,571429	HTGAGI LSMANAGK	0,002224694
Q39165	Oleosin type 2	<i>Arabidopsis thaliana</i>	AT5G40420	09 Cell structure	09.99 Others	1,00E-22	63	emb./end.	evm_27.model.AmTr.v1.0_scaffold00014.132	-30,92082	19	15,5	9	-	3	2,25	MHESG GHMGQ QVGQR	0,005005562
Q8GWR2	Uncharacterized protein	<i>Arabidopsis thaliana</i>	AT2G31985	13 Unclassified	13 Unclassified	2,00E-50	86	emb./end.	evm_27.model.AmTr.v1.0_scaffold00071.199	-13,24642	15	21,4	2	-	2	0,285714	QCLIYD SPDADAR	0,001112347
Q8H0X6	Cysteine proteinase inhibitor	<i>Arabidopsis thaliana</i>	AT3G12490	11 Disease/defence	11.02 Defence-related	2,00E-75	82	emb./end.	evm_27.model.AmTr.v1.0_scaffold00101.77	-12,40782	13	23,2	2	-	2	0,2	EFNHVG DSSLTS SDLGAK	0,001112347
Q8H103	Phosphoglucose isomerase	<i>Arabidopsis thaliana</i>	AT4G24620	02 Energy	02.01 Glycolysis	0	92	emb./end.	evm_27.model.AmTr.v1.0_scaffold00135.20	-16,84164	4	68,4	2	-	2	0,05	QGVAIT QENSLD DNTAR	0,001112347
Q8L831	MutT/nudix family protein	<i>Arabidopsis thaliana</i>	AT1G79690	20 Secondary metabolism	20.2 Terpenoids	0	79	emb./end.	evm_27.model.AmTr.v1.0_scaffold00019.58	-205,3022	40	86	36	-	26	1,027778	#####	0,020022247
Q8VYS0	Cysteine protease (papain)	<i>Arabidopsis thaliana</i>	AT3G54940	06 Protein destination and storage	06.13 Proteolysis	e-130	77	emb./end.	evm_27.model.AmTr.v1.0_scaffold00022.391	-12,92445	6	38,4	2	-	2	0,153846	LGNRPF WIIK ISMDED	0,001112347
Q93VR4	MLP-like protein	<i>Arabidopsis thaliana</i>	AT1G24020	11 Disease/defence	11.02 Defence-related	2,00E-05	44	end.	evm_27.model.AmTr.v1.0_scaffold00003.119	-6,461426	12	17,9	2	-	2	0,181818	ASIKDV HNIIVPK FNSLIVY	0,001112347

Q941A4	Uncharacterized protein	<i>Arabidopsis thaliana</i>	AT5G45690	13 Unclassified	13 Unclassified	1,00E-74	70	emb./end.	evm_27.model.AmTr_v1.0_scaffold00162.9	-80,98527	58	28,9	15	-	11	0,882353	YGLSSE ELKESR YGLSSF	0,008342603
Q9C827	Coatomer	<i>Arabidopsis thaliana</i>	AT1G52360	09 Cell structure	09.07 ER/Golgi	0	84	end.	evm_27.model.AmTr_v1.0_scaffold00142.4	-5,354578	2	104,4	2	-	2	0,05	VFEAHT DYIR SFEVTE	0,001112347
Q9FF40	2S albumin	<i>Arabidopsis thaliana</i>	AT5G38160	06 Protein destination and storage	06.20 Storage proteins	2,7	36	emb./end.	evm_27.model.AmTr_v1.0_scaffold00005.2_12	-88,31336	40	16,8	50	44	10	7,142857	#####	0,027808676
Q9FG31	Late embryogenesis abundant protein (LEA)	<i>Arabidopsis thaliana</i>	AT5G06760	11 Disease/defence	11.05 Stress responses	4,00E-09	48	emb./end.	evm_27.model.AmTr_v1.0_scaffold00022.1_82	-17,85387	20	14,8	2	-	2	0,333333	ETAGNV AASAK VPLSGP	0,001112347
Q9FH13	Ribonuclease E inhibitor RraA/Dimethylmenaquinone	<i>Arabidopsis thaliana</i>	AT5G56260	04 Transcription	04.19 mRNA synthesis	2,00E-72	88	end.	evm_27.model.AmTr_v1.0_scaffold00061.2_5	-6,545155	13	17,7	2	-	2	0,222222	HVPISIA GTLIR MFAGPI	0,001112347
Q9FH31	2S albumin	<i>Arabidopsis thaliana</i>	AT5G54740	06 Protein destination and storage	06.20 Storage proteins	0,045	55	emb./end.	evm_27.model.AmTr_v1.0_scaffold00005.2_15	-50,426	35	17,2	15	9	6	2,142857	CCEOLE NMREEC R	0,008342603
Q9FX54	Glyceraldehyde-3-phosphate dehydrogenase	<i>Arabidopsis thaliana</i>	AT1G13440	02 Energy	02.01 Glycolysis	3,00E-51	82	emb./end.	evm_27.model.AmTr_v1.0_scaffold00177.2_3	-9,422508	16	15,5	2	1	2	0,5	TLLFGD KPVTVF GVR	0,001112347
Q9FX54	Glyceraldehyde-3-phosphate dehydrogenase	<i>Arabidopsis thaliana</i>	AT1G13440	02 Energy	02.01 Glycolysis	8,00E-95	86	emb./end.	evm_27.model.AmTr_v1.0_scaffold00177.2_4	-29,96041	24	24,7	10	9	5	1,428572	AAGFNII PSSTGA AK	0,005561735
Q9LFA3	Monodehydroascorbate reductase	<i>Arabidopsis thaliana</i>	AT3G52880	11 Disease/defence	11.06 Detoxification	e-175	84	emb./end.	evm_27.model.AmTr_v1.0_scaffold00069.1_93	-9,665546	5	47,1	2	-	2	0,105263	AYLFPE GAAR VQPPVD	0,001112347
Q9LHT0	Short chain alcohol dehydrogenase	<i>Arabidopsis thaliana</i>	AT5G06060	02 Energy	02.16 Fermentation	9,00E-99	82	emb./end.	evm_27.model.AmTr_v1.0_scaffold00012.3_18	-11,06048	10	28,9	2	-	2	0,222222	LNILVNN VGTNIP K	0,001112347
Q9LKR3	HSP70 (Luminal binding protein 1)	<i>Arabidopsis thaliana</i>	AT5G28540	06 Protein destination and storage	06.01 Folding and stability	0	90	emb./end.	evm_27.model.AmTr_v1.0_scaffold00002.5_4	-28,54088	4	74,2	5	-	3	0,185185	IINEPTA AAIAYGL DKK	0,002780868
Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	4,00E-53	48	emb./end.	evm_27.model.AmTr_v1.0_scaffold00002.6_57	-650,1507	68	59,8	298	-	83	10,75	#####	0,165739711
Q9M040	Pyruvate decarboxylase-like protein	<i>Arabidopsis thaliana</i>	AT5G01320	02 Energy	02.16 Fermentation	0	88	emb./end.	evm_27.model.AmTr_v1.0_scaffold00007.1_42	-20,46228	8	65,3	5	-	4	0,333333	IVYPEG VPLK EPVPCFI	0,002780868
Q9M132	Late embryogenesis abundant protein (LEA)	<i>Arabidopsis thaliana</i>	AT4G01410	11 Disease/defence	11.05 Stress responses	6,00E-49	70	end.	evm_27.model.AmTr_v1.0_scaffold00001.4_93	-12,70246	16	23,8	2	-	2	0,285714	LPSGPK PPSPS PAPAGA	0,001112347
Q9M5K5	Dihydroliipoamide dehydrogenase	<i>Arabidopsis thaliana</i>	AT3G16950	02 Energy	02.10 TCA pathway	0,00E+00	82	end.	evm_27.model.AmTr_v1.0_scaffold00003.1_6	-13,91364	4	59,3	2	-	2	0,090909	LVPHVY CIGDAN GK	0,001112347
Q9SAJ4	Phosphoglycerate kinase	<i>Arabidopsis thaliana</i>	AT1G79550	02 Energy	02.01 Glycolysis	0	93	emb./end.	evm_27.model.AmTr_v1.0_scaffold00062.1_99	-36,97078	27	42,4	7	-	6	0,363636	VDLNVP LDDNQK ITDDTR	0,003893215
Q9SF20	MD-2-related lipid recognition domain-containing protein	<i>Arabidopsis thaliana</i>	AT3G11780	11 Disease/defence	11.02 Defence-related	4,00E-46	74	emb./end.	evm_27.model.AmTr_v1.0_scaffold00004.1_91	-16,91722	19	16,4	2	-	2	0,333333	VSGMEV DPDPVE R	0,001112347
Q9SJK9	Fructose-bisphosphate aldolase	<i>Arabidopsis thaliana</i>	AT2G36460	02 Energy	02.01 Glycolysis	e-178	91	emb./end.	evm_27.model.AmTr_v1.0_scaffold00040.2_04	-16,58503	7	38,2	3	-	2	0,1875	GILAADE STGTIG KR	0,001668521
Q9SK09	Cupin family protein (Vicilin)	<i>Arabidopsis thaliana</i>	AT2G28490	06 Protein destination and storage	06.20 Storage proteins	e-118	66	emb./end.	evm_27.model.AmTr_v1.0_scaffold00080.8_2	-87,19413	36	50,4	25	-	14	1,444444	#####	0,013904338
Q9SRT9	UDP-L-arabinose mutase	<i>Arabidopsis thaliana</i>	AT3G02230	09 Cell structure	09.01 Cell wall	0	95	emb./end.	evm_27.model.AmTr_v1.0_scaffold00047.1_49	-26,94539	14	40,9	6	3	4	0,272727	VICDHL GLGLK VICDHL	0,003337041
Q9SRT9	UDP-L-arabinose mutase	<i>Arabidopsis thaliana</i>	AT3G02230	09 Cell structure	09.01 Cell wall	0	93	end.	evm_27.model.AmTr_v1.0_scaffold00013.8_6	-17,29034	11	41,3	5	2	4	0,263158	VICDHL GLGVK LADELDI	0,002780868
Q9SRZ6	Isocitrate dehydrogenase	<i>Arabidopsis thaliana</i>	AT1G65930	02 Energy	02.10 TCA pathway	0	87	end.	evm_27.model.AmTr_v1.0_scaffold00085.1_12	-5,449527	5	55,8	2	-	2	0,083333	GGPVAL AMFNVD ESIR	0,001112347
Q9T0G0	Hydroxysteroid dehydrogenase (Steroleosin-B)	<i>Arabidopsis thaliana</i>	AT4G10020	01 Metabolism	01.06 Lipid and sterol	7,00E-88	84	emb./end.	evm_27.model.AmTr_v1.0_scaffold00099.1_3	-16,94091	18	24,8	5	-	5	0,833333	RGANLV LVAR MSLYAA	0,002780868
Q9ZP06	Malate dehydrogenase	<i>Arabidopsis thaliana</i>	AT1G53240	02 Energy	02.10 TCA pathway	e-143	90	emb./end.	evm_27.model.AmTr_v1.0_scaffold00021.8_7	-23,16765	17	36,1	4	-	4	0,666667	KLFGVT TLDVVR LFGVTT	0,002224694

Q9ZRW8	Glutathione S-transferase	<i>Arabidopsis thaliana</i>	AT1G78380	11 Disease/defence	11.06 Detoxification	4,00E-74	76	emb./end.	evm_27.model.AmTr_v1.0_scaffold00092.81	-83,52095	40	24,5	13	-	11	1,444444	EENLAN KGELLL K	0,007230256
Q9ZU52	Fructose-bisphosphate aldolase (chloroplastic)	<i>Arabidopsis thaliana</i>	AT2G01140	02 Energy	02.01 Glycolysis	0	89	emb./end.	evm_27.model.AmTr_v1.0_scaffold00001.161	-12,80521	6	42,4	2	-	2	0,142857	LSSIGLD NTEPNR ASPETIA SGCEAF	0,001112347
Q9ZV34	Thaumatococcus putative	<i>Arabidopsis thaliana</i>	AT2G28790	11 Disease/defence	11.01 Resistance genes	6,00E-91	81	emb./end.	evm_27.model.AmTr_v1.0_scaffold00012.94	-12,11521	10	26,5	2	-	2	0,2	GTDELC CR	0,001112347
Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	2,00E-64	51	emb./end.	evm_27.model.AmTr_v1.0_scaffold00067.11	-623,0742	71	49,1	293	185	77	15,47368	#####	0,162958843
Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	7,00E-70	51	emb./end.	evm_27.model.AmTr_v1.0_scaffold00067.7	-921,9827	81	54,5	497	389	126	24	#####	0,276418242

Supplemental table 3: list of the proteins identified from the albumin fraction of *Amborella trichopoda* whole mature seed by 2-DE

Proteins have been analyzed by two-dimensional electrophoresis and identified by mass spectrometry LC/MS-MS. The protein spots were analysed by LC-MS/MS on the PAPPISO platform (Benoit Valot, Thierry Balliau, Michel Zivy, INRA Moulon, France; <http://pappiso.inra.fr>). Based on the spectrum generated, proteins were identified using the X-Tandem software. "Spot ID" relates to the protein position on the 2DE reference map. "Number of id per spot" reflect the number of single identifications in the same spot. "NCBI accession number" is the accession number in NCBI database. "Protein name", "Organism" relates to the organism from which the identified protein comes from for functional analysis - efforts were focus on *Arabidopsis thaliana* as a plant model. "AGI", "Function category" and "Function description" relate to the functional categories defined according to the ontological classification of Bevan *et al.* (Bevan *et al.* (1998) Nature 391:485-488). "log(Evalue) identification" reflects the statistical power of the identification by BLAST (performed on TAIR or BLAST). "Identity" indicates in % the recovery of the *Amborella* protein sequence against the identified protein. "Description" was taken from the Amborella EVM 27 Predicted Proteins (<http://www.amborella.org>). The "log (E value)" is a statistical parameter that represents the number of peptides present at random in the database. It was calculated by the product of the Evaluate of unique peptides identified in the protein spot (Valot *et al.*, 2011). "Coverage" refers to the recovery rate of the protein by the identified peptides, expressed in %. "MW" relates to the molecular weight expressed in kDa. "Spectra" corresponds to the number of spectra which allowed the protein identification from 2DE protein single spot. "Specifics" corresponds to the number of specific spectrum corresponding to the identification among the other identifications of the group. "Uniques" refers to the number of unique peptides (different sequences) that led to the protein identification. "PAI" is the protein abundance index in the spot. "Peptide sequences" displays identified peptides for each protein spot.

Functional identification										Mass spec data								
Spot ID	Number of id per spot	NCBI accession number	Protein name	Organism	AGI	Function category	Function description	log (Evalue) identification	Identity	Description	log(E value)	Coverage	MW	Spectra	Specifics	Uniques	PAI	Peptide sequence
1	1	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-102,8897	55	43,5	30	-	20	1,34783	IEMACPH KGDATATIPAGK KGDATATIPAGK
2	1	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-135,6284	65	43,5	42	-	24	2	IEMACPH KGDATATIPAGK KGDATATIPAGK
3	1	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-125,5967	57	43,5	39	-	22	1,82609	IEMACPH KGDATATIPAGK KGDATATIPAGK
4	1	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-143,6343	61	43,5	44	-	26	2,17391	IEMACPH KGDATATIPAGK KGDATATIPAGK
5	3	Q9SIB9	Aconitase	<i>Arabidopsis thaliana</i>	AT2G05710	02 Energy	02.10 TCA pathway	0	84	evm_27.model.AmTr_v1.0_scaffold00001.143	-63,1981	14	107	11	6	11	0,30556	ATYEAITK IDKLPYSIR MFVDYNEPQT YLLQSLGK YLDQQGFHIV GYGCTTC
5	3	Q42560	Aconitase	<i>Arabidopsis thaliana</i>	AT4G35830	02 Energy	02.10 TCA pathway	0	84	evm_27.model.AmTr_v1.0_scaffold00115.1	-41,84522	13	93,2	8	3	8	0,2963	KGDATATIPAGK KGDATATIPAGK IEMACPHVSG
5	3	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-63,96007	47	43,5	15	-	13	0,65217	ATYEAITK PGQDVTVVTD SGK
6	3	Q9SIB9	Aconitase	<i>Arabidopsis thaliana</i>	AT2G05710	02 Energy	02.10 TCA pathway	0	84	evm_27.model.AmTr_v1.0_scaffold00001.143	-100,0359	30	107	21	10	20	0,61111	MFVDYKEPQT ER TIHVPTGEELY
6	3	Q42560	Aconitase	<i>Arabidopsis thaliana</i>	AT4G35830	02 Energy	02.10 TCA pathway	0	84	evm_27.model.AmTr_v1.0_scaffold00115.1	-66,72593	28	93,2	15	4	15	0,62963	KGDATATIPAGK KGDATATIPAGK PSSEQLQGLIH
6	3	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-52,41807	39	43,5	13	-	10	0,6087	ATYEAITK PGQDVTVVTD SGK
7	3	Q9SIB9	Aconitase	<i>Arabidopsis thaliana</i>	AT2G05710	02 Energy	02.10 TCA pathway	0	84	evm_27.model.AmTr_v1.0_scaffold00001.143	-136,3309	32	107	28	16	24	0,80556	KDFNSYGSR YLLQSLGK TIHVPTGEELY
7	3	Q42560	Aconitase	<i>Arabidopsis thaliana</i>	AT4G35830	02 Energy	02.10 TCA pathway	0	84	evm_27.model.AmTr_v1.0_scaffold00115.1	-66,94725	22	93,2	16	4	15	0,62963	KGDATATIPAGK EVSFNVPSR AQSDSVFVVG
7	3	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-30,92339	23	43,5	7	-	6	0,3913	AIKEEISK KISQEDYVK ISOEDYVK
8	3	O50008	5-methyltetrahydropteroyl triolotate-	<i>Arabidopsis thaliana</i>	AT5G17920	01 Metabolism	01.01 Amino Acid	0	85	evm_27.model.AmTr_v1.0_scaffold00004.99	-75,21515	23	84,5	16	-	15	0,54545	RGNDVEMAR GNDEVMAR ATYEAITK
8	3	Q9SIB9	Aconitase	<i>Arabidopsis thaliana</i>	AT2G05710	02 Energy	02.10 TCA pathway	0	84	evm_27.model.AmTr_v1.0_scaffold00001.143	-38,92142	10	107	12	-	10	0,33333	IYSSGNEK TILYEQANK
8	3	F4HWR0	Dessication-related protein	<i>Arabidopsis thaliana</i>	AT1G47980	11 Disease/defence	11.05 Stress responses	e-106	70	evm_27.model.AmTr_v1.0_scaffold00016.315	-4,930702	5	33,4	2	-	2	0,15385	

9	1	O50008	5-methyltetrahydropteroyl tripartate-	<i>Arabidopsis thaliana</i>	AT5G17920	01 Metabolism	01.01 Amino Acid	0	85	evm_27.model.AmTr_v1.0_scaffold00004.9	-99,53852	29	84,5	27	21	19	0,84848	AIKEEISK FSYASHK GNASL PAMEM
10	1	O50008	5-methyltetrahydropteroyl tripartate-	<i>Arabidopsis thaliana</i>	AT5G17920	01 Metabolism	01.01 Amino Acid	0	85	evm_27.model.AmTr_v1.0_scaffold00004.9	-89,65131	28	84,5	21	-	19	0,66667	AIKEEISK KISQEDYVK ISOEDYVK
11	1	Q9S9P4	S-adenosyl-L-methionine-dependent methyltransferase (7-	<i>Arabidopsis thaliana</i>	AT1G30550	04 Transcription	04.22 mRNA processing	2e-79	68	evm_27.model.AmTr_v1.0_scaffold00019.5	-198,9159	35	122	57	-	35	1,30435	SSLSEDDQK AGYVSAGDK SKGVTAAPIR
12	5	Q9S9P4	S-adenosyl-L-methionine-dependent methyltransferase (7-	<i>Arabidopsis thaliana</i>	AT1G30550	04 Transcription	04.22 mRNA processing	2e-79	68	evm_27.model.AmTr_v1.0_scaffold00019.5	-173,9084	30	122	42	-	30	1,04348	SSLSEDDQK AGYVSAGDK GLDFAHGK
12	5	P22953	HSC70 (Heat shock cognate 70 kDa protein)	<i>Arabidopsis thaliana</i>	AT5G02500	06 Protein destination and storage	06.01 Folding and stability	0	83	evm_27.model.AmTr_v1.0_scaffold00072.1	-90,39309	36	71,9	19	14	16	0,95455	RFSASVQSD IK STAGDTHLGG
12	5	Q9S9N1	HSP70 (heat shock protein)	<i>Arabidopsis thaliana</i>	AT1G16030	06 Protein destination and storage	06.01 Folding and stability	0	80	evm_27.model.AmTr_v1.0_scaffold00137.8	-41,69191	16	71,6	6	2	6	0,42857	FSDPSVQADM K NOVALNPENT
12	5	Q9LKR3	HSP70 (Luminal binding protein 1)	<i>Arabidopsis thaliana</i>	AT5G28540	06 Protein destination and storage	06.01 Folding and stability	0	82	evm_27.model.AmTr_v1.0_scaffold00002.5	-105,775	35	74,2	23	17	22	0,88889	SSQHQRV ALSSQHQVR LADKIESDDKE
12	5	Q39043	HSP70 (Luminal binding protein 2)	<i>Arabidopsis thaliana</i>	AT5G42020	06 Protein destination and storage	06.01 Folding and stability	0	88	evm_27.model.AmTr_v1.0_scaffold00009.3	-57,07122	17	73,2	9	4	9	0,36	AMDAGLEK SGHVEIANDQ GNR
13	4	Q8L831	Nudix hydrolase	<i>Arabidopsis thaliana</i>	AT1G79690	01 Metabolism	01.03 Nucleotides	0	66	evm_27.model.AmTr_v1.0_scaffold00036.8	-26,68328	7	88,2	7	1	5	0,22581	GGFILDSTGTF SVNFSE
13	4	Q9S9P4	S-adenosyl-L-methionine-dependent methyltransferase (7-	<i>Arabidopsis thaliana</i>	AT1G30550	04 Transcription	04.22 mRNA processing	2e-79	68	evm_27.model.AmTr_v1.0_scaffold00019.5	-202,468	35	122	55	49	36	1,26087	SSLSEDDQK EHSDDSDLDK AGYVSAGDK
13	4	Q9LKR3	HSP70 (Luminal binding protein 1)	<i>Arabidopsis thaliana</i>	AT5G28540	06 Protein destination and storage	06.01 Folding and stability	0	82	evm_27.model.AmTr_v1.0_scaffold00002.5	-23,75381	9	74,2	6	4	6	0,22222	NQAALNPER LSQEIER ALEDASLQK
13	4	P22953	HSC70 (Heat shock cognate 70 kDa protein)	<i>Arabidopsis thaliana</i>	AT5G02500	06 Protein destination and storage	06.01 Folding and stability	0	83	evm_27.model.AmTr_v1.0_scaffold00072.1	-41,57169	13	71,9	7	5	7	0,31818	FSDASVQSDIK NALENYANR
14	2	Q8L831	Nudix hydrolase	<i>Arabidopsis thaliana</i>	AT1G79690	01 Metabolism	01.03 Nucleotides	0	66	evm_27.model.AmTr_v1.0_scaffold00036.8	-23,37306	8	88,2	8	2	6	0,25806	SPWSSLDENK TITLPSGQOST VR
14	2	Q9S9P4	S-adenosyl-L-methionine-dependent methyltransferase (7-	<i>Arabidopsis thaliana</i>	AT1G30550	04 Transcription	04.22 mRNA processing	2e-79	68	evm_27.model.AmTr_v1.0_scaffold00019.5	-281,661	39	122	90	84	49	2,02174	SSLSEDDQK EHSDDSDLDK SKGVTAAPIR
15	3	Q8L831	Nudix hydrolase	<i>Arabidopsis thaliana</i>	AT1G79690	01 Metabolism	01.03 Nucleotides	0	66	evm_27.model.AmTr_v1.0_scaffold00036.8	-23,93043	8	88,2	9	1	6	0,32258	TITLPSGQOST VR
15	3	Q9S9P4	S-adenosyl-L-methionine-dependent methyltransferase (7-	<i>Arabidopsis thaliana</i>	AT1G30550	04 Transcription	04.22 mRNA processing	2e-79	68	evm_27.model.AmTr_v1.0_scaffold00019.5	-232,509	36	122	70	62	44	1,6087	SSLSEDDQK EHSDDSDLDK EHSDDSDLDK
15	3	Q9S9N1	HSP70 (heat shock protein)	<i>Arabidopsis thaliana</i>	AT1G16030	06 Protein destination and storage	06.01 Folding and stability	0	80	evm_27.model.AmTr_v1.0_scaffold00137.8	-77,01826	23	71,6	13	-	12	0,66667	LSKEIEK TKDNNLLGK FSDPSVQADM
16	2	Q9S9P4	S-adenosyl-L-methionine-dependent methyltransferase (7-	<i>Arabidopsis thaliana</i>	AT1G30550	04 Transcription	04.22 mRNA processing	2e-79	68	evm_27.model.AmTr_v1.0_scaffold00019.5	-133,7371	24	122	32	-	25	0,73913	SSLSEDDQK KASDLLQK EHSDDSDLDK
16	2	Q9S9N1	HSP70 (heat shock protein)	<i>Arabidopsis thaliana</i>	AT1G16030	06 Protein destination and storage	06.01 Folding and stability	0	80	evm_27.model.AmTr_v1.0_scaffold00137.8	-75,12224	23	71,6	15	-	13	0,7619	TKDNNLLGK FSDPSVQADM K
17	2	Q9S9P4	S-adenosyl-L-methionine-dependent methyltransferase (7-	<i>Arabidopsis thaliana</i>	AT1G30550	04 Transcription	04.22 mRNA processing	2e-79	68	evm_27.model.AmTr_v1.0_scaffold00019.5	-82,98392	18	122	17	-	16	0,3913	DDLATSEK AYEVANTPSLK AFLTTADSAVK
17	2	Q9S9N1	HSP70 (heat shock protein)	<i>Arabidopsis thaliana</i>	AT1G16030	06 Protein destination and storage	06.01 Folding and stability	0	80	evm_27.model.AmTr_v1.0_scaffold00137.8	-205,7307	47	71,6	56	-	32	2,66667	KCLETVEK AAEQYKAEDE EVKR
18	3	Q9S9P4	S-adenosyl-L-methionine-dependent methyltransferase (7-	<i>Arabidopsis thaliana</i>	AT1G30550	04 Transcription	04.22 mRNA processing	2e-79	68	evm_27.model.AmTr_v1.0_scaffold00019.5	-301,8307	45	122	88	-	54	2,04348	SSLSEDDQK EHSDDSDLDK SKGVTAAPIR
18	3	Q9S9N1	HSP70 (heat shock protein)	<i>Arabidopsis thaliana</i>	AT1G16030	06 Protein destination and storage	06.01 Folding and stability	0	80	evm_27.model.AmTr_v1.0_scaffold00137.8	-46,21963	21	71,6	11	8	11	0,57143	TKDNNLLGK FSDPSVQADM K
18	3	P22953	HSC70 (Heat shock cognate 70 kDa protein)	<i>Arabidopsis thaliana</i>	AT5G02500	06 Protein destination and storage	06.01 Folding and stability	0	83	evm_27.model.AmTr_v1.0_scaffold00072.1	-19,53139	7	71,9	4	1	4	0,18182	VEIANDQGNR

19	6	Q8L831	Nudix hydrolase	<i>Arabidopsis thaliana</i>	AT1G79690	01 Metabolism	01.03 Nucleotides	0	66	evm_27.model.AmTr_v1.0_scaffold00036.84	-14,56268	5	88,2	4	1	4	0,12903	LQEAESVAVK
19	6	Q9S9P4	S-adenosyl-L-methionine-dependent methyltransferase (7-	<i>Arabidopsis thaliana</i>	AT1G30550	04 Transcription	04.22 mRNA processing	2e-79	68	evm_27.model.AmTr_v1.0_scaffold00019.57	-131,5984	30	122	33	30	26	0,73913	KASDLLQK AYEVANTPSLK EGLDEAH FSDPSVQADM K
19	6	Q9S9N1	HSP70 (heat shock protein)	<i>Arabidopsis thaliana</i>	AT1G16030	06 Protein destination and storage	06.01 Folding and stability	0	80	evm_27.model.AmTr_v1.0_scaffold00137.8	-37,42429	14	71,6	7	-	7	0,33333	VEIIPNDQGNR FAGDDAPR VGMGQKDAYV GDEAQS
19	6	P53492	Actin 7	<i>Arabidopsis thaliana</i>	AT5G09810	09 Cell structure	09.04 Cytoskeleton	0	97	evm_27.model.AmTr_v1.0_scaffold00018.104	-21,83434	14	41,6	6	-	6	0,4	FAGDDAPR VGMGQKDAYV GDEAQS
19	6	P53496	Actin 11	<i>Arabidopsis thaliana</i>	AT3G12110	09 Cell structure	09.04 Cytoskeleton	0	96	evm_27.model.AmTr_v1.0_scaffold00044.61	-21,83434	14	43,9	6	-	6	0,375	FAGDDAPR VGMGQKDAYV GDEAQS
19	6	P53492	Actin 7	<i>Arabidopsis thaliana</i>	AT5G09810	09 Cell structure	09.04 Cytoskeleton	0	97	evm_27.model.AmTr_v1.0_scaffold00062.182	-21,83434	14	41,5	6	-	6	0,4	FAGDDAPR VGMGQKDAYV GDEAQS
20	3	Q9S9P4	S-adenosyl-L-methionine-dependent methyltransferase (7-	<i>Arabidopsis thaliana</i>	AT1G30550	04 Transcription	04.22 mRNA processing	2e-79	68	evm_27.model.AmTr_v1.0_scaffold00019.57	-55,2701	13	122	13	-	11	0,28261	KASDLLQK FGLDEAHGK AFLTADSAVK
20	3	P29197	Chaperonin (Chaperonin-60kD, ch60, CPN60)	<i>Arabidopsis thaliana</i>	AT3G23990	06 Protein destination and storage	06.01 Folding and stability	0	86	evm_27.model.AmTr_v1.0_scaffold00003.261	-208,6805	56	61,2	47	-	33	1,6	MPVHTIASN LHTANFDQK IGGASEVEVS
20	3	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5e-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-21,1972	14	43,5	4	-	4	0,17391	KGDTATIPAGK AQSDSVFVVG PR
21	2	Q9M9K1	Phosphoglycerate mutase	<i>Arabidopsis thaliana</i>	AT3G08590	02 Energy	02.01 Glycolysis	0	82	evm_27.model.AmTr_v1.0_scaffold00077.211	-134,2158	56	61,3	31	-	26	1,375	SALEAVKK TPTMDSLK TFACSETVK
21	2	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-36,50215	26	43,5	10	-	7	0,47826	KGDTATIPAGK KGDTATIPAGK AQSDSVFVVG
22	2	Q9CA83	Malate dehydrogenase	<i>Arabidopsis thaliana</i>	AT1G79750	02 Energy	02.10 TCA pathway	0	76	evm_27.model.AmTr_v1.0_scaffold00056.87	-40,91504	16	71,9	9	-	8	0,31034	ISAHIAANVTK YAMAMDLQER
22	2	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5e-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-51,201	37	43,5	11	-	9	0,52174	KGDTATIPAGK PSSEQLQLLH GSGGGK
23	2	Q9CA83	Malate dehydrogenase	<i>Arabidopsis thaliana</i>	AT1G79750	02 Energy	02.10 TCA pathway	0	76	evm_27.model.AmTr_v1.0_scaffold00056.87	-134,8279	42	71,9	31	-	23	1,10345	IPVEEAR ISAHIAAN YAMAMDLQER
23	2	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5e-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-79,0151	47	43,5	19	-	14	0,91304	IEMACPH KGDTATIPAGK KGDTATIPAGK
24	3	O49299	Phosphoglucosyltransferase	<i>Arabidopsis thaliana</i>	AT1G23190	02 Energy	02.01 Glycolysis	0	81	evm_27.model.AmTr_v1.0_scaffold00010.123	-96,26015	43	63,7	24	-	23	0,89655	ETSPIDSQK KETSPIQSQK GTSGLR
24	3	Q9C9K3	Pyrophosphate-fructose 6-phosphate 1-phosphotransferase	<i>Arabidopsis thaliana</i>	AT1G76550	02 Energy	02.01 Glycolysis	0	79	evm_27.model.AmTr_v1.0_scaffold00022.114	-22,92995	10	73,8	5	-	5	0,17857	ATAQVPDAK PAVHPATVDLR NPGPLQFEGP
24	3	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5e-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-9,657578	9	43,5	2	-	2	0,08696	ISNDHGELYEL DETEYSPLR AFSDEILEASF
25	2	Q9C9K3	Pyrophosphate-fructose 6-phosphate 1-phosphotransferase	<i>Arabidopsis thaliana</i>	AT1G76550	02 Energy	02.01 Glycolysis	0	78	evm_27.model.AmTr_v1.0_scaffold00022.114	-43,8919	24	73,8	15	-	12	0,60714	ATAQVPDAK IIQHPVIR CGGAPITAMM
25	2	O49299	Phosphoglucosyltransferase	<i>Arabidopsis thaliana</i>	AT1G23190	02 Energy	02.01 Glycolysis	0	81	evm_27.model.AmTr_v1.0_scaffold00010.123	-66,50652	39	63,7	18	-	17	0,68966	LSGTGSEGATIR ETSPIDSQK LSGTGSEGATIR
26	1	O49299	Phosphoglucosyltransferase	<i>Arabidopsis thaliana</i>	AT1G23190	02 Energy	02.01 Glycolysis	0	81	evm_27.model.AmTr_v1.0_scaffold00010.123	-89,94231	43	63,7	25	-	22	0,89655	ETSPIDSQK LSGTGSEGATIR ETSPIDSQK
27	2	O49299	Phosphoglucosyltransferase	<i>Arabidopsis thaliana</i>	AT1G23190	02 Energy	02.01 Glycolysis	0	81	evm_27.model.AmTr_v1.0_scaffold00010.123	-47,33076	21	63,7	11	-	10	0,44828	LSGTGSEGATIR ETSPIDSQK
27	2	Q9C9K3	Pyrophosphate-fructose 6-phosphate 1-phosphotransferase	<i>Arabidopsis thaliana</i>	AT1G76550	02 Energy	02.01 Glycolysis	0	78	evm_27.model.AmTr_v1.0_scaffold00022.114	-78,99382	31	73,8	17	-	16	0,64286	ATAQVPDAK PAVHPATVDLR ASHVALECTL
28	2	O49299	Phosphoglucosyltransferase	<i>Arabidopsis thaliana</i>	AT1G23190	02 Energy	02.01 Glycolysis	0	81	evm_27.model.AmTr_v1.0_scaffold00010.123	-96,3412	42	63,7	24	-	20	0,82759	ETSPIDSQK GTSGLR GGPAPEAITDK

28	2	Q9C9K3	Pyrophosphate-fructose 6-phosphate 1-phosphotransferase	<i>Arabidopsis thaliana</i>	AT1G76550	02 Energy	02.01 Glycolysis	0	78	evm_27.model.AmTr_v1.0_scaffold00022.114	-33,60399	15	73,8	8	-	8	0,28571	ATAQVPDAK PAVHPATVDLDR VEFGDGTITTA
29	2	O49299	Phosphoglucosmutase	<i>Arabidopsis thaliana</i>	AT1G23190	02 Energy	02.01 Glycolysis	0	81	evm_27.model.AmTr_v1.0_scaffold00010.123	-210,3922	66	63,7	56	-	42	2,03448	DPVDGVSVK MQEFTGR LSCGTGSEGATL
29	2	Q9S9P4	S-adenosyl-L-methionine-dependent methyltransferase (7-	<i>Arabidopsis thaliana</i>	AT1G30550	04 Transcription	04.22 mRNA processing	2e-79	68	evm_27.model.AmTr_v1.0_scaffold00019.57	-46,09355	8	122	12	-	6	0,26087	IQVPIVDIAPK ATFEAFVGVGR GGFVMDTNG
30	1	Q9FX54	Glyceraldehyde-3-phosphate dehydrogenase	<i>Arabidopsis thaliana</i>	AT1G13440	02 Energy	02.01 Glycolysis	6e-94	82	evm_27.model.AmTr_v1.0_scaffold00177.24	-18,55315	24	24,7	5	-	4	0,85714	PVTVEGNR AAGFNIPSST GAAK
31	2	Q9SAJ6	Glyceraldehyde-3-phosphate dehydrogenase	<i>Arabidopsis thaliana</i>	AT1G79530	02 Energy	02.01 Glycolysis	e-165	70,0000	evm_27.model.AmTr_v1.0_scaffold00039.188	-4,832092	3	45,2	2	1	2	0,1	LTGMAFR
31	2	Q9FX54	Glyceraldehyde-3-phosphate dehydrogenase	<i>Arabidopsis thaliana</i>	AT1G13440	02 Energy	02.01 Glycolysis	6,00E-94	74	evm_27.model.AmTr_v1.0_scaffold00177.24	-28,31506	34	24,7	9	8	6	1,28571	DAPMFVVGVN EHYEK AAGFNIPSST
32	3	Q5E924	Glyceraldehyde-3-phosphate dehydrogenase	<i>Arabidopsis thaliana</i>	AT1G79530	02 Energy	02.01 Glycolysis	e-162	77	evm_27.model.AmTr_v1.0_scaffold00039.188	-10,0716	6	45,2	5	2	4	0,3	SSIFDAK SSIFDAK
32	3	Q9SAJ6	Glyceraldehyde-3-phosphate dehydrogenase	<i>Arabidopsis thaliana</i>	AT1G16300	02 Energy	02.01 Glycolysis	e-165	70	evm_27.model.AmTr_v1.0_scaffold00032.283	-10,0716	8	45,4	5	2	4	0,33333	SSIFDAK SSIFDAK
32	3	Q9FX54	Glyceraldehyde-3-phosphate dehydrogenase	<i>Arabidopsis thaliana</i>	AT1G13440	02 Energy	02.01 Glycolysis	6,00E-94	82	evm_27.model.AmTr_v1.0_scaffold00177.24	-65,27201	58	24,7	20	17	16	3	KVVISAPSK VVISAPSK KVVISAPSK
33	3	O49485	Phosphoglycerate dehydrogenase	<i>Arabidopsis thaliana</i>	AT4G34200	01 Metabolism	01.01 Amino Acid	0	74	evm_27.model.AmTr_v1.0_scaffold00051.59	-51,54272	27	65,2	15	-	12	0,55172	NIQAQADASKM KHAVMAIGVD EFPNK
33	3	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-76,13778	50	43,5	20	-	15	0,91304	IEMACPH KGDATIPAGK KGDATIPAGK
33	3	Q9STS1	Betaine aldehyde dehydrogenase	<i>Arabidopsis thaliana</i>	AT3G48170	11 Disease/defence	11.05 Stress responses	0	78	evm_27.model.AmTr_v1.0_scaffold00055.145	-68,0287	24	54,6	15	-	11	0,88889	DLEQCDR VSDPLQDGR IAFTGSSMTG
34	2	Q9S9P4	S-adenosyl-L-methionine-dependent methyltransferase (7-	<i>Arabidopsis thaliana</i>	AT1G30550	04 Transcription	04.22 mRNA processing	2e-79	68	evm_27.model.AmTr_v1.0_scaffold00019.57	-39,7301	6	122	7	-	4	0,15217	ATFEAFVGVGR GGFVMDTNG AESVDFSK
34	2	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5e-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-118,9046	59	43,5	39	-	24	1,86957	IEMACPH KGDATIPAGK KGDATIPAGK
35	2	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5e-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-79,45148	47	43,5	23	-	15	1,08696	IEMACPH KGDATIPAGK IEMACPHVSG
35	2	Q9STS1	Betaine aldehyde dehydrogenase	<i>Arabidopsis thaliana</i>	AT3G48170	11 Disease/defence	11.05 Stress responses	0	78	evm_27.model.AmTr_v1.0_scaffold00055.145	-66,07894	27	54,6	16	-	12	1	IAFTGSSMTG R VSDPLQDGR
36	2	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-90,44898	44	43,5	21	-	15	0,91304	KGDATIPAGK KGDATIPAGK ARIEMACPHV
36	2	Q9STS1	Betaine aldehyde dehydrogenase	<i>Arabidopsis thaliana</i>	AT3G48170	11 Disease/defence	11.05 Stress responses	0	78	evm_27.model.AmTr_v1.0_scaffold00055.145	-55,57142	23	54,6	14	-	10	0,83333	IAFTGSSMTG R VSDPLQDGR
37	2	Q9M5K2	Dihydropolipoamide dehydrogenase	<i>Arabidopsis thaliana</i>	AT3G17240	01 Metabolism	01.06 Lipid and sterol	0	77	evm_27.model.AmTr_v1.0_scaffold00064.49	-114,5202	49	53,8	23	21	18	1,04348	TCHAHPTLSE AVK VTGVDAASDSG
37	2	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-34,46526	29	43,5	8	-	8	0,43478	KGDATIPAGK EVSFNVPSR AQSDSVFVVG
38	2	P94078	Alpha-mannosidase	<i>Arabidopsis thaliana</i>	AT3G26720	01 Metabolism	01.05 Sugars and polysaccharides	0	67	evm_27.model.AmTr_v1.0_scaffold00016.68	-30,27021	6	114,9	7	-	6	0,16279	IDYQDR VMSGYMAA R
38	2	Q9M5K2	Dihydropolipoamide dehydrogenase	<i>Arabidopsis thaliana</i>	AT3G17240	01 Metabolism	01.06 Lipid and sterol	0	77	evm_27.model.AmTr_v1.0_scaffold00064.49	-82,45521	40	53,8	19	2	17	0,82609	AAQLGLK GALGGTCLNV GCIPSK
39	2	P94078	Alpha-mannosidase	<i>Arabidopsis thaliana</i>	AT3G26720	01 Metabolism	01.05 Sugars and polysaccharides	0	67	evm_27.model.AmTr_v1.0_scaffold00016.68	-84,31109	18	114,9	24	-	17	0,60465	QHWANDYAK EQSEAMQAVV K
39	2	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-16,97535	15	43,5	4	-	4	0,21739	KGDATIPAGK AQSDSVFVVG PR

40	1	P34795	Phosphoglucose isomerase	<i>Arabidopsis thaliana</i>	AT5G42740	02 Energy	02.01 Glycolysis	0	82	evm_27.model.AmTr_v1.0_scaffold00111.63	-139,5044	49	62,4	38	-	29	1,39286	IQQVSMESNGK VHVEDINK
41	2	P34795	Phosphoglucose isomerase	<i>Arabidopsis thaliana</i>	AT5G42740	02 Energy	02.01 Glycolysis	0	82	evm_27.model.AmTr_v1.0_scaffold00111.63	-179,9548	58	62,4	54	-	32	2	IQQVSMESNGK DLMNDSEK
41	2	Q9LZC3	Malate synthase	<i>Arabidopsis thaliana</i>	AT5G03860	02 Energy	02.10 TCA pathway	0	75	evm_27.model.AmTr_v1.0_scaffold00049.86	-6,466546	6	64,8	3	-	3	0,11111	DHSVGLNCGR HGAVLDGDGVK
42	2	P34795	Phosphoglucose isomerase	<i>Arabidopsis thaliana</i>	AT5G42740	02 Energy	02.01 Glycolysis	0	82	evm_27.model.AmTr_v1.0_scaffold00111.63	-108,225	41	62,4	25	-	20	0,92857	VHVEDINK LAEAAHLR SLASQVR
42	2	Q9LZC3	Malate synthase	<i>Arabidopsis thaliana</i>	AT5G03860	02 Energy	02.10 TCA pathway	0	75	evm_27.model.AmTr_v1.0_scaffold00049.86	-72,23691	31	64,8	19	-	17	0,74074	HIVQLHPSSR DHSVGLNCGR HGAVLDGDGVK
43	2	P34795	Phosphoglucose isomerase	<i>Arabidopsis thaliana</i>	AT5G42740	02 Energy	02.01 Glycolysis	0	82	evm_27.model.AmTr_v1.0_scaffold00111.63	-83,19611	39	62,4	26	-	22	0,96429	IQQVSMESNGK DLMNDSEK
43	2	Q9LZC3	Malate synthase	<i>Arabidopsis thaliana</i>	AT5G03860	02 Energy	02.10 TCA pathway	0	75	evm_27.model.AmTr_v1.0_scaffold00049.86	-21,17397	8	64,8	5	-	5	0,18519	HIVQLHPSSR HGAVLDGDGVK
44	1	P30184	Leucine aminopeptidase	<i>Arabidopsis thaliana</i>	AT2G24200	06 Protein destination and storage	06.13 Proteolysis	0	68	evm_27.model.AmTr_v1.0_scaffold00065.204	-143,7936	56	54,5	31	-	25	1,06897	SGVADMVNTG GR PGDIVTASNG
45	2	P30184	Leucine aminopeptidase	<i>Arabidopsis thaliana</i>	AT2G24200	06 Protein destination and storage	06.13 Proteolysis	0	68	evm_27.model.AmTr_v1.0_scaffold00065.204	-161,4386	56	54,5	38	-	29	1,37931	GSAALGAAR ILNEDQCR SGVADMVNTG
45	2	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-37,20856	29	43,5	7	-	7	0,34783	KGDTATIPAGK PSSEQLQGLIH GSGGGGK
46	2	Q9S9P4	S-adenosyl-L-methionine-dependent methyltransferase (7-	<i>Arabidopsis thaliana</i>	AT1G30550	04 Transcription	04.22 mRNA processing	2e-79	68	evm_27.model.AmTr_v1.0_scaffold00019.57	-100,4046	22	122	21	-	19	0,47826	VEGAVESLSR AYEVANTPSLK SEQYGYVLK
46	2	P30184	Leucine aminopeptidase	<i>Arabidopsis thaliana</i>	AT2G24200	06 Protein destination and storage	06.13 Proteolysis	0	68	evm_27.model.AmTr_v1.0_scaffold00065.204	-156,4525	60	54,5	28	-	23	1	PGGSTVLR ILNEDQCR SGVADMVNTG
47	2	P94078	Alpha-mannosidase	<i>Arabidopsis thaliana</i>	AT3G26720	01 Metabolism	01.05 Sugars and polysaccharides	0	67	evm_27.model.AmTr_v1.0_scaffold00016.68	-61,07647	11	114,9	17	-	12	0,39535	ITEMSLSANQER R
47	2	Q9S9P4	S-adenosyl-L-methionine-dependent methyltransferase (7-	<i>Arabidopsis thaliana</i>	AT1G30550	04 Transcription	04.22 mRNA processing	2e-79	68	evm_27.model.AmTr_v1.0_scaffold00019.57	-33,80976	8	122	8	-	7	0,17391	DDLATSELK LFSEHLQEME DNLPMDDSYK
48	2	P94078	Alpha-mannosidase	<i>Arabidopsis thaliana</i>	AT3G26720	01 Metabolism	01.05 Sugars and polysaccharides	0	67	evm_27.model.AmTr_v1.0_scaffold00016.68	-77,10317	18	114,9	22	-	16	0,5814	ITEMSLSANQER R
48	2	Q9S9P4	S-adenosyl-L-methionine-dependent methyltransferase (7-	<i>Arabidopsis thaliana</i>	AT1G30550	04 Transcription	04.22 mRNA processing	2e-79	68	evm_27.model.AmTr_v1.0_scaffold00019.57	-12,86923	5	122	4	-	4	0,08696	FGLDEAHGK LFSEHLQEME DNLPMDDSYK
49	3	Q8L831	Nudix hydrolase	<i>Arabidopsis thaliana</i>	AT1G79690	01 Metabolism	01.03 Nucleotides	0	66	evm_27.model.AmTr_v1.0_scaffold00036.84	-15,41464	5	88,2	5	1	4	0,16129	TITLPSGQQST VR
49	3	Q9S9P4	S-adenosyl-L-methionine-dependent methyltransferase (7-	<i>Arabidopsis thaliana</i>	AT1G30550	04 Transcription	04.22 mRNA processing	2e-79	68	evm_27.model.AmTr_v1.0_scaffold00019.57	-186,0687	27	122	46	42	30	1,06522	SSLSEDQK GLDEAHGK FGLDEAHGK
49	3	P30184	Leucine aminopeptidase	<i>Arabidopsis thaliana</i>	AT2G24200	06 Protein destination and storage	06.13 Proteolysis	0	68	evm_27.model.AmTr_v1.0_scaffold00065.204	-13,34161	10	54,5	4	-	4	0,13793	TIEVNNTDAEGR GFGEAVASSA
50	3	P94078	Alpha-mannosidase	<i>Arabidopsis thaliana</i>	AT3G26720	01 Metabolism	01.05 Sugars and polysaccharides	0	67	evm_27.model.AmTr_v1.0_scaffold00016.68	-16,74112	4	114,9	4	-	3	0,09302	ITEMSLSANQER R
50	3	A7WM73	Beta-hexosaminidase	<i>Arabidopsis thaliana</i>	AT3G55260	01 Metabolism	01.05 Sugars and polysaccharides	0	67	evm_27.model.AmTr_v1.0_scaffold00061.152	-11,00568	4	61,6	2	-	2	0,11111	QQQIAIAQK DATSTGLDVLQ R
50	3	Q9S9P4	S-adenosyl-L-methionine-dependent methyltransferase (7-	<i>Arabidopsis thaliana</i>	AT1G30550	04 Transcription	04.22 mRNA processing	2e-79	68	evm_27.model.AmTr_v1.0_scaffold00019.57	-202,5784	31	122	52	-	38	1,15217	SSLSEDQK SKGVTAAPIR KASDLLQK
51	3	P57751	UDP-glucose pyrophosphorylase	<i>Arabidopsis thaliana</i>	AT5G17310	01 Metabolism	01.05 Sugars and polysaccharides	0	78	evm_27.model.AmTr_v1.0_scaffold00044.2	-41,9648	16	52,2	6	-	6	0,23077	LQSAVAGLNQI SESEK FGCINLYSR
51	3	Q94CC6	Serine carboxypeptidase	<i>Arabidopsis thaliana</i>	AT4G36195	06 Protein destination and storage	06.13 Proteolysis	0	67	evm_27.model.AmTr_v1.0_scaffold00182.29	-12,44433	9	54,3	4	-	4	0,26667	QVGVSGAPDC K QYYQDSLNVK

51	3	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5e-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-193,2189	68	43,5	78	-	39	3,56522	ARIEMACPH IEMACPH KGD TATIPAGK
52	1	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-165,0144	57	43,5	57	-	32	2,52174	IEMACPH KGD TATIPAGK KGD TATIPAGK
53	1	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5e-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-227,5835	69	43,5	94	-	44	4,26087	PHVSGGR IEMACPH KGD TATIPAGK
54	1	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5e-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-216,7958	69	43,5	85	-	42	3,91304	IEMACPH ARIEMACPH KGD TATIPAGK
55	1	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-221,2022	60	43,5	87	-	43	3,91304	ARIEMACPH KGD TATIPAGK KGD TATIPAGK
56	1	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5e-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-191,816	63	43,5	74	-	38	3,3913	ARIEMACPH KGD TATIPAGK KGD TATIPAGK
57	1	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-157,6953	61	43,5	54	-	29	2,47826	KGD TATIPAGK KGD TATIPAGK IEMACPHVSG
58	3	P57751	UDP-glucose pyrophosphorylase	<i>Arabidopsis thaliana</i>	AT5G17310	01 Metabolism	01.05 Sugars and polysaccharides	0	78	evm_27.model.AmTr_v1.0_scaffold00044.42	-44,99591	27	52,2	9	-	9	0,34615	AAVATKPASSE SEK LQSAVAGLNQI
58	3	P25696	Enolase	<i>Arabidopsis thaliana</i>	AT2G36530	02 Energy	02.01 Glycolysis	0	88	evm_27.model.AmTr_v1.0_scaffold00041.34	-28,99833	12	47,9	4	-	4	0,19048	HIANLAGNK VQIVGDDLLVT NPK
58	3	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5e-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-161,6647	60	43,5	58	-	28	2,65217	IEMACPH KGD TATIPAGK KGD TATIPAGK
59	5	O23255	S-Adenosylhomocysteine hydrolase	<i>Arabidopsis thaliana</i>	AT4G13940	01 Metabolism	01.01 Amino Acid	0	88	evm_27.model.AmTr_v1.0_scaffold00013.277	-24,42131	15	53	6	-	6	0,33333	LGAHLTK AEEFEFK VASLHLGK
59	5	P57751	UDP-glucose pyrophosphorylase	<i>Arabidopsis thaliana</i>	AT5G17310	01 Metabolism	01.05 Sugars and polysaccharides	0	78	evm_27.model.AmTr_v1.0_scaffold00044.42	-25,94099	12	52,2	6	-	6	0,23077	AVATKPASSE EK AAVATKPASSE
59	5	P25696	Enolase	<i>Arabidopsis thaliana</i>	AT2G36530	02 Energy	02.01 Glycolysis	0	88	evm_27.model.AmTr_v1.0_scaffold00041.34	-166,3612	66	47,9	33	-	22	1,61905	HIANLAGNK HAGWGVMS HR
59	5	Q94CC6	Serine carboxypeptidase	<i>Arabidopsis thaliana</i>	AT4G36195	06 Protein destination and storage	06.13 Proteolysis	0	67	evm_27.model.AmTr_v1.0_scaffold00182.29	-25,14634	13	54,3	7	-	7	0,46667	QVGVSAAGPDC K GALQEITR
59	5	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5e-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-160,0221	59	43,5	53	-	29	2,52174	IEMACPH KGD TATIPAGK IEMACPHVSG
60	5	O23255	S-Adenosylhomocysteine hydrolase	<i>Arabidopsis thaliana</i>	AT4G13940	01 Metabolism	01.01 Amino Acid	0	88	evm_27.model.AmTr_v1.0_scaffold00013.277	-64,23125	37	53	17	-	15	0,94444	NTIKPQTR LGAHLTK ATDVMIAGK
60	5	P57751	UDP-glucose pyrophosphorylase	<i>Arabidopsis thaliana</i>	AT5G17310	01 Metabolism	01.05 Sugars and polysaccharides	0	78	evm_27.model.AmTr_v1.0_scaffold00044.42	-78,06896	38	52,2	15	-	13	0,61538	AVATKPASSE EK AAVATKPASSE
60	5	P25696	Enolase	<i>Arabidopsis thaliana</i>	AT2G36530	02 Energy	02.01 Glycolysis	0	88	evm_27.model.AmTr_v1.0_scaffold00041.34	-206,1951	72	47,9	48	-	26	2,57143	HIANLAGNK HAGWGVMS HAGWGVMS
60	5	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5e-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-158,8514	60	43,5	53	-	29	2,43478	IEMACPH KGD TATIPAGK IEMACPHVSG
60	5	P92947	Monodehydroascorbate reductase	<i>Arabidopsis thaliana</i>	AT1G63940	11 Disease/defence	11.06 Detoxification	0	68	evm_27.model.AmTr_v1.0_scaffold00001.90	-22,06298	13	53,9	6	-	5	0,26087	GMMVDKLEA GSDGR IVTASSAAFAN GQVITIAKPG EK
61	3	P57751	UDP-glucose pyrophosphorylase	<i>Arabidopsis thaliana</i>	AT5G17310	01 Metabolism	01.05 Sugars and polysaccharides	0	78	evm_27.model.AmTr_v1.0_scaffold00044.42	-60,84567	36	52,2	12	-	12	0,57692	AAVATKPASSE EK
61	3	P25696	Enolase	<i>Arabidopsis thaliana</i>	AT2G36530	02 Energy	02.01 Glycolysis	0	88	evm_27.model.AmTr_v1.0_scaffold00041.34	-191,806	74	47,9	45	-	26	2,19048	HIANLAGNK HAGWGVMS HR
61	3	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5e-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-175,9548	62	43,5	58	-	33	2,65217	IEMACPH ARIEMACPH KGD TATIPAGK
62	6	F4K6N3	Amidase family protein	<i>Arabidopsis thaliana</i>	AT5G07360	01 Metabolism	01.02 Nitrogen and sulphur	0	65	evm_27.model.AmTr_v1.0_scaffold00016.285	-35,68095	18	67,1	9	-	8	0,34615	TGVMSISESLD K DQVLDMEASV

62	6	Q9M088	glucan endo-1,3-beta-glucosidase	<i>Arabidopsis thaliana</i>	AT4G31140	01 Metabolism	01.05 Sugars and polysaccharides	e-172	66	evm_27.model.AmTr_v1.0_scaffold00025.307	-14,28534	6	53,4	3	-	3	0,16667	NNQLQVACK FNQGLFTR YQI.GVGNLSOL
62	6	P57751	UDP-glucose pyrophosphorylase	<i>Arabidopsis thaliana</i>	AT5G17310	01 Metabolism	01.05 Sugars and polysaccharides	0	78	evm_27.model.AmTr_v1.0_scaffold00044.42	-45,12743	26	52,2	9	-	9	0,38462	AAVATKPASSL SEK MEIIPNPK
62	6	P25696	Enolase	<i>Arabidopsis thaliana</i>	AT2G36530	02 Energy	02.01 Glycolysis	0	88	evm_27.model.AmTr_v1.0_scaffold00041.34	-152,5721	55	47,9	35	-	20	1,90476	HIANLAGNK HIANLAGNK HAGWGVMSK QVGSAGPDC K
62	6	Q94CC6	Serine carboxypeptidase	<i>Arabidopsis thaliana</i>	AT4G36195	06 Protein destination and storage	06.13 Proteolysis	0	67	evm_27.model.AmTr_v1.0_scaffold00182.29	-8,59468	8	54,3	4	-	4	0,26667	QYYODSLNVK IEMACPH ARIEMACPH
62	6	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5e-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-136,3923	62	43,5	39	-	25	1,78261	KGDTATIPAGK LITSGVESGAR DAQGDVFR VNAGTEPGTD
63	5	Q0WM29	Methylmalonate-semialdehyde dehydrogenase	<i>Arabidopsis thaliana</i>	AT2G14170	01 Metabolism	01.01 Amino Acid	0	76	evm_27.model.AmTr_v1.0_scaffold00033.188	-28,87696	11	84,3	7	-	7	0,24138	SNLTNSMK ALAENEGGL AK
63	5	Q9M5K5	Dihydroliipoamide dehydrogenase	<i>Arabidopsis thaliana</i>	AT3G16950	01 Metabolism	01.06 Lipid and sterol	0	75	evm_27.model.AmTr_v1.0_scaffold00003.16	-48,93916	19	57,1	10	-	9	0,47619	TPNSVYDHDM STNSVTLK
63	5	Q9SX53	Oligopeptidase B	<i>Arabidopsis thaliana</i>	AT1G50380	06 Protein destination and storage	06.13 Proteolysis	0	70	evm_27.model.AmTr_v1.0_scaffold00171.48	-24,10355	13	80,9	8	1	7	0,27778	IEMACPH ARIEMACPH KGDTATIPAGK
63	5	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5e-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-125,4206	58	43,5	41	-	21	1,86957	RLSDAQQCR GRQEGVGE EQRGEQGGK
63	5	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr_v1.0_scaffold00067.7	-110,4516	46	54,5	24	-	21	1,14286	ISNQQAQDIK ANVIGVGER GEGQIQIGTN
64	2	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr_v1.0_scaffold00067.7	-14,57331	11	54,5	4	-	4	0,2381	IEMACPH KGDTATIPAGK KGDTATIPAGK
64	2	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5e-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-146,988	62	43,5	58	-	30	2,69565	SNLTNSMK QGVADHANNL ASK
65	3	Q9M5K5	Dihydroliipoamide dehydrogenase	<i>Arabidopsis thaliana</i>	AT3G16950	01 Metabolism	01.06 Lipid and sterol	0	75	evm_27.model.AmTr_v1.0_scaffold00003.16	-106,2833	40	57,1	22	-	17	1,09524	IVGLQTR MESQFSSHIL R
65	3	Q9SX53	Oligopeptidase B	<i>Arabidopsis thaliana</i>	AT1G50380	06 Protein destination and storage	06.13 Proteolysis	0	70	evm_27.model.AmTr_v1.0_scaffold00171.48	-44,13302	17	80,9	11	-	11	0,30556	ISNQQAQDIK GEGQIQIGTN GOK
65	3	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr_v1.0_scaffold00067.7	-11,71652	6	54,5	3	-	3	0,14286	MMLAHTASQ QGVADHANNL ASK
66	3	Q9M5K5	Dihydroliipoamide dehydrogenase	<i>Arabidopsis thaliana</i>	AT3G16950	01 Metabolism	01.06 Lipid and sterol	0	75	evm_27.model.AmTr_v1.0_scaffold00003.16	-104,0757	42	57,1	26	-	19	1,33333	IEMACPH KGDTATIPAGK KGDTATIPAGK
66	3	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-119,1544	60	43,5	38	-	24	1,82609	NTISGRPEK SEQQAVEQAK LVNHSHTVEVT
66	3	P48641	Glutathione reductase	<i>Arabidopsis thaliana</i>	AT3G24170	11 Disease/defence	11.06 Detoxification	0	69	evm_27.model.AmTr_v1.0_scaffold00067.136	-56,20296	30	57,5	11	-	11	0,45833	VQACTQEEVN K TGGDTGIAISK
67	2	Q1WIQ6	Glyceraldehyde-3-phosphate dehydrogenase	<i>Arabidopsis thaliana</i>	AT2G24270	02 Energy	02.01 Glycolysis	0	87	evm_27.model.AmTr_v1.0_scaffold00065.146	-68,10373	39	54,2	17	-	14	0,86364	IEMACPH KGDTATIPAGK IEMACPHVSG
67	2	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5e-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-87,61553	50	43,5	24	-	17	1,08696	VQACTQEEVN K AELLHR
68	2	Q1WIQ6	Glyceraldehyde-3-phosphate dehydrogenase	<i>Arabidopsis thaliana</i>	AT2G24270	02 Energy	02.01 Glycolysis	0	87	evm_27.model.AmTr_v1.0_scaffold00065.146	-101,5984	48	54,2	28	-	21	1,36364	IVDALSDTR SLYDDEAVIVG GTNHSHTATK
68	2	P25819	Catalase 2	<i>Arabidopsis thaliana</i>	AT4G35090	11 Disease/defence	11.06 Detoxification	0	79	evm_27.model.AmTr_v1.0_scaffold00001.7	-22,60983	19	54,9	7	5	7	0,35	LTMGAFR SSIFDAK SSIFDAK
69	4	Q9SAJ6	Glyceraldehyde-3-phosphate dehydrogenase	<i>Arabidopsis thaliana</i>	AT1G79530	02 Energy	02.01 Glycolysis	e-165	70	evm_27.model.AmTr_v1.0_scaffold00039.188	-5,244125	5	45,2	4	3	3	0,2	CLAPLAK TTNCLAPLAK ASCCTINCLAP
69	4	Q9FX54	Glyceraldehyde-3-phosphate dehydrogenase	<i>Arabidopsis thaliana</i>	AT1G13440	02 Energy	02.01 Glycolysis	6,00E-94	74	evm_27.model.AmTr_v1.0_scaffold00177.24	-170,0313	52	24,7	49	42	28	7,14286	

69	4	Q9SCV3	Beta-galactosidase	<i>Arabidopsis thaliana</i>	AT2G32810	09 Cell structure	09.01 Cell wall	0	68	evm_27.model.AmTr_v1.0_scaffold00117.17	-15,97429	8	74,6	7	-	6	0,26667	LGNQEAH SAGLHYPR RMLVSAAGLHY
70	3	Q5E924	Glyceraldehyde-3-phosphate dehydrogenase	<i>Arabidopsis thaliana</i>	AT1G79530	02 Energy	02.01 Glycolysis	e-162	77	evm_27.model.AmTr_v1.0_scaffold00039.188	-27,03456	16	45,2	13	4	9	0,7	LTGMAFR LTGMAFR
70	3	Q9SAJ6	Glyceraldehyde-3-phosphate dehydrogenase	<i>Arabidopsis thaliana</i>	AT1G16300	02 Energy	02.01 Glycolysis	e-165	70	evm_27.model.AmTr_v1.0_scaffold00032.283	-35,11374	12	45,4	10	1	8	0,52381	PSMDIVSNAS CTTNCLAPLAK
70	3	Q9FX54	Glyceraldehyde-3-phosphate dehydrogenase	<i>Arabidopsis thaliana</i>	AT1G13440	02 Energy	02.01 Glycolysis	6,00E-94	74	evm_27.model.AmTr_v1.0_scaffold00177.24	-110,4528	64	24,7	30	19	22	4,28571	PVTVFGNR DAPMFVGVN EHEYKPDVH
70	4	Q9SJK9	Fructose-bisphosphate aldolase	<i>Arabidopsis thaliana</i>	AT2G36460	02 Energy	02.01 Glycolysis	e-172	86	evm_27.model.AmTr_v1.0_scaffold00040.204	-62,51038	30	37,7	10	-	8	0,64706	ANSEATLGT K GDAPVFGEGAS
71	2	Q9FX54	Glyceraldehyde-3-phosphate dehydrogenase	<i>Arabidopsis thaliana</i>	AT1G13440	02 Energy	02.01 Glycolysis	6,00E-94	74	evm_27.model.AmTr_v1.0_scaffold00177.24	-96,00919	48	24,7	29	25	20	4,57143	PSSTGAOK CLAPLAK TNCLAPLAK
71	2	Q9SJK9	Fructose-bisphosphate aldolase	<i>Arabidopsis thaliana</i>	AT2G36460	02 Energy	02.01 Glycolysis	e-172	86	evm_27.model.AmTr_v1.0_scaffold00040.204	-9,857892	9	37,7	3	-	3	0,17647	MVTPGSDAPK CQQYYAAGAR GILAADESTGT
72	4	Q5E924	Glyceraldehyde-3-phosphate dehydrogenase	<i>Arabidopsis thaliana</i>	AT1G16300	02 Energy	02.01 Glycolysis	e-162	77	evm_27.model.AmTr_v1.0_scaffold00032.283	-19,77956	10	45,4	4	1	4	0,2381	PSMDIVSNAS CTTNCLAPLAK
72	4	Q9SAJ6	Glyceraldehyde-3-phosphate dehydrogenase	<i>Arabidopsis thaliana</i>	AT1G79530	02 Energy	02.01 Glycolysis	e-165	70	evm_27.model.AmTr_v1.0_scaffold00039.188	-9,485707	7	45,2	4	1	4	0,25	LTGMAFR
72	4	Q9FX54	Glyceraldehyde-3-phosphate dehydrogenase	<i>Arabidopsis thaliana</i>	AT1G13440	02 Energy	02.01 Glycolysis	6,00E-94	74	evm_27.model.AmTr_v1.0_scaffold00177.24	-78,84562	64	24,7	18	13	16	2,71429	DAPMFVGVN EHEYK DAPMFVGVN
72	4	Q9SJK9	Fructose-bisphosphate aldolase	<i>Arabidopsis thaliana</i>	AT2G36460	02 Energy	02.01 Glycolysis	e-172	86	evm_27.model.AmTr_v1.0_scaffold00040.204	-140,9961	66	37,7	39	-	28	2,35294	MVTPGSDAPK CQQYYAAGAR ANDEMTGIGK PNMVTGSDA
73	5	Q9SAJ6	Glyceraldehyde-3-phosphate dehydrogenase	<i>Arabidopsis thaliana</i>	AT1G79530	02 Energy	02.01 Glycolysis	e-165	70	evm_27.model.AmTr_v1.0_scaffold00039.188	-3,764472	3	45,2	2	1	2	0,1	LTGMAFR
73	5	Q9FX54	Glyceraldehyde-3-phosphate dehydrogenase	<i>Arabidopsis thaliana</i>	AT1G13440	02 Energy	02.01 Glycolysis	6,00E-94	82	evm_27.model.AmTr_v1.0_scaffold00177.24	-28,92995	30	24,7	6	5	5	0,85714	DAPMFVGVN EHEYK AAGENIPSS
73	5	Q9SJK9	Fructose-bisphosphate aldolase	<i>Arabidopsis thaliana</i>	AT2G36460	02 Energy	02.01 Glycolysis	e-172	86	evm_27.model.AmTr_v1.0_scaffold00040.204	-23,44074	19	37,7	6	-	6	0,35294	ALQOSTLK CQQYYAAGAR NAAYIGTPGR
73	5	P06525	Alcohol dehydrogenase	<i>Arabidopsis thaliana</i>	AT1G77120	02 Energy	02.16 Fermentation	e-159	71	evm_27.model.AmTr_v1.0_scaffold00071.65	-34,66493	33	34,2	13	-	8	1,16667	GVMLSDGK GVMLSDGK GAVGLAAEAG
73	5	Q9S9N1	HSC70 (Heat shock cognate 70 kDa protein)	<i>Arabidopsis thaliana</i>	AT1G16030	06 Protein destination and storage	06.01 Folding and stability	0	80	evm_27.model.AmTr_v1.0_scaffold00137.8	-85,82221	24	71,6	18	-	13	0,85714	FSDPSVQADM K AAILTGESEK
74	2	Q9FIK7	acetyl-CoA acetyltransferase	<i>Arabidopsis thaliana</i>	AT5G47720	01 Metabolism	01.06 Lipid and sterol	e-176	76	evm_27.model.AmTr_v1.0_scaffold00061.248	-8,714389	8	48	3	-	3	0,2	APAAVSDSLK R QAALGAGIPN
74	2	Q9S9N1	HSP70 (heat shock protein)	<i>Arabidopsis thaliana</i>	AT1G16030	06 Protein destination and storage	06.01 Folding and stability	0	80	evm_27.model.AmTr_v1.0_scaffold00137.8	-253,2506	41	71,6	86	-	45	4,38095	ILTGESEK CLETVEK RFSDPSPVQAD
75	3	P06525	Alcohol dehydrogenase	<i>Arabidopsis thaliana</i>	AT1G77120	02 Energy	02.16 Fermentation	e-159	71	evm_27.model.AmTr_v1.0_scaffold00071.65	-122,7848	60	34,2	40	-	24	3,75	GVMLSDGK ASTAGQVIR TVVHVGCVAK
75	3	Q9LDZ0	HSC70 (Heat shock cognate 70 kDa protein)	<i>Arabidopsis thaliana</i>	AT5G09590	06 Protein destination and storage	06.01 Folding and stability	0	86	evm_27.model.AmTr_v1.0_scaffold00046.170	-13,70146	7	73,3	5	-	5	0,16129	KFDDPQTOK TEGIDLSK IAGLDVQR
75	3	Q9S9N1	HPS70	<i>Arabidopsis thaliana</i>	AT1G16030	06 Protein destination and storage	06.01 Folding and stability	0	80	evm_27.model.AmTr_v1.0_scaffold00137.8	-79,78307	25	71,6	14	-	13	0,71429	FSDPSVQADM K AAILTGESEK
76	3	P06525	Alcohol dehydrogenase	<i>Arabidopsis thaliana</i>	AT1G77120	02 Energy	02.16 Fermentation	e-159	71	evm_27.model.AmTr_v1.0_scaffold00071.65	-8,424766	12	34,2	4	-	3	0,41667	GQKPLFPR ASTAGQVIR ASTAGQVIR
76	3	Q9S9N1	HSP70 (heat shock protein)	<i>Arabidopsis thaliana</i>	AT1G16030	06 Protein destination and storage	06.01 Folding and stability	0	80	evm_27.model.AmTr_v1.0_scaffold00137.8	-199,1009	41	71,6	71	65	37	3,52381	ATAGDTHLGG RFSDPSPVQAD MK
76	3	Q9LKR3	HSP70 (Luminal binding protein 1)	<i>Arabidopsis thaliana</i>	AT5G28540	06 Protein destination and storage	06.01 Folding and stability	0	82	evm_27.model.AmTr_v1.0_scaffold00002.54	-27,73322	4	74,2	7	1	5	0,25926	AGVIAGLNVAR IINEPTAAAIAY GLDK

77	2	P06525	Alcohol dehydrogenase	<i>Arabidopsis thaliana</i>	AT1G77120	02 Energy	02.16 Fermentation	e-159	71	evm_27.model.AmTr_v1.0_scaffold00071.65	-83,37369	52	34,2	27	-	17	2,25	GVMLSDGK GVMLSDGK GVMLSDGK
77	2	Q9S9N1	HSP70 (heat shock protein)	<i>Arabidopsis thaliana</i>	AT1G16030	06 Protein destination and storage	06.01 Folding and stability	0	80	evm_27.model.AmTr_v1.0_scaffold00137.8	-149,6076	36	71,6	34	-	24	1,7619	ATAGDTHLGG RFSDPSVQAD MK
78	4	P06525	Alcohol dehydrogenase	<i>Arabidopsis thaliana</i>	AT1G77120	02 Energy	02.16 Fermentation	e-159	71	evm_27.model.AmTr_v1.0_scaffold00071.65	-63,23336	52	34,2	18	-	15	1,58333	TVVHYGCVAK GQKPLFPR REGCTEFVNS FSDPSVQADM
78	4	Q9S9N1	HSP70 (heat shock protein)	<i>Arabidopsis thaliana</i>	AT1G16030	06 Protein destination and storage	06.01 Folding and stability	0	80	evm_27.model.AmTr_v1.0_scaffold00137.8	-57,5639	18	71,6	10	9	9	0,57143	K VEIIPNDQGNR KFDPPQTQK TTPSVAFNP K
78	4	Q9LDZ0	HSC70 (Heat shock cognate 70 kDa protein)	<i>Arabidopsis thaliana</i>	AT5G09590	06 Protein destination and storage	06.01 Folding and stability	0	86	evm_27.model.AmTr_v1.0_scaffold00046.170	-6,364335	4	73,3	3	2	3	0,09677	K NQAALNPER NGHVEIANDQ GNR
78	4	Q9LKR3	HSP70 (Luminal binding protein 1)	<i>Arabidopsis thaliana</i>	AT5G28540	06 Protein destination and storage	06.01 Folding and stability	0	82	evm_27.model.AmTr_v1.0_scaffold00025.4	-14,85261	8	74,2	5	3	5	0,18519	K GVMLSDGK GVMLSDGK SEESNMCELL
79	5	P06525	Alcohol dehydrogenase	<i>Arabidopsis thaliana</i>	AT1G77120	02 Energy	02.16 Fermentation	e-159	71	evm_27.model.AmTr_v1.0_scaffold00071.65	-9,12203	11	34,2	6	-	4	0,5	NGHVEIANDQ GNR
79	5	Q9LKR3	HSP70 (Luminal binding protein 1)	<i>Arabidopsis thaliana</i>	AT5G28540	06 Protein destination and storage	06.01 Folding and stability	0	82	evm_27.model.AmTr_v1.0_scaffold00025.4	-19,77828	6	74,2	6	2	4	0,22222	AGVIAGLNVAR RFSDPSVQAD MK
79	5	Q9S9N1	HSP70	<i>Arabidopsis thaliana</i>	AT1G16030	06 Protein destination and storage	06.01 Folding and stability	0	80	evm_27.model.AmTr_v1.0_scaffold00137.8	-124,0283	32	71,6	34	30	21	1,7619	RFSDPSVQAD MK
79	5	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-29,5133	25	43,5	9	-	7	0,43478	KGDTATIPAGK EVSFNVPSR NSILNQIER
79	5	Q9FN21	FAD-dependent oxidoreductase-like protein	<i>Arabidopsis thaliana</i>	AT5G67290	13 Unclassified	13 Unclassified	e-110	58	evm_27.model.AmTr_v1.0_scaffold00092.142	-14,29633	10	40,6	5	-	4	0,2381	AMASDAAGAG AR EESVAMLHR
80	6	Q9T0K7	3-hydroxyisobutyryl-CoA hydrolase-like protein	<i>Arabidopsis thaliana</i>	AT4G13360	01 Metabolism	01.01 Amino Acid	e-148	67	evm_27.model.AmTr_v1.0_scaffold00142.40	-15,71895	17	48,7	5	-	5	0,20833	K QHQLSSEAPV K AFSAGMDIK
80	6	Q8GYB8	12-oxophytodienoate reductase	<i>Arabidopsis thaliana</i>	AT1G76690	01 Metabolism	01.06 Lipid and sterol	e-169	76	evm_27.model.AmTr_v1.0_scaffold00071.206	-61,1964	32	41,9	12	10	10	0,66667	TDHYGGSLER R TDHYGGSLER
80	6	Q9S9N1	Fructose-bisphosphate aldolase	<i>Arabidopsis thaliana</i>	AT2G36460	02 Energy	02.01 Glycolysis	e-172	86	evm_27.model.AmTr_v1.0_scaffold00040.204	-18,44806	15	37,7	5	-	5	0,29412	CQQYYAAGAR NAAYIGTPGR ANSEATLGT Y
80	6	Q9S9N1	HSP70 (heat shock protein)	<i>Arabidopsis thaliana</i>	AT1G16030	06 Protein destination and storage	06.01 Folding and stability	0	80	evm_27.model.AmTr_v1.0_scaffold00137.8	-18,87695	8	71,6	4	-	4	0,19048	VEIIPNDQGNR TTPSVYAFDT ER
80	6	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5e-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-101,0411	52	43,5	24	-	18	1,04348	IEMACPH KGDTATIPAGK IEMACPHVSG
80	6	Q9LF88	Late embryogenesis abundant protein (LEA)	<i>Arabidopsis thaliana</i>	AT3G53040	11 Disease/defence	11.05 Stress responses	3e-44	37	evm_27.model.AmTr_v1.0_scaffold00002.388	-15,04639	10	33,9	3	-	3	0,375	AGEANDSAAD ATR VTAEDAGER
81	5	Q8GYB8	12-oxophytodienoate reductase	<i>Arabidopsis thaliana</i>	AT1G76690	01 Metabolism	01.06 Lipid and sterol	e-169	76	evm_27.model.AmTr_v1.0_scaffold00071.206	-15,04692	8	41,9	3	-	3	0,16667	QLSPQVDANQ INK RFELNAPLNK
81	5	Q9LKR3	HSP70 (Luminal binding protein 1)	<i>Arabidopsis thaliana</i>	AT5G28540	06 Protein destination and storage	06.01 Folding and stability	0	82	evm_27.model.AmTr_v1.0_scaffold00025.4	-16,69379	5	74,2	4	2	3	0,14815	ALEDASLQK VEIANDQGNR
81	5	Q9S9N1	HSP70	<i>Arabidopsis thaliana</i>	AT1G16030	06 Protein destination and storage	06.01 Folding and stability	0	80	evm_27.model.AmTr_v1.0_scaffold00137.8	-77,62367	23	71,6	18	16	12	0,85714	FSDPSVQADM K ATAGDTHLGG
81	5	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5e-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-89,78651	50	43,5	22	-	15	1	KGDTATIPAGK IEMACPHVSG GR
81	5	Q9LF88	Late embryogenesis abundant protein (LEA)	<i>Arabidopsis thaliana</i>	AT3G53040	11 Disease/defence	11.05 Stress responses	3e-44	37	evm_27.model.AmTr_v1.0_scaffold00002.388	-21,18191	13	33,9	4	-	4	0,5	AGEANDSAAD ATR VTAEDAGER
82	5	P25696	Enolase	<i>Arabidopsis thaliana</i>	AT2G36530	02 Energy	02.01 Glycolysis	0	88	evm_27.model.AmTr_v1.0_scaffold00041.34	-31,70128	10	47,9	4	-	3	0,19048	AAVPSGASTG VYEALERL VVIGMDVAAS
82	5	Q9LKR3	HSP70 (Luminal binding protein 1)	<i>Arabidopsis thaliana</i>	AT5G28540	06 Protein destination and storage	06.01 Folding and stability	0	82	evm_27.model.AmTr_v1.0_scaffold00025.4	-19,09253	9	74,2	5	3	5	0,22222	K NQAALNPER NGHVEIANDQ GNR

82	5	Q39043	HSP70 (Luminal binding protein 2)	<i>Arabidopsis thaliana</i>	AT5G42020	06 Protein destination and storage	06.01 Folding and stability	0	88	evm_27.model.AmTr.v1.0_scaffold00009.363	-17,47277	6	73,2	3	1	3	0,12	IINEPTAAAIY GMDK
82	5	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5e-54	30	evm_27.model.AmTr.v1.0_scaffold00002.657	-55,64196	43	43,5	12	-	11	0,56522	KGDTATIPAGK EVSFNVP RSSEFQI QGLIHLI RVEHVDHAR RMEHVDHAK GOVEEFKGGI SGLQIDTHVSK MDAEAGLVEA LSAR
82	5	Q9LFA3	Monodehydroascorbate reductase	<i>Arabidopsis thaliana</i>	AT3G52880	11 Disease/defence	11.06 Detoxification	e-178	69	evm_27.model.AmTr.v1.0_scaffold00069.193	-104,6198	46	48	30	-	18	1,73684	AHASTEGIAK YLMENGAK FYKEEFKNDP QEGEYGEEQ RGEQK ISNQQAQDIK
83	6	F4J9A0	Glutamine synthetase	<i>Arabidopsis thaliana</i>	F4J9A0	01 Metabolism	01.01 Amino Acid	0	60	evm_27.model.AmTr.v1.0_scaffold00140.38	-16,09911	5	93,8	3	-	3	0,11111	AHASTEGIAK YLMENGAK FYKEEFKNDP QEGEYGEEQ RGEQK ISNQQAQDIK
83	6	Q9SAJ4	Phosphoglycerate kinase	<i>Arabidopsis thaliana</i>	AT1G79550	02 Energy	02.01 Glycolysis	0	85	evm_27.model.AmTr.v1.0_scaffold00062.199	-77,96169	50	42,4	16	-	15	0,72727	AHASTEGIAK YLMENGAK FYKEEFKNDP QEGEYGEEQ RGEQK ISNQQAQDIK
83	6	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr.v1.0_scaffold00067.7	-20,49852	12	54,5	6	-	6	0,28571	IEMACPH KGDTATIPAGK TTYIINK
83	6	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr.v1.0_scaffold00002.657	-48,24721	34	43,5	13	-	10	0,56522	AGEANDSAAD ATR VTAEDAGER
83	6	Q9LF88	Late embryogenesis abundant protein (LEA)	<i>Arabidopsis thaliana</i>	AT3G53040	11 Disease/defence	11.05 Stress responses	3e-44	37	evm_27.model.AmTr.v1.0_scaffold00002.388	-23,34903	13	33,9	4	-	4	0,5	AGEANDSAAD ATR VTAEDAGER
83	6	Q9LFA3	Monodehydroascorbate reductase	<i>Arabidopsis thaliana</i>	AT3G52880	11 Disease/defence	11.06 Detoxification	e-178	69	evm_27.model.AmTr.v1.0_scaffold00069.193	-14,02411	5	48	2	-	2	0,10526	LSDFGVGGAD AK ALEADIVIVGV
84	7	F4J9A0	Glutamine synthetase	<i>Arabidopsis thaliana</i>	F4J9A0	01 Metabolism	01.01 Amino Acid	0	60	evm_27.model.AmTr.v1.0_scaffold00140.38	-32,10002	12	93,8	7	-	7	0,22222	SSGIDSICSK SGLQIDTHVSK LSNPLHLR
84	7	Q9M5K2	Dihydropyridyl dehydrogenase	<i>Arabidopsis thaliana</i>	AT3G17240	01 Metabolism	01.06 Lipid and sterol	0	77	evm_27.model.AmTr.v1.0_scaffold00064.49	-43,6454	26	53,8	12	1	10	0,56522	VTGVDASDSSG VR
84	7	Q9SAJ4	Phosphoglycerate kinase	<i>Arabidopsis thaliana</i>	AT1G79550	02 Energy	02.01 Glycolysis	0	85	evm_27.model.AmTr.v1.0_scaffold00062.199	-166,2025	70	42,4	41	-	30	1,95455	AHASTEGIAK YLMENGAK MSHISTGGGA SHVDDVVLVG GSTR TTPSYVAFTDT
84	7	Q9S9N1	HSP70 (heat shock protein)	<i>Arabidopsis thaliana</i>	AT1G16030	06 Protein destination and storage	06.01 Folding and stability	0	80	evm_27.model.AmTr.v1.0_scaffold00137.8	-14,19339	8	71,6	4	-	4	0,19048	ISNQQAQDIK GEGSISQHRK QFFIAGGQPR
84	7	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr.v1.0_scaffold00067.7	-13,29685	8	54,5	4	-	4	0,19048	IEMACPH KGDTATIPAGK IEMACPHVSG
84	7	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr.v1.0_scaffold00002.657	-36,05587	23	43,5	9	-	8	0,43478	AGEANDSAAD ATR VTAEDAGER
84	7	Q9LF88	Late embryogenesis abundant protein (LEA)	<i>Arabidopsis thaliana</i>	AT3G53040	11 Disease/defence	11.05 Stress responses	3e-44	37	evm_27.model.AmTr.v1.0_scaffold00002.388	-31,07862	18	33,9	8	-	6	1	KSSGIDSICSK SSGIDSICSK SGLQIDTHVSK VTGVDASDSSG VR HIIATGSDVK
85	6	F4J9A0	Glutamine synthetase	<i>Arabidopsis thaliana</i>	F4J9A0	01 Metabolism	01.01 Amino Acid	0	60	evm_27.model.AmTr.v1.0_scaffold00140.38	-51,95196	14	93,8	12	-	10	0,33333	AHASTEGIAK AHASTEGIAK AHASTEGIAK QEGEYGEEQ RGEQK ANVIGVGER
85	6	Q9M5K2	Dihydropyridyl dehydrogenase	<i>Arabidopsis thaliana</i>	AT3G17240	01 Metabolism	01.06 Lipid and sterol	0	77	evm_27.model.AmTr.v1.0_scaffold00064.49	-16,67381	15	53,8	5	-	5	0,26087	AHASTEGIAK AHASTEGIAK AHASTEGIAK QEGEYGEEQ RGEQK ANVIGVGER
85	6	Q9SAJ4	Phosphoglycerate kinase	<i>Arabidopsis thaliana</i>	AT1G79550	02 Energy	02.01 Glycolysis	0	85	evm_27.model.AmTr.v1.0_scaffold00062.199	-244,1428	80	42,4	68	-	37	3,18182	AGEANDSAAD ATR VTAEDAGER
85	6	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr.v1.0_scaffold00067.7	-7,47502	7	54,5	3	-	3	0,14286	IEMACPH KGDTATIPAGK IEMACPHVSG
85	6	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr.v1.0_scaffold00002.657	-80,90527	38	43,5	24	-	15	1,08696	AGEANDSAAD ATR VTAEDAGER
85	6	Q9LF88	Late embryogenesis abundant protein (LEA)	<i>Arabidopsis thaliana</i>	AT3G53040	11 Disease/defence	11.05 Stress responses	3e-44	37	evm_27.model.AmTr.v1.0_scaffold00002.388	-24,06704	13	33,9	4	-	4	0,5	EAMATYDK TCHAPTLSE AVK
86	4	Q9M5K2	Dihydropyridyl dehydrogenase	<i>Arabidopsis thaliana</i>	AT3G17240	01 Metabolism	01.06 Lipid and sterol	0	77	evm_27.model.AmTr.v1.0_scaffold00064.49	-118,1488	42	53,8	30	-	18	1,34783	KGDTATIPAGK ATEIYVLEGR ASQENLQIC
86	4	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr.v1.0_scaffold00002.657	-27,02939	15	43,5	6	-	4	0,30435	

86	4	P93026	Vacuolar sorting receptor	<i>Arabidopsis thaliana</i>	AT3G52850	08 Intracellular traffic	08.13 Vacuolar	0	73	evm_27.model.AmTr_v1.0_scaffold00077.78	-76,06812	26	69,4	20	-	15	0,73333	AEQDSQIGHG AR ESLPHPDFER AGEANDSAAD ATR VTAEDAGER SGLQIDTHVSK SGLQIDTHVSK LSNPLHLR
86	4	Q9LF88	Late embryogenesis abundant protein (LEA)	<i>Arabidopsis thaliana</i>	AT3G53040	11 Disease/defence	11.05 Stress responses	3e-44	37	evm_27.model.AmTr_v1.0_scaffold00002.388	-19,2832	13	33,9	3	-	3	0,5	LTDQSAVVNR AGSDVVVASV EK
87	4	F4J9A0	Glutamine synthetase	<i>Arabidopsis thaliana</i>	F4J9A0	01 Metabolism	01.01 Amino Acid	0	60	evm_27.model.AmTr_v1.0_scaffold00140.38	-39,44092	14	93,8	8	-	7	0,25	AHASTEGLIAK FYKEEEK YLMENGAK
87	4	Q9MAH3	4-Methyl-5(B-hydroxyethyl)-thiazole monophosphate	<i>Arabidopsis thaliana</i>	AT1G53280	01 Metabolism	01.07 Cofactors	e-137	62	evm_27.model.AmTr_v1.0_scaffold00021.43	-28,02428	15	45,5	6	-	6	0,31579	IEMACPH KGD TATIPAGK ARIEMACPHV KSSGSDICSCK SSGSDICSCK SGLQIDTHVSK
87	4	Q9SAJ4	Phosphoglycerate kinase	<i>Arabidopsis thaliana</i>	AT1G79550	02 Energy	02.01 Glycolysis	0	85	evm_27.model.AmTr_v1.0_scaffold00062.199	-191,4477	75	42,4	49	-	31	2,27273	LTDQSAVVNR AGSDVVVASV EK
87	4	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-46,76115	31	43,5	13	-	10	0,56522	AHASTEGLIAK FYKEEEK YLMENGAK
88	4	F4J9A0	Glutamine synthetase	<i>Arabidopsis thaliana</i>	F4J9A0	01 Metabolism	01.01 Amino Acid	0	60	evm_27.model.AmTr_v1.0_scaffold00140.38	-68,07385	18	93,8	16	-	12	0,44444	KSSGSDICSCK SSGSDICSCK SGLQIDTHVSK
88	4	Q9MAH3	4-Methyl-5(B-hydroxyethyl)-thiazole monophosphate	<i>Arabidopsis thaliana</i>	AT1G53280	01 Metabolism	01.07 Cofactors	e-137	62	evm_27.model.AmTr_v1.0_scaffold00021.43	-18,3662	10	45,5	4	-	4	0,21053	LTDQSAVVNR AGSDVVVASV EK
88	4	Q9SAJ4	Phosphoglycerate kinase	<i>Arabidopsis thaliana</i>	AT1G79550	02 Energy	02.01 Glycolysis	0	85	evm_27.model.AmTr_v1.0_scaffold00062.199	-76,25341	55	42,4	18	-	17	0,81818	AHASTEGLIAK EEEKNDPEFS K
88	4	Q9LF88	Late embryogenesis abundant protein (LEA)	<i>Arabidopsis thaliana</i>	AT3G53040	11 Disease/defence	11.05 Stress responses	3e-44	37	evm_27.model.AmTr_v1.0_scaffold00002.388	-17,31786	10	33,9	3	-	3	0,375	AGEANDSAAD ATR VTAEDAGER
89	2	Q9SAJ4	Phosphoglycerate kinase	<i>Arabidopsis thaliana</i>	AT1G79550	02 Energy	02.01 Glycolysis	0	85	evm_27.model.AmTr_v1.0_scaffold00062.199	-85,7233	53	42,4	20	-	16	0,90909	AHASTEGLIAK SVGSSLVEED K
89	2	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-89,61781	36	43,5	35	-	19	1,78261	YVANGDAR IEMACPH KGD TATIPAGK
90	2	Q9SAJ4	Phosphoglycerate kinase	<i>Arabidopsis thaliana</i>	AT1G79550	02 Energy	02.01 Glycolysis	0	85	evm_27.model.AmTr_v1.0_scaffold00062.199	-24,2739	20	42,4	4	-	4	0,22727	RPFPAIVGGSK VDLNVLDDN OK
90	2	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-204,7133	49	43,5	79	-	39	3,69565	ACPHVSGGR KGD TATIPAGK TIPAGK
91	2	Q9SJQ9	Fructose-bisphosphate aldolase	<i>Arabidopsis thaliana</i>	AT2G36460	02 Energy	02.01 Glycolysis	e-172	86	evm_27.model.AmTr_v1.0_scaffold00040.204	-33,67435	30	37,7	8	-	8	0,47059	MVTPGSDAPK EENIPAAQK ANSEATLGT Y
91	2	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-176,7037	46	43,5	72	-	35	3,52174	ACPHVSGGR IEMACPH KGD TATIPAGK
92	3	Q9SAJ4	Phosphoglycerate kinase	<i>Arabidopsis thaliana</i>	AT1G79550	02 Energy	02.01 Glycolysis	0	85	evm_27.model.AmTr_v1.0_scaffold00062.199	-5,063486	6	42,4	0	-	0	0,09091	FYKEEEKNDP EFSK RPFPAIVGGSK
92	3	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5e-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-161,7377	44	43,5	55	-	33	2,6087	IEMACPH ARIEMACPH ARIEMACPH
92	3	Q9M8R4	Glyoxalase	<i>Arabidopsis thaliana</i>	AT3G02720	11 Disease/defence	11.06 Detoxification	e-171	73	evm_27.model.AmTr_v1.0_scaffold00029.215	-57,40573	31	42,9	11	-	10	0,85714	KAGEACTTAV HER GEACTTAVHE
93	4	Q9SCX9	Glycerol-3-phosphate dehydrogenase	<i>Arabidopsis thaliana</i>	AT5G40610	01 Metabolism	01.06 Lipid and sterol	e-164	78	evm_27.model.AmTr_v1.0_scaffold00049.111	-10,13709	15	42,5	3	-	3	0,3125	LSSFHDEV RVRPDAQISL I K
93	4	Q9SJQ9	Fructose-bisphosphate aldolase	<i>Arabidopsis thaliana</i>	AT2G36460	02 Energy	02.01 Glycolysis	e-172	86	evm_27.model.AmTr_v1.0_scaffold00040.204	-19,73206	12	37,7	5	-	4	0,29412	MVTPGSDAPK MVTPGSDAPK CQQYYAAGAR
93	4	Q94CC6	Serine carboxypeptidase	<i>Arabidopsis thaliana</i>	AT4G36195	06 Protein destination and storage	06.13 Proteolysis	0	67	evm_27.model.AmTr_v1.0_scaffold00182.29	-26,60629	15	54,3	7	-	7	0,53333	QVGVSGAPDC K GALQEITR
93	4	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5e-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-160,3658	57	43,5	57	-	31	2,86957	IEMACPH ARIEMACPH KGD TATIPAGK
94	2	Q9SJQ9	Fructose-bisphosphate aldolase	<i>Arabidopsis thaliana</i>	AT2G36460	02 Energy	02.01 Glycolysis	e-172	86	evm_27.model.AmTr_v1.0_scaffold00040.204	-18,15937	14	37,7	5	-	5	0,35294	MVTPGSDAPK CQQYYAAGAR VAPEVIAEHTI

94	2	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-163,5763	44	43,5	64	-	31	3,08696	ACPHVSGGR IEMACPH ARIEMACPH
95	6	O50008	5-methyltetrahydropteroyl triqlutamate-	<i>Arabidopsis thaliana</i>	AT5G17920	01 Metabolism	01.01 Amino Acid	0	85	evm_27.model.AmTr_v1.0_scaffold00004.99	-27,82609	7	84,5	5	-	5	0,15152	ASHVGYPR GNASLPAMEM TK
95	6	Q9LVC5	Phosphoglucose isomerase	<i>Arabidopsis thaliana</i>	AT5G57330	02 Energy	02.01 Glycolysis	e-143	76	evm_27.model.AmTr_v1.0_scaffold00019.39	-39,61237	33	35,2	8	-	7	0,64706	IAVLDEHK QELSAVPSY CSGOLDPQR
95	6	Q9SJQ9	Fructose-bisphosphate aldolase	<i>Arabidopsis thaliana</i>	AT2G36460	02 Energy	02.01 Glycolysis	e-172	86	evm_27.model.AmTr_v1.0_scaffold00040.204	-47,16173	33	37,7	9	-	9	0,52941	MVTPGSDAPK NAAYIGTPGR ANSEATLGT Y
95	6	Q9LQQ3	12S Globulin	<i>Arabidopsis thaliana</i>	AT1G07750	06 Protein destination and storage	06.20 Storage proteins	e-129	63	evm_27.model.AmTr_v1.0_scaffold00044.174	-71,78135	45	38,4	18	-	14	1,63636	VQVVGVDGK VAYVIOGK VAYVIOGK
95	6	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-98,02804	54	43,5	23	-	17	1,13043	IEMACPHVSG GR MACPHVSGG
95	6	Q9SRT9	UDP-L-arabinose mutase	<i>Arabidopsis thaliana</i>	AT3G02230	09 Cell structure	09.01 Cell wall	0	89	evm_27.model.AmTr_v1.0_scaffold00047.149	-59,14184	35	40,9	13	-	11	0,59091	DGADFVR HLIVQDGDPT K
96	6	O50008	5-methyltetrahydropteroyl triqlutamate-	<i>Arabidopsis thaliana</i>	AT5G17920	01 Metabolism	01.01 Amino Acid	0	85	evm_27.model.AmTr_v1.0_scaffold00004.99	-18,97627	7	84,5	4	-	4	0,12121	GNASLPAMEM TK VVEVNLATAL
96	6	Q9SJQ9	Fructose-bisphosphate aldolase	<i>Arabidopsis thaliana</i>	AT2G36460	02 Energy	02.01 Glycolysis	e-172	86	evm_27.model.AmTr_v1.0_scaffold00040.204	-25,3498	14	37,7	4	-	4	0,23529	ANSEATLGT Y VAPEVIAEHTI
96	6	P57106	Malate dehydrogenase	<i>Arabidopsis thaliana</i>	AT5G43330	02 Energy	02.10 TCA pathway	e-130	78 ; 68	evm_27.model.AmTr_v1.0_scaffold01428.1	-31,22846	60	6,9	8	-	6	3	KKLDATADELS EEK KLDATADELSE
96	6	Q9ZP06	Malate dehydrogenase	<i>Arabidopsis thaliana</i>	AT1G53240	02 Energy	02.10 TCA pathway	e-148	83	evm_27.model.AmTr_v1.0_scaffold00021.87	-20,65793	26	36,1	5	-	5	0,83333	TQDGGTEVVE AK SLCTAIK
96	6	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-28,06645	33	43,5	6	-	6	0,47826	KGDTATIPAGK IEMACPHVSG GR
96	6	Q9SRT9	UDP-L-arabinose mutase	<i>Arabidopsis thaliana</i>	AT3G02230	09 Cell structure	09.01 Cell wall	0	89	evm_27.model.AmTr_v1.0_scaffold00047.149	-24,40149	20	40,9	5	-	5	0,31818	DGADFVR HLIVQDGDPT K
97	8	O50008	5-methyltetrahydropteroyl triqlutamate-	<i>Arabidopsis thaliana</i>	AT5G17920	01 Metabolism	01.01 Amino Acid	0	85	evm_27.model.AmTr_v1.0_scaffold00004.99	-69,92527	19	84,5	12	-	10	0,42424	GNASLPAMEM TK GNASLPAMEM
97	8	Q9LVC5	Phosphoglucose isomerase	<i>Arabidopsis thaliana</i>	AT5G57330	02 Energy	02.01 Glycolysis	e-143	76	evm_27.model.AmTr_v1.0_scaffold00019.39	-35,01493	26	35,2	7	-	7	0,47059	CSGOLDPQR IAVLDEHK AVLDHEK
97	8	Q9SJQ9	Fructose-bisphosphate aldolase	<i>Arabidopsis thaliana</i>	AT2G36460	02 Energy	02.01 Glycolysis	e-172	86	evm_27.model.AmTr_v1.0_scaffold00040.204	-21,69191	18	37,7	5	-	5	0,29412	NAAYIGTPGR ANSEATLGT Y
97	8	P57106	Malate dehydrogenase	<i>Arabidopsis thaliana</i>	AT5G43330	02 Energy	02.10 TCA pathway	2,00E-47	78	evm_27.model.AmTr_v1.0_scaffold01428.1	-18,81684	46	6,9	4	-	3	1,33333	KLDATADELSE EK KLDATADELSE
97	8	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-35,48082	29	43,5	9	-	8	0,3913	IEMACPH KGD TATIPAGK KGD TATIPAGK
97	8	Q9FF40	2S albumin	<i>Arabidopsis thaliana</i>	AT5G38160	06 Protein destination and storage	06.20 Storage proteins	2,7	36	evm_27.model.AmTr_v1.0_scaffold00005.212	-23,72816	20	16,8	5	4	2	0,71429	SLMSEAGGQE QQQIER SLMSEAGGQE
97	8	Q9SRT9	UDP-L-arabinose mutase	<i>Arabidopsis thaliana</i>	AT3G02230	09 Cell structure	09.01 Cell wall	0	89	evm_27.model.AmTr_v1.0_scaffold00047.149	-49,3939	34	40,9	11	5	10	0,5	HLIVQDGDPT K VICDHLGLGLK
97	8	Q9SRT9	UDP-arabinopyranose mutase	<i>Arabidopsis thaliana</i>	AT3G02230	09 Cell structure	09.01 Cell wall	0,00E+00	89	evm_27.model.AmTr_v1.0_scaffold00013.86	-32,61085	23	41,3	8	2	8	0,42105	VICDHLGLGLK GTLFFMCGMN LGFNR
98	4	Q9TOG0	Hydroxysteroid dehydrogenase (Steroleosin-B)	<i>Arabidopsis thaliana</i>	AT4G10020	01 Metabolism	01.06 Lipid and sterol	2,00E-86	66	evm_27.model.AmTr_v1.0_scaffold01428.1	-18,81684	46	6,9	4	-	3	1,33333	KLDATADELSE EK KLDATADELSE
98	4	Q9SJQ9	Fructose-bisphosphate aldolase	<i>Arabidopsis thaliana</i>	AT2G36460	02 Energy	02.01 Glycolysis	e-172	86	evm_27.model.AmTr_v1.0_scaffold00040.204	-47,79874	35	37,7	10	-	10	0,70588	MVTPGSDAPK ANSEATLGT Y
98	4	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-91,23316	45	43,5	27	-	18	1,34783	IEMACPH KGD TATIPAGK IEMACPHVSG

98	4	O65398	Glyoxalase I (Lactoylglutathione lyase)	<i>Arabidopsis thaliana</i>	AT1G11840	11 Disease/defence	11.06 Detoxification	e-130	78	evm_27.model.AmTr_v1.0_scaffold00037.106	-52,4241	33	33,2	11	-	10	0,85714	LVTQELGGK YGVTEYTK AIATEDVYK
99	7	Q9T0A7	UDP-glucose 4-epimerase	<i>Arabidopsis thaliana</i>	AT4G23920	01 Metabolism	01.05 Sugars and polysaccharides	e-156	76	evm_27.model.AmTr_v1.0_scaffold00024.78	-37,96322	29	37,9	8	-	8	0,47059	VTELAGESSGK RPDGAEIVYAS TDK
99	7	Q9SJK9	Fructose-bisphosphate aldolase	<i>Arabidopsis thaliana</i>	AT2G36460	02 Energy	02.01 Glycolysis	e-172	86	evm_27.model.AmTr_v1.0_scaffold00040.204	-27,46824	34	37,7	8	-	8	0,52941	MVTPGSDAPK CQQYYAAGAR NAAYIGTPGR
99	7	P57106	Malate dehydrogenase	<i>Arabidopsis thaliana</i>	AT5G43330	02 Energy	02.10 TCA pathway	2e-47	78	evm_27.model.AmTr_v1.0_scaffold01428.1	-25,57344	60	6,9	6	-	5	2	KKLDATADELS EEK
99	7	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-23,54799	25	43,5	6	-	6	0,30435	KLDATELSE KGDATATIPACK ISNDHGELYEL DTFEYSPLR
99	7	Q9SRT9	UDP-arabinopyranose mutase	<i>Arabidopsis thaliana</i>	AT3G02230	09 Cell structure	09.01 Cell wall	0,00E+00	89	evm_27.model.AmTr_v1.0_scaffold00013.86	-19,98794	16	41,3	4	2	4	0,26316	GTLPFMCGMN LGFNR
99	7	Q9SRT9	UDP-L-arabinose mutase	<i>Arabidopsis thaliana</i>	AT3G02230	09 Cell structure	09.01 Cell wall	0	89	evm_27.model.AmTr_v1.0_scaffold00047.149	-18,96312	14	40,9	4	2	4	0,18182	LADELDIVIPTI SDSALPNPGA K
99	7	O65398	Glyoxalase I (Lactoylglutathione lyase)	<i>Arabidopsis thaliana</i>	AT1G11840	11 Disease/defence	11.06 Detoxification	e-130	78	evm_27.model.AmTr_v1.0_scaffold00037.106	-95,03111	45	33,2	26	-	18	1,92857	MGYAEK LVTQELGGK YGVTEYTK
100	5	Q9FX54	Glyceraldehyde-3-phosphate dehydrogenase	<i>Arabidopsis thaliana</i>	AT1G13440	02 Energy	02.01 Glycolysis	6,00E-94	74,00	evm_27.model.AmTr_v1.0_scaffold00177.21	-13,39276	45	15,5	4	3	3	1,75	TLLFGDKPVTV FGVN
100	5	Q9SJK9	Fructose-bisphosphate aldolase	<i>Arabidopsis thaliana</i>	AT2G36460	02 Energy	02.01 Glycolysis	e-172	86,00	evm_27.model.AmTr_v1.0_scaffold00040.204	-81,92661	49	37,7	17	-	14	1,17647	MVTPGSDAPK MVTPGSDAPK CQQYYAAGAR
100	5	P06525	Alcohol dehydrogenase	<i>Arabidopsis thaliana</i>	AT1G77120	02 Energy	02.16 Fermentation	e-159	71	evm_27.model.AmTr_v1.0_scaffold00071.65	-15,55679	19	34,2	5	-	5	0,58333	GQKPLFPR ASTAGQVIR CSDKPVQEVIV
100	5	Q94EJ2	Histone deacetylase	<i>Arabidopsis thaliana</i>	AT1G08460	04 Transcription	04.1907 Chromatin modification	e-154	68,00	evm_27.model.AmTr_v1.0_scaffold00030.113	-18,41451	14	42,2	4	-	4	0,28571	GYEYAMTK ELIEADENGG K
100	5	Q9S9N1	HSP70 (heat shock protein)	<i>Arabidopsis thaliana</i>	AT1G16030	06 Protein destination and storage	06.01 Folding and stability	0	80,00	evm_27.model.AmTr_v1.0_scaffold00137.8	-68,78564	22	71,6	13	-	12	0,61905	FSDPSVQADM K
101	3	Q9T0A7	UDP-glucose 4-epimerase	<i>Arabidopsis thaliana</i>	AT4G23920	01 Metabolism	01.05 Sugars and polysaccharides	e-156	76	evm_27.model.AmTr_v1.0_scaffold00024.78	-122,0852	57	37,9	31	-	21	1,94118	ATAGDTHLGG RVTELAGESSG K
101	3	Q9T0G0	Hydroxysteroid dehydrogenase (Steroleosin-B)	<i>Arabidopsis thaliana</i>	AT4G10020	01 Metabolism	01.06 Lipid and sterol	2e-86	66	evm_27.model.AmTr_v1.0_scaffold00099.13	-18,70341	23	24,8	4	-	4	0,66667	VQOQVAVGR MSLYAAK GANLNLVLR VVIVTGASSGI
101	3	Q9SJK9	Fructose-bisphosphate aldolase	<i>Arabidopsis thaliana</i>	AT2G36460	02 Energy	02.01 Glycolysis	e-172	86	evm_27.model.AmTr_v1.0_scaffold00040.204	-48,21319	37	37,7	10	-	10	0,58824	MVTPGSDAPK CQQYYAAGAR NAAYIGTPGR
102	4	Q9T0A7	UDP-glucose 4-epimerase	<i>Arabidopsis thaliana</i>	AT4G23920	01 Metabolism	01.05 Sugars and polysaccharides	e-156	76	evm_27.model.AmTr_v1.0_scaffold00024.78	-84,19937	51	37,9	20	-	16	1,23529	RVTELAGESSG K
102	4	Q9T0G0	Hydroxysteroid dehydrogenase (Steroleosin-B)	<i>Arabidopsis thaliana</i>	AT4G10020	01 Metabolism	01.06 Lipid and sterol	2,00E-86	66	evm_27.model.AmTr_v1.0_scaffold00099.13	-38,52873	45	24,8	7	-	6	2	DVVKEEDCR R
102	4	Q9SJK9	Fructose-bisphosphate aldolase	<i>Arabidopsis thaliana</i>	AT2G36460	02 Energy	02.01 Glycolysis	e-172	86	evm_27.model.AmTr_v1.0_scaffold00040.204	-28,02059	26	37,7	7	-	6	0,47059	MVTPGSDAPK VAPVIAEHTI R
102	4	P57106	Malate dehydrogenase	<i>Arabidopsis thaliana</i>	AT5G43330	02 Energy	02.10 TCA pathway	2e-47	78	evm_27.model.AmTr_v1.0_scaffold01428.1	-22,42187	60	6,9	6	-	4	2	KKLDATADELS EEK
103	4	Q9T0A7	UDP-glucose 4-epimerase	<i>Arabidopsis thaliana</i>	AT4G23920	01 Metabolism	01.05 Sugars and polysaccharides	e-156	76	evm_27.model.AmTr_v1.0_scaffold00024.78	-22,81451	23	37,9	5	-	5	0,35294	KLDATELSE RPDGAEIVYAS TDK
103	4	Q9T0G0	Hydroxysteroid dehydrogenase (Steroleosin-B)	<i>Arabidopsis thaliana</i>	AT4G10020	01 Metabolism	01.06 Lipid and sterol	2,00E-86	66	evm_27.model.AmTr_v1.0_scaffold00099.13	-22,01412	22	24,8	4	-	4	0,66667	YFNPVGAHPS AADVKEEDCR
103	4	Q9SJK9	Fructose-bisphosphate aldolase	<i>Arabidopsis thaliana</i>	AT2G36460	02 Energy	02.01 Glycolysis	e-172	86	evm_27.model.AmTr_v1.0_scaffold00040.204	-12,57306	18	37,7	4	-	4	0,35294	MSLYAAK EENIPAAQK CQQYYAAGAR ANSEATLGT
103	4	P57106	Malate dehydrogenase	<i>Arabidopsis thaliana</i>	AT5G43330	02 Energy	02.10 TCA pathway	e-130	78	evm_27.model.AmTr_v1.0_scaffold01428.1	-32,9069	60	6,9	9	-	6	3	ADELSEK KKLDATADELS EEK

105	3	Q9FX54	Glyceraldehyde-3-phosphate dehydrogenase	<i>Arabidopsis thaliana</i>	AT1G13440	02 Energy	02.01 Glycolysis	6,00E-94	74	evm_27.model.AmTr.v1.0_scaffold00177.2	-35,02179	16	15,5	6	5	5	1,5	PVTVFGVR TLLFGDKPVTV EGVR
105	3	Q9SJK9	Fructose-bisphosphate aldolase	<i>Arabidopsis thaliana</i>	AT2G36460	02 Energy	02.01 Glycolysis	e-172	86	evm_27.model.AmTr.v1.0_scaffold00040.2	-76,81541	47	37,7	16	-	14	1,05822	MVTPGSDAPK ALQOQSTLK CQOYYAAGAR
105	3	P06525	Alcohol dehydrogenase	<i>Arabidopsis thaliana</i>	AT1G77120	02 Energy	02.16 Fermentation	e-159	71	evm_27.model.AmTr.v1.0_scaffold00071.6	-21,02055	19	34,2	6	-	6	0,66667	GVMLSDGK AAVAWEAGK ASTAGQVIR
106	3	O81884	L-galactose dehydrogenase	<i>Arabidopsis thaliana</i>	AT4G33670	01 Metabolism	01.05 Sugars and polysaccharides	e-135	75,00	evm_27.model.AmTr.v1.0_scaffold00033.2	-7,187782	12	34,5	3	-	3	0,33333	ALOSLNVPFR ENVSSALEISS AEK
106	3	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr.v1.0_scaffold00067.7	-159,0974	32	54,5	55	-	35	2,95238	LSDAQQCR SFHSGESGSI QHR
106	3	Q9FGH3	Cinnamoyl-CoA reductase	<i>Arabidopsis thaliana</i>	AT5G58490	20 Secondary metabolism	20.1 Phenylpropanoids/phenolics	e-124	67	evm_27.model.AmTr.v1.0_scaffold00153.3	-18,73758	14	24,8	4	-	4	0,44444	HLQGLEAGERS AAWDFAK
107	2	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr.v1.0_scaffold00067.7	-224,2515	39	54,5	70	-	46	3,57143	RLSDAQQCR LSDAQQCR GROEGEYGE
107	2	O65398	Glyoxalase I (Lactoylglutathione lyase)	<i>Arabidopsis thaliana</i>	AT1G11840	11 Disease/defence	11.06 Detoxification	e-130	78,00	evm_27.model.AmTr.v1.0_scaffold00037.1	-20,13407	19	33,2	3	-	3	0,35714	GPTPEPLCHV MLR VVFVDHSDFL
108	2	P47998	Cysteine synthase	<i>Arabidopsis thaliana</i>	AT4G14880	01 Metabolism	01.01 Amino Acid	e-126	73	evm_27.model.AmTr.v1.0_scaffold00033.2	-15,0158	16	34,8	5	-	4	0,3125	GISSGAAAA AIK LIITMPTMSL
108	2	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr.v1.0_scaffold00067.7	-198,0258	39	54,5	63	-	41	3,71429	RLSDAQQCR LSDAQQCR GROEGEYGE
109	2	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr.v1.0_scaffold00067.7	-281,075	39	54,5	102	-	62	5,38095	RLSDAQQCR GROEGEYGE EEOEGEQK
109	2	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5e-54	30	evm_27.model.AmTr.v1.0_scaffold00002.6	-24,793	18	43,5	5	-	5	0,21739	PSSEQLQLIHL GQGGPVRPSS
110	1	P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	5e-72	32	evm_27.model.AmTr.v1.0_scaffold00067.1	-196,643	42	53	77	-	40	5	VGEGEQQQ GIKDRHQK RGQEGQQE
111	4	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr.v1.0_scaffold00067.7	-27,14046	11	54,5	5	2	5	0,2381	QFFIAGGQPR LIQTILPQIDTR
111	4	P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	5e-72	32	evm_27.model.AmTr.v1.0_scaffold00067.1	-33,11552	21	53	7	-	6	0,47059	RGQEEGQQE QEQEQEQR VGEGEQQQ
111	4	O65398	Glyoxalase I (Lactoylglutathione lyase)	<i>Arabidopsis thaliana</i>	AT1G11840	11 Disease/defence	11.06 Detoxification	e-130	78	evm_27.model.AmTr.v1.0_scaffold00037.1	-89,89387	58	33,2	23	22	16	1,92857	MGYAEEK ISDNPAYK LVTQELGGK
111	4	Q8W593	Glyoxalase I (Lactoylglutathione lyase)	<i>Arabidopsis thaliana</i>	AT1G67280	11 Disease/defence	11.06 Detoxification	e-151	78	evm_27.model.AmTr.v1.0_scaffold00109.1	-9,438898	8	32	3	2	2	0,28571	GPTPEPLCQV MLR GPTPEPLCQV
112	2	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr.v1.0_scaffold00002.6	-20,71018	19	43,5	6	-	6	0,26087	GQGGPVR PSSEQLQLIHL GSGGGK
112	2	Q941A4	Uncharacterized protein	<i>Arabidopsis thaliana</i>	AT5G45690	13 Unclassified	13 Unclassified	5,00E-74	55	evm_27.model.AmTr.v1.0_scaffold00162.9	-98,95898	71	28,9	28	-	20	1,82353	VYDSDSSDAR AVYDSDSSDAR
113	2	Q9SF20	MD-2-related lipid recognition domain-containing protein	<i>Arabidopsis thaliana</i>	AT3G11780	11 Disease/defence	11.02 Defence-regulated	1,00E-45	59	evm_27.model.AmTr.v1.0_scaffold00004.1	-14,92609	26	16,4	3	-	3	0,5	SISASTEAPLS EGK VSGMEVDDPP
113	2	Q941A4	Uncharacterized protein	<i>Arabidopsis thaliana</i>	AT5G45690	13 Unclassified	13 Unclassified	5,00E-74	55	evm_27.model.AmTr.v1.0_scaffold00162.9	-152,7677	75	28,9	49	-	29	3,41176	VYDSDSSDAR AVYDSDSSDAR
114	5	P53492	Actin 7	<i>Arabidopsis thaliana</i>	AT5G09810	09 Cell structure	09.04 Cytoskeleton	0	97	evm_27.model.AmTr.v1.0_scaffold00018.1	-19,37329	19	41,6	4	-	4	0,46667	VGMGQKDAYV GDEAQS AGFAGDDAPR
114	5	P53496	Actin 11	<i>Arabidopsis thaliana</i>	AT3G12110	09 Cell structure	09.04 Cytoskeleton	0	96	evm_27.model.AmTr.v1.0_scaffold00044.6	-19,37329	13	43,9	4	-	4	0,375	VGMGQKDAYV GDEAQS AGFAGDDAPR
114	5	P53492	Actin 7	<i>Arabidopsis thaliana</i>	AT5G09810	09 Cell structure	09.04 Cytoskeleton	0	97	evm_27.model.AmTr.v1.0_scaffold00030.1	-19,37329	14	41,5	4	-	4	0,4	VGMGQKDAYV GDEAQS AGFAGDDAPR

114	5	F4HWR0	Dessication-related protein	<i>Arabidopsis thaliana</i>	AT1G47980	11 Disease/defence	11.05 Stress responses	e-106	70	evm_27.model.AmTr_v1.0_scaffold00016.315	-30,22254	19	33,4	6	-	5	0,46154	TPQEILR TILYEQANK PLLDLSSENFA
114	5	O65398	Glyoxalase I (Lactoylglutathione lyase)	<i>Arabidopsis thaliana</i>	AT1G11840	11 Disease/defence	11.06 Detoxification	e-130	78	evm_27.model.AmTr_v1.0_scaffold00037.106	-87,23048	48	33,2	26	-	15	1,85714	ISDNPAYK AIATEDVYK YTLAMMGYAE
115	2	F4HWR0	Dessication-related protein	<i>Arabidopsis thaliana</i>	AT1G47980	11 Disease/defence	11.05 Stress responses	e-106	70	evm_27.model.AmTr_v1.0_scaffold00016.315	-236,193	62	33,4	83	-	51	7,38462	VMNSAFGHK QEYGHLR IVYSSGNEK
115	2	Q941A4	Uncharacterized protein	<i>Arabidopsis thaliana</i>	AT5G45690	13 Unclassified	13 Unclassified	5,00E-74	55	evm_27.model.AmTr_v1.0_scaffold00162.9	-10,42555	12	28,9	3	-	3	0,17647	GAQMLQSLKP VK IFESLPDFEK
116	2	F4HWR0	Dessication-related protein	<i>Arabidopsis thaliana</i>	AT1G47980	11 Disease/defence	11.05 Stress responses	e-106	70	evm_27.model.AmTr_v1.0_scaffold00016.315	-210,402	63	33,4	74	-	42	6,76923	VMNSAFGHK IVYSSGNEK KVDPPYPH
116	2	O65398	Glyoxalase I (Lactoylglutathione lyase)	<i>Arabidopsis thaliana</i>	AT1G11840	11 Disease/defence	11.06 Detoxification	e-130	78	evm_27.model.AmTr_v1.0_scaffold00037.106	-22,12679	20	33,2	6	-	5	0,42857	YTLAMMGYAE EK IALSTEDVYK
117	2	F4HWR0	Dessication-related protein	<i>Arabidopsis thaliana</i>	AT1G47980	11 Disease/defence	11.05 Stress responses	e-106	70	evm_27.model.AmTr_v1.0_scaffold00016.315	-195,2634	57	33,4	63	-	39	5,15385	VMNSAFGHK KVDPPYPH GPPPIGATK
117	2	O65398	Glyoxalase I (Lactoylglutathione lyase)	<i>Arabidopsis thaliana</i>	AT1G11840	11 Disease/defence	11.06 Detoxification	e-130	78	evm_27.model.AmTr_v1.0_scaffold00037.106	-24,57457	15	33,2	6	-	4	0,42857	LVTQELGGK YTLAMMGYAE EK
118	2	F4HWR0	Dessication-related protein	<i>Arabidopsis thaliana</i>	AT1G47980	11 Disease/defence	11.05 Stress responses	e-106	70	evm_27.model.AmTr_v1.0_scaffold00016.315	-105,9725	49	33,4	25	-	19	2,23077	VMNSAFGHK KVDPPYPH GGPPPIGATK
118	2	O65398	Glyoxalase I (Lactoylglutathione lyase)	<i>Arabidopsis thaliana</i>	AT1G11840	11 Disease/defence	11.06 Detoxification	e-130	78	evm_27.model.AmTr_v1.0_scaffold00037.106	-97,64965	49	33,2	33	-	19	2,5	MGYAEK ISDNPAYK KDKHRELHAV
119	3	F4HWR0	Dessication-related protein	<i>Arabidopsis thaliana</i>	AT1G47980	11 Disease/defence	11.05 Stress responses	e-106	70	evm_27.model.AmTr_v1.0_scaffold00016.315	-62,39283	43	33,4	17	-	14	1,46154	VMNSAFGHK IVYSSGNEK IVYSSGNEK
119	3	O65398	Glyoxalase I (Lactoylglutathione lyase)	<i>Arabidopsis thaliana</i>	AT1G11840	11 Disease/defence	11.06 Detoxification	e-130	78	evm_27.model.AmTr_v1.0_scaffold00037.106	-106,2738	57	33,2	31	29	23	2,42857	ISDNPAYK MGYAEK KDKHRELHAV
119	3	Q8W593	Glyoxalase I (Lactoylglutathione lyase)	<i>Arabidopsis thaliana</i>	AT1G67280	11 Disease/defence	11.06 Detoxification	e-151	78	evm_27.model.AmTr_v1.0_scaffold00109.150	-6,629117	8	32	3	1	2	0,21429	GPTPEPLCQV MLR
120	5	Q9FX54	Glyceraldehyde-3-phosphate dehydrogenase	<i>Arabidopsis thaliana</i>	AT1G13440	02 Energy	02.01 Glycolysis	6e-94	82	evm_27.model.AmTr_v1.0_scaffold00177.24	-59,69678	42	24,7	16	-	13	2,42857	VVESTGVFTD K DAPMFVVGVN
120	5	P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	5e-72	32	evm_27.model.AmTr_v1.0_scaffold00067.12	-51,37841	31	53	9	-	9	0,52941	RGQEEGOQE QEQEEOEER VGFEGQQQQ
120	5	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5e-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-32,53067	27	43,5	8	-	7	0,3913	IEMACPH AQSDSVFVVG PR
120	5	F4HWR0	Dessication-related protein	<i>Arabidopsis thaliana</i>	AT1G47980	11 Disease/defence	11.05 Stress responses	e-106	70	evm_27.model.AmTr_v1.0_scaffold00016.315	-33,70228	23	33,4	7	-	7	0,53846	GGPPPIGATK AYQEVGHLR TILYEQANK
120	5	O65398	Glyoxalase I (Lactoylglutathione lyase)	<i>Arabidopsis thaliana</i>	AT1G11840	11 Disease/defence	11.06 Detoxification	e-130	78,00	evm_27.model.AmTr_v1.0_scaffold00037.106	-23,30103	25	33,2	4	-	4	0,5	YTLAMMGYAE EK FYTECFGMK
121	5	Q9S9P4	S-adenosyl-L-methionine-dependent methyltransferase (7-)	<i>Arabidopsis thaliana</i>	AT1G30550	04 Transcription	04.22 mRNA processing	2e-79	68	evm_27.model.AmTr_v1.0_scaffold00019.57	-14,8412	3	122	4	-	4	0,08696	EHSDDSDLK LK AFLTTADSAVK
121	5	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5e-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-35,44227	36	43,5	11	-	10	0,47826	ARIEMACPHV SGGR LVTIGEER
121	5	F4HWR0	Dessication-related protein	<i>Arabidopsis thaliana</i>	AT1G47980	11 Disease/defence	11.05 Stress responses	e-106	70	evm_27.model.AmTr_v1.0_scaffold00016.315	-44,59486	35	33,4	10	-	10	0,76923	IVYSSGNEK GGPPPIGATK TILYEQANK
121	5	O24496	Glyoxalase II (Hydroxyacylglutathione hydrolase)	<i>Arabidopsis thaliana</i>	AT3G10850	11 Disease/defence	11.06 Detoxification	e-113	70	evm_27.model.AmTr_v1.0_scaffold00077.152	-72,79105	64	28,8	16	-	14	1,21429	VYGGHEYTVK AEAVHADIK EAAVDPPEP
121	5	Q941A4	Uncharacterized protein	<i>Arabidopsis thaliana</i>	AT5G45690	13 Unclassified	13 Unclassified	5,00E-74	55	evm_27.model.AmTr_v1.0_scaffold00162.9	-41,33185	38	28,9	10	-	9	0,58824	IFESLPDEEKK YGLSSEELK IFESLPDEEK
122	3	Q9FX54	Glyceraldehyde-3-phosphate dehydrogenase	<i>Arabidopsis thaliana</i>	AT1G13440	02 Energy	02.01 Glycolysis	6e-94	82	evm_27.model.AmTr_v1.0_scaffold00177.24	-14,7612	26	24,7	5	-	4	0,71429	VVESTGVFTD K AAGFNIPSST

122	3	F4HWR0	Dessication-related protein	<i>Arabidopsis thaliana</i>	AT1G47980	11 Disease/defence	11.05 Stress responses	e-106	70	evm_27.model.AmTr_v1.0_scaffold00016.3_15	-15,13949	30	33,4	7	-	7	0,61538	IVYSSGNEK TILYEQANK TPOEILR
122	3	Q941A4	Uncharacterized protein	<i>Arabidopsis thaliana</i>	AT5G45690	13 Unclassified	13 Unclassified	5,00E-74	55	evm_27.model.AmTr_v1.0_scaffold00162.9	-77,77918	60	28,9	24	-	14	1,58824	VYDSDSSDAR AVYDSDSSDAR
123	6	Q9FX54	Glyceraldehyde-3-phosphate dehydrogenase	<i>Arabidopsis thaliana</i>	AT1G13440	02 Energy	02.01 Glycolysis	6e-94	82	evm_27.model.AmTr_v1.0_scaffold00177.2_4	-34,19664	33	24,7	9	-	6	1,42857	KVVISAPSK DAPMFVVGVN FHEYKDDVH FGLDEAHGK
123	6	Q9S9P4	S-adenosyl-L-methionine-dependent methyltransferase (7-	<i>Arabidopsis thaliana</i>	AT1G30550	04 Transcription	04.22 mRNA processing	2e-79	68	evm_27.model.AmTr_v1.0_scaffold00019.5_7	-59,43711	11	122	11	-	11	0,28261	PAASLLDK EILTGAQGDGK GVASGMAPLAR
123	6	Q9LUM3	Subtilase family protein	<i>Arabidopsis thaliana</i>	AT3G14240	06 Protein destination and storage	06.13 Proteolysis	0	55	evm_27.model.AmTr_v1.0_scaffold00003.1_07	-18,20918	8	61	6	-	5	0,33333	ASALGYAR IEMACPH IEMACPHVSGGR
123	6	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5e-54	30	evm_27.model.AmTr_v1.0_scaffold00002.6_57	-45,37548	28	43,5	11	-	8	0,52174	IEMACPH IEMACPHVSGGR
123	6	F4HWR0	Dessication-related protein	<i>Arabidopsis thaliana</i>	AT1G47980	11 Disease/defence	11.05 Stress responses	e-106	70	evm_27.model.AmTr_v1.0_scaffold00016.3_15	-33,79751	27	33,4	6	-	6	0,53846	TILYEQANK ANLDPILTR SPGGFFPK
123	6	O65398	Glyoxalase I (Lactoylglutathione lyase)	<i>Arabidopsis thaliana</i>	AT1G11840	11 Disease/defence	11.06 Detoxification	e-130	78,00	evm_27.model.AmTr_v1.0_scaffold00037.1_06	-22,55939	21	33,2	6	-	5	0,57143	EPGPIPIGINTK FYTECFGNMK YTLAMMGYAE
124	3	Q9FX54	Glyceraldehyde-3-phosphate dehydrogenase	<i>Arabidopsis thaliana</i>	AT1G13440	02 Energy	02.01 Glycolysis	6e-94	82	evm_27.model.AmTr_v1.0_scaffold00177.2_4	-33,5574	42	24,7	9	-	6	1,42857	KVVISAPSK DAPMFVVGVN
124	3	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.6_57	-55,72472	35	43,5	14	-	11	0,65217	IEMACPH ARIEMACPHVSGGR
124	3	F4HWR0	Dessication-related protein	<i>Arabidopsis thaliana</i>	AT1G47980	11 Disease/defence	11.05 Stress responses	e-106	70	evm_27.model.AmTr_v1.0_scaffold00016.3_15	-23,42779	21	33,4	5	-	4	0,46154	TILYEQANK VDPYPHTISEF TNNISQLR
125	3	Q9SAJ4	Phosphoglycerate kinase	<i>Arabidopsis thaliana</i>	AT1G79550	02 Energy	02.01 Glycolysis	0	85	evm_27.model.AmTr_v1.0_scaffold00062.1_99	-123,7533	60	42,4	26	-	20	1,22727	AHASTEGLIAK YLMENGAKE EEEKNDPEFS
125	3	B9DGL8	Alpha-galactosidase	<i>Arabidopsis thaliana</i>	AT5G08370	09 Cell structure	09.01 Cell wall	e-171	75	evm_27.model.AmTr_v1.0_scaffold00171.3_2	-37,9204	24	45,1	8	-	8	0,52381	YDNCNNDGV DPR GQLTATVDSH
125	3	Q9LF88	Late embryogenesis abundant protein (LEA)	<i>Arabidopsis thaliana</i>	AT3G53040	11 Disease/defence	11.05 Stress responses	3e-44	37	evm_27.model.AmTr_v1.0_scaffold00002.3_88	-17,61332	11	33,9	3	-	3	0,375	AGEANDSAAD ATR EAAAEFAAAQ
126	4	Q9SAJ4	Phosphoglycerate kinase	<i>Arabidopsis thaliana</i>	AT1G79550	02 Energy	02.01 Glycolysis	0	85	evm_27.model.AmTr_v1.0_scaffold00062.1_99	-116,7739	63	42,4	24	-	19	1,13636	AHASTEGLIAK YLMENGAKE VILASHLGR
126	4	B9DGL8	Alpha-galactosidase	<i>Arabidopsis thaliana</i>	AT5G08370	09 Cell structure	09.01 Cell wall	e-171	75	evm_27.model.AmTr_v1.0_scaffold00171.3_2	-23,9537	16	45,1	5	-	5	0,33333	YDNCNNDGV DPR DSQGNLVPK
126	4	Q9LF88	Late embryogenesis abundant protein (LEA)	<i>Arabidopsis thaliana</i>	AT3G53040	11 Disease/defence	11.05 Stress responses	3e-44	37	evm_27.model.AmTr_v1.0_scaffold00002.3_88	-21,74325	16	33,9	4	-	4	0,75	AGEANDSAAD ATR VTAEDAGER
126	4	F4HWR0	Dessication-related protein	<i>Arabidopsis thaliana</i>	AT1G47980	11 Disease/defence	11.05 Stress responses	e-106	70	evm_27.model.AmTr_v1.0_scaffold00016.3_15	-53,98155	34	33,4	15	-	8	1,38462	TILYEQANK VDPYPHTISEF TNNISQLR
127	5	Q9SAJ4	Phosphoglycerate kinase	<i>Arabidopsis thaliana</i>	AT1G79550	02 Energy	02.01 Glycolysis	0	85	evm_27.model.AmTr_v1.0_scaffold00062.1_99	-43,92173	37	42,4	11	-	10	0,63636	AHASTEGLIAK VILASHLGR RPFPAIVGGSK
127	5	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.6_57	-30,63027	30	43,5	8	-	7	0,47826	IEMACPH KGDATIPAGK IEMACPHVSG
127	5	B9DGL8	Alpha-galactosidase	<i>Arabidopsis thaliana</i>	AT5G08370	09 Cell structure	09.01 Cell wall	e-171	75	evm_27.model.AmTr_v1.0_scaffold00171.3_2	-99,74345	54	45,1	25	-	19	1,42857	YDNCNNDGV DPR GQLTATVDSH
127	5	Q9LF88	Late embryogenesis abundant protein (LEA)	<i>Arabidopsis thaliana</i>	AT3G53040	11 Disease/defence	11.05 Stress responses	3e-44	37	evm_27.model.AmTr_v1.0_scaffold00002.3_88	-25,91492	23	33,9	6	-	5	0,75	AGEANDSAAD ATR EAAAEFAAAQ
127	5	F4HWR0	Dessication-related protein	<i>Arabidopsis thaliana</i>	AT1G47980	11 Disease/defence	11.05 Stress responses	e-106	70	evm_27.model.AmTr_v1.0_scaffold00016.3_15	-53,5281	25	33,4	12	-	7	0,92308	TILYEQANK PLLDLSSENFAK
128	3	Q9LF88	Late embryogenesis abundant protein (LEA)	<i>Arabidopsis thaliana</i>	AT3G53040	11 Disease/defence	11.05 Stress responses	3e-44	37	evm_27.model.AmTr_v1.0_scaffold00002.3_88	-22,06585	13	33,9	4	-	4	0,5	AGEANDSAAD ATR VTAEDAGER

128	3	F4HWR0	Dessication-related protein	<i>Arabidopsis thaliana</i>	AT1G47980	11 Disease/defence	11.05 Stress responses	e-106	70	evm_27.model.AmTr_v1.0_scaffold00016.315	-53,35379	26	33,4	13	-	7	1,15385	SPGGFFPK LVAGLLGVES GQDAIR
128	3	Q9SD45	Epoxide hydrolase	<i>Arabidopsis thaliana</i>	AT3G51000	11 Disease/defence	11.06 Detoxification	1e-22	34	evm_27.model.AmTr_v1.0_scaffold00009.414	-21,76501	42	21,7	9	-	7	2	DEADHPMPTD LK VPAMLVMGNK AFLTITADSAVK IQVFPVDIAPK ILQIPSDICITE SVAAGMINAMD LR SAIFASTSDYD AQSDSVFVVG PR NSLNQIER
129	4	Q9S9P4	S-adenosyl-L-methionine-dependent methyltransferase (7- Chaperonin (Chaperonin-60kD, ch60_CPN60)	<i>Arabidopsis thaliana</i>	AT1G30550	04 Transcription	04.22 mRNA processing	2e-79	68	evm_27.model.AmTr_v1.0_scaffold00019.57	-16,79904	5	122	3	-	3	0,1087	YTLAMMGYAE EK ETTIVLELTNY GAIANPDEGR FSEVDTR ALIAEGSCGSP GEYVDMVK IGGASEVEVS EK
129	4	P29197	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.01 Folding and stability	0	86	evm_27.model.AmTr_v1.0_scaffold00003.261	-118,1769	45	61,2	22	-	19	0,9	IEMACPH KGD TATIPAGK PSSEQLQGLIH
129	4	Q9LUJ7	Glyoxalase I (Lactoylglutathione lyase)	<i>Arabidopsis thaliana</i>	AT1G11840	11 Disease/defence	11.06 Detoxification	e-130	78,00	evm_27.model.AmTr_v1.0_scaffold00037.106	-14,69357	10	33,2	3	-	2	0,21429	FLAALDPIEL AQ FLAALDPIEL AEQDSQIGHG AR QDSQIGHGAR AVTAATNYNN R EAVSSELSDE
130	5	Q8H103	Phosphoglucose isomerase	<i>Arabidopsis thaliana</i>	AT4G24620	02 Energy	02.01 Glycolysis	0	84	evm_27.model.AmTr_v1.0_scaffold00135.20	-54,99657	22	68,4	12	-	12	0,325	ITTAALANK ISAQMLQDAV SR
130	5	P29197	Chaperonin (Chaperonin-60kD, ch60_CPN60)	<i>Arabidopsis thaliana</i>	AT3G23990	06 Protein destination and storage	06.01 Folding and stability	9	86	evm_27.model.AmTr_v1.0_scaffold00003.261	-17,98158	9	61,2	4	-	4	0,16667	IVAHMAANDR GAIANPDEGR SALYANNR RGQEEGOQE QEQEEOEER GIISIVFPGCTE
130	5	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5e-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-33,37077	29	43,5	9	-	8	0,43478	IEMACPH KGD TATIPAGK PSSEQLQGLIH
130	5	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr_v1.0_scaffold00067.7	-21,81942	17	54,5	6	-	5	0,28571	FLAALDPIEL AQ FLAALDPIEL AEQDSQIGHG AR QDSQIGHGAR AVTAATNYNN R EAVSSELSDE
130	5	P93026	Vacuolar sorting receptor	<i>Arabidopsis thaliana</i>	AT3G52850	08 Intracellular traffic	08.13 Vacuolar	0	73	evm_27.model.AmTr_v1.0_scaffold00077.78	-154,5848	47	69,4	36	-	30	1,23333	ITTAALANK ISAQMLQDAV SR
131	5	Q9SEE5	Galactokinase	<i>Arabidopsis thaliana</i>	AT3G06580	01 Metabolism	01.05 Sugars and polysaccharides	0	73	evm_27.model.AmTr_v1.0_scaffold00003.234	-67,84259	38	50,9	14	-	14	0,7	IVAHMAANDR GAIANPDEGR SALYANNR RGQEEGOQE QEQEEOEER GIISIVFPGCTE
131	5	Q8W4R0	Phosphoglucosamine mutase family protein	<i>Arabidopsis thaliana</i>	AT5G17530	02 Energy	02.01 Glycolysis	0	66	evm_27.model.AmTr_v1.0_scaffold00148.23	-15,22458	11	64	4	-	4	0,18519	IEMACPH KGD TATIPAGK IEMACPHVSG HIVQLHPSSR DHSVGLNCGR YDHEFAR
131	5	Q8H103	Phosphoglucose isomerase	<i>Arabidopsis thaliana</i>	AT4G24620	02 Energy	02.01 Glycolysis	0	84	evm_27.model.AmTr_v1.0_scaffold00135.20	-144,4526	49	68,4	41	-	28	1,15	ADSSMTVAYE K TIEAEAHTGTV TR EPI MCK
131	5	P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	5e-72	32	evm_27.model.AmTr_v1.0_scaffold00067.12	-16,54061	8	53	3	-	2	0,17647	GVMLSDGK AAVAWEAGK ASTAGQVIR NKPPVMIGGK VTGVAILHYSN GPSAGPLPDP
131	5	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5e-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-89,63732	60	43,5	23	-	18	1,08696	AQSDSVFVVG PR AFSDEILEASF ARIEMACPHV SGGR IEMACPHVSG
135	1	Q9LZC3	Malate synthase	<i>Arabidopsis thaliana</i>	AT5G03860	02 Energy	02.10 TCA pathway	0	75	evm_27.model.AmTr_v1.0_scaffold00049.86	-133,2511	50	64,8	42	-	33	1,7037	EGALAEENMR GGGQIPTAR AYLPVVESEFG
136	1	Q9SRZ6	Isocitrate dehydrogenase	<i>Arabidopsis thaliana</i>	AT1G65930	02 Energy	02.10 TCA pathway	0	84	evm_27.model.AmTr_v1.0_scaffold00071.147	-93,68179	46	46,7	20	-	18	1,2	
137	2	Q9SRZ6	Isocitrate dehydrogenase	<i>Arabidopsis thaliana</i>	AT1G65930	02 Energy	02.10 TCA pathway	0	84	evm_27.model.AmTr_v1.0_scaffold00071.147	-87,87887	38	46,7	17	-	16	0,85	
137	2	P06525	Alcohol dehydrogenase	<i>Arabidopsis thaliana</i>	AT1G77120	02 Energy	02.16 Fermentation	e-159	71	evm_27.model.AmTr_v1.0_scaffold00071.65	-15,1439	21	34,2	6	-	6	0,58333	
138	1	Q9SU40	Monocopper oxidase-like protein	<i>Arabidopsis thaliana</i>	AT4G12420	03 Cell growth/division	03.01 Cell growth	0	72	evm_27.model.AmTr_v1.0_scaffold00085.6	-13,71894	9	66,3	4	-	4	0,18182	
139	1	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5e-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-11,31876	6	43,5	2	-	2	0,08696	
140	1	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5e-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-63,06705	53	43,5	19	-	15	1	
141	3	Q9ASR1	Translation elongation factor 2	<i>Arabidopsis thaliana</i>	AT1G56070	05 Protein synthesis	05.04 Translation factors	0	88,00	evm_27.model.AmTr_v1.0_scaffold00032.93	-14,30627	5	93,9	3	-	3	0,13333	

141	3	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30,00	evm_27.model.AmTr_v1.0_scaffold00002.657	-12,82754	12	43,5	3	-	3	0,17391	PSSEQLQLGHL GGSGGGK AQSDSVFVVG KISGNLLASDQ
141	3	F4HWR0	Dessiccation-related protein	<i>Arabidopsis thaliana</i>	AT1G47980	11 Disease/defence	11.05 Stress responses	e-106	70	evm_27.model.AmTr_v1.0_scaffold00016.315	-23,48096	10	33,4	6	-	3	0,53846	FSLSFDRTPQ EILR
142	1	Q9ASR1	Translation elongation factor 2	<i>Arabidopsis thaliana</i>	AT1G56070	05 Protein synthesis	05.04 Translation factors	0	88	evm_27.model.AmTr_v1.0_scaffold00032.93	-43,36718	11	93,9	7	-	7	0,3	ASQLTATPR GGGQIIPTR IMGPNYVPGQ
143	2	O50008	5-methyltetrahydropteroyl triolylamide	<i>Arabidopsis thaliana</i>	AT5G17920	01 Metabolism	01.01 Amino Acid	0	85	evm_27.model.AmTr_v1.0_scaffold00004.99	-38,62024	21	84,5	9	-	9	0,39394	AIKEEISK GNASLPAMEM TK
143	2	Q9SIB9	Aconitase	<i>Arabidopsis thaliana</i>	AT2G05710	02 Energy	02.10 TCA pathway	0	84	evm_27.model.AmTr_v1.0_scaffold00001.143	-16,18549	5	107	4	-	4	0,11111	ATYEAITK DFNSYGR VVFESFHGAP
145	2	Q9LF46	2-hydroxyacyl-CoA lyase	<i>Arabidopsis thaliana</i>	AT5G17380	01 Metabolism	01.06 Lipid and sterol	0	62	evm_27.model.AmTr_v1.0_scaffold00011.8	-23,28614	12	61,3	6	-	6	0,28571	AVLVQTEPR NPEEISGPYK SALTDPSFAR
145	2	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-41,80081	41	43,5	10	-	9	0,6087	IEMACPH EVSFNVPSR GGQPVRPSS
146	5	Q05758	Ketol-acid reductoisomerase	<i>Arabidopsis thaliana</i>	AT3G58610	01 Metabolism	01.01 Amino Acid	0	80	evm_27.model.AmTr_v1.0_scaffold00021.42	-60,59471	18	71,8	13	-	8	0,71429	GVSFMVDCNS TTAR DSLAEFAQSNII
146	5	Q8W4M5	Pyrophosphate-fructose 6-phosphate 1-phosphotransferase	<i>Arabidopsis thaliana</i>	AT1G12000	02 Energy	02.01 Glycolysis	0	79	evm_27.model.AmTr_v1.0_scaffold00136.32	-27,16793	10	61,9	4	-	4	0,26316	TIDGDLK LQDGPSSAA GNPDEIAK
146	5	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5e-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-132,7554	58	43,5	35	-	21	1,78261	KGDTATIPAGK KGDTATIPAGK ARIEMACPHV
146	5	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr_v1.0_scaffold00067.7	-9,608218	7	54,5	3	-	3	0,14286	FLAEALDPIEL AQK OFFIAGGQPR
146	5	O65398	Glyoxalase I (Lactoylglutathione lyase)	<i>Arabidopsis thaliana</i>	AT1G11840	11 Disease/defence	11.06 Detoxification	e-130	78	evm_27.model.AmTr_v1.0_scaffold00037.106	-15,84164	13	33,2	3	-	2	0,21429	ETTIVLELTNY GDTEYTK ETTIVLELTNY
147	1	Q9FX54	Glyceraldehyde-3-phosphate dehydrogenase	<i>Arabidopsis thaliana</i>	AT1G13440	02 Energy	02.01 Glycolysis	6e-94	82	evm_27.model.AmTr_v1.0_scaffold00177.24	-17,40528	17	24,7	3	-	3	0,42857	PVTVFGNR TLLFGEKPVTV FGNR
148	3	Q5E924	Glyceraldehyde-3-phosphate dehydrogenase	<i>Arabidopsis thaliana</i>	AT1G16300	02 Energy	02.01 Glycolysis	e-162	77	evm_27.model.AmTr_v1.0_scaffold00032.83	-4,053548	3	45,4	2	1	2	0,14286	SSIFDAK
148	3	Q9SAJ6	Glyceraldehyde-3-phosphate dehydrogenase	<i>Arabidopsis thaliana</i>	AT1G79530	02 Energy	02.01 Glycolysis	e-165	70	evm_27.model.AmTr_v1.0_scaffold00039.188	-4,053548	3	45,2	2	1	2	0,15	SSIFDAK
148	3	Q9FX54	Glyceraldehyde-3-phosphate dehydrogenase	<i>Arabidopsis thaliana</i>	AT1G13440	02 Energy	02.01 Glycolysis	6,00E-94	82	evm_27.model.AmTr_v1.0_scaffold00177.24	-38,82905	50	24,7	10	9	8	1,42857	KVVISAPSK YDSVHGQWK PVTVFGNR
149	3	Q9S9N1	HSP70 (heat shock protein)	<i>Arabidopsis thaliana</i>	AT1G16030	06 Protein destination and storage	06.01 Folding and stability	0	80	evm_27.model.AmTr_v1.0_scaffold00137.8	-22,18977	5	71,6	4	-	3	0,19048	SHVDDVVLVG GSTR SHVDDVVLVG
149	3	Q9SYT0	Annexin 1	<i>Arabidopsis thaliana</i>	AT1G35720	10 Signal transduction	10.99 Others	e-106	61	evm_27.model.AmTr_v1.0_scaffold00060.114	-71,67432	48	35,5	17	-	16	1,05263	DLKGAEDK AIASDTSGDYT YDGEVNGHL
149	3	A1L4Y4	NADPH:quinone reductase	<i>Arabidopsis thaliana</i>	AT5G61510	11 Disease/defence	11.06 Detoxification	e-132	69	evm_27.model.AmTr_v1.0_scaffold00111.28	-58,49009	30	40,1	12	-	9	0,8	IHENGGPEVL K IHENGGPEVL
153	1	P29197	Chaperonin (Chaperonin-60kD, ch60, CPN60)	<i>Arabidopsis thaliana</i>	AT3G23990	06 Protein destination and storage	06.01 Folding and stability	0	86	evm_27.model.AmTr_v1.0_scaffold00003.261	-103,7673	31	61,2	12	13	0,86667	AIYAEGCK GVEELADAVQ VTMGPK	
155	2	P54904	Pyroline-5-carboxylate reductase	<i>Arabidopsis thaliana</i>	AT5G14800	01 Metabolism	01.01 Amino Acid	4e-88	64	evm_27.model.AmTr_v1.0_scaffold00053.25	-65,84887	43	28,8	13	-	11	1,55556	MAEAIAR MAEAIAR GTIMGAVMAA
155	2	Q9LY84	GDSL esterase/lipase	<i>Arabidopsis thaliana</i>	AT5G14450	01 Metabolism	01.06 Lipid and sterol	e-119	58	evm_27.model.AmTr_v1.0_scaffold00049.280	-28,48466	14	41,7	3	-	3	0,33333	FCCGHAGDYT VGGCR YGCVYTQNDV
156	4	Q9XFK7	protein MOTHER of FT and TF 1	<i>Arabidopsis thaliana</i>	AT1G18100	03 Cell growth/division	03.26 Growth regulators	3,00E-70	67	evm_27.model.AmTr_v1.0_scaffold00024.325	-10,88739	34	19	3	-	3	0,44444	TVDPVLVVG QQTPLSLVAH PLPSTR
156	4	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr_v1.0_scaffold00067.7	-18,16629	12	54,5	4	-	4	0,19048	ISNQAQADIK GEGQIQIGTN GQK

156	4	P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	5e-72	32	evm_27.model.AmTr_v1.0_scaffold00067.12	-88,3251	22	53	36	-	22	2,41176	TSDLPMK GHLHPNAL AGHIQIVNR
156	4	F4HWR0	Dessication-related protein	<i>Arabidopsis thaliana</i>	AT1G47980	11 Disease/defence	11.05 Stress responses	e-106	70	evm_27.model.AmTr_v1.0_scaffold00016.315	-8,332547	11	33,4	4	-	2	0,30769	LVAGLLGVES GQDAIR ISGNLLASDQF VIGDVMDFM PSVR VIGDVMDFM ISNQAQDIK GEGQIQIGTN GQK
157	3	Q9XFK7	protein MOTHER of FT and TF 1	<i>Arabidopsis thaliana</i>	AT1G18100	03 Cell growth/division	03.26 Growth regulators	3,00E-70	67	evm_27.model.AmTr_v1.0_scaffold00024.325	-13,17005	24	19	3	-	2	0,44444	RADIYSR GHLHPNAL RADIYSR SINAHTIAYITR YNREDQIMIFP SSSR
157	3	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr_v1.0_scaffold00067.7	-63,52174	33	54,5	12	11	12	0,57143	RADIYSR GHLHPNAL RADIYSR SINAHTIAYITR YNREDQIMIFP SSSR
157	3	P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	5e-72	32	evm_27.model.AmTr_v1.0_scaffold00067.12	-56,7614	25	53	23	22	17	1,64706	RADIYSR GHLHPNAL RADIYSR SINAHTIAYITR YNREDQIMIFP SSSR
158	2	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr_v1.0_scaffold00067.7	-61,01322	25	54,5	29	16	12	1,57143	RADIYSR GHLHPNAL RADIYSR SINAHTIAYITR YNREDQIMIFP SSSR
158	2	P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	5e-72	32	evm_27.model.AmTr_v1.0_scaffold00067.12	-22,296	17	53	9	-	7	0,52941	RADIYSR QAQGHQIVNR SPILGHASAIK TVTDTVSDYN QLDTK YNREDQIMIFP
159	2	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr_v1.0_scaffold00067.7	-84,79927	31	54,5	30	15	17	1,57143	IQVIGTNGR GEGNIQVIGTN GR
159	2	P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	5e-72	32	evm_27.model.AmTr_v1.0_scaffold00067.12	-15,46066	14	53	6	5	6	0,52941	FLAEALDPIEL AQK FLAEALDPIEL VEIIPNDQGNR TTPSYVAFDTT ER
160	1	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr_v1.0_scaffold00067.7	-78,29639	33	54,5	32	14	17	1,61905	YNREDQIMIFP SSSR QFFIAGGQPR VGGEGQQQQ GIK QAQGHQIVNR HGGHLKTINR ISNQAQDIK NQQAQDIK NR
161	3	Q9S9N1	HSP70 (heat shock protein)	<i>Arabidopsis thaliana</i>	AT1G16030	06 Protein destination and storage	06.01 Folding and stability	0	80	evm_27.model.AmTr_v1.0_scaffold00137.8	-20,85821	8	71,6	4	-	4	0,19048	ISNQAQDIK ISNQAQDIKY NR
161	3	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr_v1.0_scaffold00067.7	-38,75304	21	54,5	14	9	8	0,80952	ISNQAQDIK ISNQAQDIK GEGQIQIGTN
161	3	P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	5e-72	32	evm_27.model.AmTr_v1.0_scaffold00067.12	-14,51578	14	53	4	-	4	0,41176	DYHPQASLR VPEVQPGVR
162	1	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr_v1.0_scaffold00067.7	-116,9934	29	54,5	49	-	25	2,66667	KGDTATIPAGK LVTIGEER GQGPIVRPSS
163	1	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr_v1.0_scaffold00067.7	-62,33001	20	54,5	22	-	12	1,19048	KGDTATIPAGK LVTIGEER GQGPIVRPSS
164	1	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr_v1.0_scaffold00067.7	-57,60686	20	54,5	17	-	12	0,95238	HTTDSYNLYK PETIHAPPHGK LPETHAPPHG
166	2	Q8H114	Protein-synthesizing GTPase (Appr-1-p processing enzyme)	<i>Arabidopsis thaliana</i>	AT2G40600	05 Protein synthesis	05.04 Translation factors	3e-63	67	evm_27.model.AmTr_v1.0_scaffold00077.36	-4,503763	13	23,2	2	-	2	0,36364	ISNQAQDIK ISNQAQDIK GEGQIQIGTN
166	2	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5e-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-17,83135	14	43,5	5	-	4	0,21739	KGDTATIPAGK LVTIGEER GQGPIVRPSS
168	2	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5e-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-24,56667	18	43,5	6	-	5	0,30435	HTTDSYNLYK PETIHAPPHGK LPETHAPPHG
168	2	Q9SK09	Cupin family protein (Viciin)	<i>Arabidopsis thaliana</i>	AT2G28490	06 Protein destination and storage	06.20 Storage proteins	e-115	50	evm_27.model.AmTr_v1.0_scaffold00080.82	-103,5694	28	43,1	26	-	20	1,8125	ISNQAQDIK TVTDTVSDYN QLDTK
169	4	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr_v1.0_scaffold00067.7	-29,20573	13	54,5	5	-	4	0,2381	LAMDINVK HTTDSYNLYK HTTDSYNLYK
169	4	Q9SK09	Cupin family protein (Viciin)	<i>Arabidopsis thaliana</i>	AT2G28490	06 Protein destination and storage	06.20 Storage proteins	e-115	50	evm_27.model.AmTr_v1.0_scaffold00080.82	-164,3304	30	43,1	47	-	29	3,1875	KGDTATIPAGK LVTIGEER GQGPIVRPSS
169	4	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-22,20325	14	43,5	6	-	6	0,26087	HLYGVGK SVTLTATAA ASPEVHEANL
169	4	Q93Z51	Isochorismatase family protein	<i>Arabidopsis thaliana</i>	AT3G16190	20 Secondary metabolism	20.3 Alkaloids	1e-64	64	evm_27.model.AmTr_v1.0_scaffold00067.182	-46,11492	59	21,1	8	-	7	1,6	

170	4	Q9SK09	Cupin family protein (Vicilin)	<i>Arabidopsis thaliana</i>	AT2G28490	06 Protein destination and storage	06.20 Storage proteins	e-115	50	evm_27.model.AmTr.v1.0_scaffold00080.82	-47,33563	17	43,1	13	-	9	0,8125	ESVILPETIHAPHG ESVILPETIHAPKGD TATIPAGK
170	4	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5e-54	30	evm_27.model.AmTr.v1.0_scaffold00002.657	-29,79026	21	43,5	6	-	6	0,30435	PSSEQLQLLIHGGSGGGK KISGNLLASDQ FSLSDFRTPQ FILR
170	4	F4HWR0	Dessication-related protein	<i>Arabidopsis thaliana</i>	AT1G47980	11 Disease/defence	11.05 Stress responses	e-106	70	evm_27.model.AmTr.v1.0_scaffold00016.315	-27,0314	13	33,4	6	-	3	0,46154	IFESLPDEEKK QIQOHVCSFR LIGVFYIVSDR KGD TATIPAGK
170	4	Q941A4	Uncharacterized protein	<i>Arabidopsis thaliana</i>	AT5G45690	13 Unclassified	13 Unclassified	5,00E-74	55	evm_27.model.AmTr.v1.0_scaffold00162.9	-13,21274	21	28,9	4	-	4	0,23529	VATPANWNPGDR PGLTIGDTIPNI KGD TATIPAGK
171	2	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr.v1.0_scaffold00002.657	-31,94739	20	43,5	8	-	6	0,47826	KGD TATIPAGK AFVLP PHHK
171	2	O04005	1-Cys peroxiredoxin	<i>Arabidopsis thaliana</i>	AT1G48130	11 Disease/defence	11.05 Stress responses	9,00E-89	69	evm_27.model.AmTr.v1.0_scaffold00045.37	-20,15629	35	24,2	5	-	5	0,54545	VATPANWNPGDR PGLTIGDTIPNI KGD TATIPAGK
172	1	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr.v1.0_scaffold00002.657	-93,13646	28	43,5	29	-	17	1,52174	TIPAGK KGD TATIPAGK
173	2	P48491	Triosephosphate isomerase	<i>Arabidopsis thaliana</i>	AT3G55440	02 Energy	02.01 Glycolysis	e-112	77	evm_27.model.AmTr.v1.0_scaffold00012.164	-45,03304	36	27,3	12	-	8	1,08333	CNGTVEEVKK CNGTVEEVKK CNGTVEEVKK
173	2	Q8GWR2	Uncharacterized protein	<i>Arabidopsis thaliana</i>	AT2G31985	13 Unclassified	13 Unclassified	5,00E-50	68	evm_27.model.AmTr.v1.0_scaffold00071.199	-116,8762	59	28,7	37	-	27	4	HYCSHPSEDMR HYCSHPSEDMR
174	1	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5e-54	30	evm_27.model.AmTr.v1.0_scaffold00002.657	-82,543	24	43,5	22	-	14	1,08696	KGD TATIPAGK KGD TATIPAGK GDTATIPAGK
175	1	P49206	40S ribosomal protein S26	<i>Arabidopsis thaliana</i>	AT2G40590	05 Protein synthesis	05.01 Ribosomal proteins	2e-31	75	evm_27.model.AmTr.v1.0_scaffold00077.25	-130,2098	33	42,6	38	-	25	3,30769	FNGGGHINH NLAPVNEGGG EPPK
176	2	P49206	40S ribosomal protein S26	<i>Arabidopsis thaliana</i>	AT2G40590	05 Protein synthesis	05.01 Ribosomal proteins	2e-31	75	evm_27.model.AmTr.v1.0_scaffold00077.25	-186,183	34	42,6	58	-	36	4,69231	HHQAYVTN FNGGGHINH KNLAPVNEGGG
176	2	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr.v1.0_scaffold00067.7	-16,09367	10	54,5	3	-	3	0,19048	GMPIEVLTNAYR VTLYSDAILAP NLAPVNEGGG EPPK
177	1	P49206	40S ribosomal protein S26	<i>Arabidopsis thaliana</i>	AT2G40590	05 Protein synthesis	05.01 Ribosomal proteins	2e-31	75	evm_27.model.AmTr.v1.0_scaffold00077.25	-17,92082	11	42,6	3	-	3	0,23077	GDASSTVQLQ APWSSLDENK IQVPVDIAPK ADIVCLWALK
178	2	Q9S9P4	S-adenosyl-L-methionine-dependent methyltransferase (7-	<i>Arabidopsis thaliana</i>	AT1G30550	04 Transcription	04.22 mRNA processing	2e-79	68	evm_27.model.AmTr.v1.0_scaffold00019.57	-6,913854	2	122	3	-	3	0,06522	VMNSAFGHHK GGPPPIGATK AYQEVGHLR
178	2	F4HWR0	Dessication-related protein	<i>Arabidopsis thaliana</i>	AT1G47980	11 Disease/defence	11.05 Stress responses	e-106	70	evm_27.model.AmTr.v1.0_scaffold00016.315	-50,42506	32	33,4	17	-	14	1,46154	CNGTVEEVKK CNGTVEEVKK ESGSTMDVVA
179	2	P48491	Triosephosphate isomerase	<i>Arabidopsis thaliana</i>	AT3G55440	02 Energy	02.01 Glycolysis	e-112	77	evm_27.model.AmTr.v1.0_scaffold00012.164	-33,73265	26	27,3	7	-	6	0,58333	VMNSAFGHHK KVDPPYPH QEVGHLR
179	2	F4HWR0	Dessication-related protein	<i>Arabidopsis thaliana</i>	AT1G47980	11 Disease/defence	11.05 Stress responses	e-106	70	evm_27.model.AmTr.v1.0_scaffold00016.315	-62,46827	37	33,4	19	-	16	1,46154	ESGSTMDVVA AQTK IYGGSVNGAN
180	2	P48491	Triosephosphate isomerase	<i>Arabidopsis thaliana</i>	AT3G55440	02 Energy	02.01 Glycolysis	e-112	77	evm_27.model.AmTr.v1.0_scaffold00012.164	-12,05661	15	27,3	3	-	3	0,25	VMNSAFGHHK KVDPPYPH PPPIGATK
180	2	F4HWR0	Dessication-related protein	<i>Arabidopsis thaliana</i>	AT1G47980	11 Disease/defence	11.05 Stress responses	e-106	70	evm_27.model.AmTr.v1.0_scaffold00016.315	-96,53965	37	33,4	25	-	20	2,15385	KNVSAEAVSK VATPQQAQDVH
181	3	Q9SKP6	Triosephosphate isomerase	<i>Arabidopsis thaliana</i>	AT2G21170	02 Energy	02.01 Glycolysis	3e-48	80	evm_27.model.AmTr.v1.0_scaffold00041.261	-95,86256	43	34,2	30	29	15	1,76471	ESGSTMDVVA AQTK
181	3	P48491	Triosephosphate isomerase	<i>Arabidopsis thaliana</i>	AT3G55440	02 Energy	02.01 Glycolysis	e-112	77	evm_27.model.AmTr.v1.0_scaffold00012.164	-12,3808	11	27,3	2	1	2	0,25	GGPPPIGATK AYQEVGHLR TILYEQANK
181	3	F4HWR0	Dessication-related protein	<i>Arabidopsis thaliana</i>	AT1G47980	11 Disease/defence	11.05 Stress responses	e-106	70	evm_27.model.AmTr.v1.0_scaffold00016.315	-15,88573	15	33,4	5	-	5	0,38462	AHSDDSYLDR TLQAEAVSK
182	7	Q8L831	Nudix hydrolase	<i>Arabidopsis thaliana</i>	AT1G79690	01 Metabolism	01.03 Nucleotides	0	66	evm_27.model.AmTr.v1.0_scaffold00036.84	-25,27815	9	88,2	5	-	5	0,16129	

182	7	Q9SKP6	Triosephosphate isomerase	<i>Arabidopsis thaliana</i>	AT2G21170	02 Energy	02.01 Glycolysis	3,00E-48	80	evm_27.model.AmTr_v1.0_scaffold00041.2_61	-88,59711	42	34,2	22	-	16	1,47059	KNVSAEVASK GNSNCAELAK NVSAEVASK
182	7	O23708	Proteasome subunit similaire 20S	<i>Arabidopsis thaliana</i>	AT1G16470	06 Protein destination and storage	06.13 Proteolysis	5e-25	76	evm_27.model.AmTr_v1.0_scaffold00029.5_0	-12,48149	20	20,3	3	-	3	0,3	AADGVVIATEK IGVVYSGMGP DSR
182	7	O81148	Proteasome subunit similaire 20S	<i>Arabidopsis thaliana</i>	AT3G22110	06 Protein destination and storage	06.13 Proteolysis	e-111	80	evm_27.model.AmTr_v1.0_scaffold00010.4_31	-24,79183	27	27,5	7	-	4	0,72727	TMDSTSLTSE K AAAIGANNOA DQVFIATK
182	7	O65390	Aspartic proteinase	<i>Arabidopsis thaliana</i>	AT1G11910	06 Protein destination and storage	06.13 Proteolysis	0	68,00	evm_27.model.AmTr_v1.0_scaffold00106.4_8	-57,54134	30	55	10	-	10	0,58824	LSQDHVQVGD LVYK
182	7	F4HWR0	Dessication-related protein	<i>Arabidopsis thaliana</i>	AT1G47980	11 Disease/defence	11.05 Stress responses	e-106	70	evm_27.model.AmTr_v1.0_scaffold00016.3_15	-16,33649	11	33,4	6	-	3	0,46154	TILYEQANK ANLDP LTR ISGNLLASDQF
182	7	Q42539	Protein-L-isoaspartate O-methyltransferase	<i>Arabidopsis thaliana</i>	AT3G48330	11 Disease/defence	11.06 Detoxification	7e-92	68	evm_27.model.AmTr_v1.0_scaffold00166.1_4	-11,17809	11	29	3	-	2	0,3	VAEVMETIDR VAEVMETIDR SPAAPLLOEG
183	3	Q1WIQ6	Glyceraldehyde-3-phosphate dehydrogenase	<i>Arabidopsis thaliana</i>	AT2G24270	02 Energy	02.01 Glycolysis	0	87	evm_27.model.AmTr_v1.0_scaffold00065.1_46	-34,89249	18	54,2	7	-	7	0,36364	GGFSYSGQR GATFCQEQYK FIEGLVMDAK
183	3	P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	5e-72	32	evm_27.model.AmTr_v1.0_scaffold00067.1_2	-10,96337	8	53	3	-	3	0,17647	RGQEEGGQEQ QEQEQEQR VGGEGQQQQ
183	3	F4HWR0	Dessication-related protein	<i>Arabidopsis thaliana</i>	AT1G47980	11 Disease/defence	11.05 Stress responses	e-106	70	evm_27.model.AmTr_v1.0_scaffold00016.3_15	-19,73898	11	33,4	4	-	2	0,30769	LVAGLLGVES GQDAIIR ISGNLLASDQF
184	2	Q1WIQ6	Glyceraldehyde-3-phosphate dehydrogenase	<i>Arabidopsis thaliana</i>	AT2G24270	02 Energy	02.01 Glycolysis	0	87	evm_27.model.AmTr_v1.0_scaffold00065.1_46	-10,05869	10	54,2	3	-	3	0,18182	TGGDTGAIASK GGFSYSGQR GATFCQEQYK
184	2	Q84WW2	6-Phosphogluconolactonase	<i>Arabidopsis thaliana</i>	AT5G24400	02 Energy	02.07 Pentose phosphate	4,00E-89	62	evm_27.model.AmTr_v1.0_scaffold00027.2_7	-53,44355	30	29,6	11	-	8	1,44444	QAAMGEATSV K MNQAAMGEAT
185	2	Q84WW2	6-Phosphogluconolactonase	<i>Arabidopsis thaliana</i>	AT5G24400	02 Energy	02.07 Pentose phosphate	4,00E-89	62	evm_27.model.AmTr_v1.0_scaffold00027.2_7	-34,37076	23	29,6	7	-	7	0,88889	PKPPPER AAMGEATSVK QAAMGEATSV
186	1	Q9SK09	Cupin family protein (Vicilin)	<i>Arabidopsis thaliana</i>	AT2G28490	06 Protein destination and storage	06.20 Storage proteins	e-115	50	evm_27.model.AmTr_v1.0_scaffold00080.8_2	-77,90117	22	43,1	28	-	16	1,875	TGAHEPPK MTGAHEPPK LVNIGEGOR
187	2	Q9SK09	Cupin family protein (Vicilin)	<i>Arabidopsis thaliana</i>	AT2G28490	06 Protein destination and storage	06.20 Storage proteins	e-115	50	evm_27.model.AmTr_v1.0_scaffold00080.8_2	-66,56586	22	43,1	29	-	14	1,875	TGAHEPPK INRDDLVEK LVNIGEGOR
187	2	O48646	Glutathione peroxidase	<i>Arabidopsis thaliana</i>	AT4G11600	11 Disease/defence	11.06 Detoxification	4e-78	67	evm_27.model.AmTr_v1.0_scaffold00009.2_77	-24,5495	40	18,9	6	-	6	0,88889	VEVNGDNATP VYK DOTSVHDFTV QEQYGEEEQ
188	2	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr_v1.0_scaffold00067.7	-16,11422	9	54,5	5	-	5	0,2381	RGEQGG ISNQQAQDIK DDLVEKELR
188	2	Q9SK09	Cupin family protein (Vicilin)	<i>Arabidopsis thaliana</i>	AT2G28490	06 Protein destination and storage	06.20 Storage proteins	e-115	50	evm_27.model.AmTr_v1.0_scaffold00080.8_2	-54,17469	19	43,1	13	-	10	0,9375	YLVNIGEGQR IGWINRDDLVE HTGVMMVGMG
189	2	P53492	Actin 7	<i>Arabidopsis thaliana</i>	AT5G09810	09 Cell structure	09.04 Cytoskeleton	0	97	evm_27.model.AmTr_v1.0_scaffold00018.1_04	-7,735872	8	41,6	3	2	3	0,2	QKDAY AVFPSIVGR HTGVMMVGMG
189	2	P53496	Actin 11	<i>Arabidopsis thaliana</i>	AT3G12110	09 Cell structure	09.04 Cytoskeleton	0	96	evm_27.model.AmTr_v1.0_scaffold00044.6_1	-7,735872	8	43,9	3	2	3	0,1875	QKDAY AVFPSIVGR PSAGPIIYMTG
190	2	Q9SK09	Cupin family protein (Vicilin)	<i>Arabidopsis thaliana</i>	AT2G28490	06 Protein destination and storage	06.20 Storage proteins	e-115	50	evm_27.model.AmTr_v1.0_scaffold00080.8_2	-32,29284	20	43,1	7	-	7	0,4375	AHEPPK IGWINRDDLVE CGLTNSNYK
190	2	O48646	Glutathione peroxidase	<i>Arabidopsis thaliana</i>	AT4G11600	11 Disease/defence	11.06 Detoxification	4,00E-78	67	evm_27.model.AmTr_v1.0_scaffold00009.2_77	-17,51021	24	18,9	4	-	4	0,44444	VEVNGDNATP VYK DDLVEKELR
191	3	Q9SK09	Cupin family protein (Vicilin)	<i>Arabidopsis thaliana</i>	AT2G28490	06 Protein destination and storage	06.20 Storage proteins	e-115	50	evm_27.model.AmTr_v1.0_scaffold00080.8_2	-14,31734	17	43,1	5	-	5	0,375	IGWINRDDLVE K GNAYAIALST
191	3	O65398	Glyoxalase I (Lactoylglutathione lyase)	<i>Arabidopsis thaliana</i>	AT1G11840	11 Disease/defence	11.06 Detoxification	e-130	78	evm_27.model.AmTr_v1.0_scaffold00037.1_06	-15,93742	11	33,2	2	-	2	0,14286	EDVYK ETTIVLELTNY AVYDSDSSDA
191	3	Q941A4	Uncharacterized protein	<i>Arabidopsis thaliana</i>	AT5G45690	13 Unclassified	13 Unclassified	5,00E-74	55	evm_27.model.AmTr_v1.0_scaffold00162.9	-5,746178	7	28,9	2	-	2	0,11765	R YGLSSEELK

192	1	Q9SK09	Cupin family protein (Vicilin)	<i>Arabidopsis thaliana</i>	AT2G28490	06 Protein destination and storage	06.20 Storage proteins	e-115	50	evm_27.model.AmTr_v1.0_scaffold00080.82	-28,79982	16	43,1	8	-	6	0,5	PSAGPIIYMTG AHEPPK PSAGPIIYMTG YLVNIGEGQR PSAGPIIYMTG AHEPPK RPBYLK NLAPVNEGGG EPPK
193	1	Q9SK09	Cupin family protein (Vicilin)	<i>Arabidopsis thaliana</i>	AT2G28490	06 Protein destination and storage	06.20 Storage proteins	e-115	50	evm_27.model.AmTr_v1.0_scaffold00080.82	-25,33827	19	43,1	8	-	6	0,5	NCFAIASDR DDKPFICTMD SIGAK
194	1	P49206	40S ribosomal protein S26	<i>Arabidopsis thaliana</i>	AT2G40590	05 Protein synthesis	05.01 Ribosomal proteins	2e-31	75	evm_27.model.AmTr_v1.0_scaffold00077.25	-43,92062	24	42,6	9	-	8	0,69231	YTVIEGER FNSLVYEVK
195	1	Q9XI05	20S proteasome beta subunit C1	<i>Arabidopsis thaliana</i>	AT1G21720	06 Protein destination and storage	06.13 Proteolysis	e-103	89	evm_27.model.AmTr_v1.0_scaffold00002.142	-20,20884	25	22,7	4	-	4	0,44444	ALGSHPLK LGSHPK VLVIDGGGSM
196	1	F4K5S5	SRPBCC ligand-binding domain-containing protein	<i>Arabidopsis thaliana</i>	AT5G28010	12 Unclear classification	12 Unclear classification	2,00E-72	88	evm_27.model.AmTr_v1.0_scaffold00003.118	-6,343327	15	12,3	2	-	2	0,25	AWAESYPENK HVPGFIAQAE ELK
197	1	Q9FH13	Ribonuclease E inhibitor RraV/Dimethylmenaqui	<i>Arabidopsis thaliana</i>	AT5G56260	04 Transcription	04.19 mRNA synthesis	7,00E-73	79	evm_27.model.AmTr_v1.0_scaffold00061.25	-32,44259	41	17,7	9	-	7	1	VKAAVLGSK AVVHADPDD LGKGGHELK
198	2	F4ID64	Peroxioredoxin	<i>Arabidopsis thaliana</i>	AT1G65980	11 Disease/defence	11.06 Detoxification	0	60	evm_27.model.AmTr_v1.0_scaffold00109.90	-36,47116	43	17,4	5	-	5	0,55556	FRLPENGKVD EVK ADLPLGLTK
198	2	P24704	Superoxide dismutase (Cu/Zn)	<i>Arabidopsis thaliana</i>	AT1G08830	11 Disease/defence	11.06 Detoxification	0	84	evm_27.model.AmTr_v1.0_scaffold00057.130	-26,74357	33	19,9	7	-	6	1,16667	ADLPGLKKEE VK
199	1	P19036	HSP17.4 (class I small heat shock protein family)	<i>Arabidopsis thaliana</i>	AT3G46230	06 Protein destination and storage	06.01 Folding and stability	0	60	evm_27.model.AmTr_v1.0_scaffold00165.36	-12,10128	21	18,1	3	-	3	0,75	LPENGVKDE VK LPENGVKDE K LPENGVKDE K KEVEYCDK KEVEYCDK EEFDDPVER
200	2	P19037	HSP18.1 (small heat shock protein family)	<i>Arabidopsis thaliana</i>	AT5G59720	06 Protein destination and storage	06.01 Folding and stability	2,00E-43	56	evm_27.model.AmTr_v1.0_scaffold00009.199	-5,815309	12	18,6	2	1	2	0,75	FLIDOGYLSK YGQAQPLSQ ALDKLEK
200	2	P19036	HSP17.4 (class I small heat shock protein)	<i>Arabidopsis thaliana</i>	AT3G46230	06 Protein destination and storage	06.01 Folding and stability	1,00E-52	60	evm_27.model.AmTr_v1.0_scaffold00165.36	-43,83231	55	18,1	20	19	11	6,5	PSAGPIIYMTG AHEPPK YLVNIGEGQR
201	1	Q9SF20	MD-2-related lipid recognition domain-containing protein	<i>Arabidopsis thaliana</i>	AT3G11780	11 Disease/defence	11.02 Defence-regulated	0	59	evm_27.model.AmTr_v1.0_scaffold00004.191	-50,40495	38	16,4	16	-	10	2,83333	RKEVEEKGD TWH ETDDAHMFK EIVKVELVDG R ATMENGVLTV
202	2	Q9S9P4	S-adenosyl-L-methionine-dependent methyltransferase (7-	<i>Arabidopsis thaliana</i>	AT1G30550	04 Transcription	04.22 mRNA processing	2e-79	68	evm_27.model.AmTr_v1.0_scaffold00019.57	-6,119758	2	122	2	-	2	0,04348	QKIEEHSTS QKIEEHSTS SA EEFDQQLQK VDVDELK
202	2	Q9SK09	Cupin family protein (Vicilin)	<i>Arabidopsis thaliana</i>	AT2G28490	06 Protein destination and storage	06.20 Storage proteins	e-115	50	evm_27.model.AmTr_v1.0_scaffold00080.82	-34,91154	23	43,1	12	-	7	0,875	LLGISCDVVNS HK PGLTIGDTIPNI LQEQPPFDK LDTEQQEIFKK LQEQPPFDK
204	1	P19037	HSP18.1 (small heat shock protein family)	<i>Arabidopsis thaliana</i>	AT5G59720	06 Protein destination and storage	06.01 Folding and stability	0	62	evm_27.model.AmTr_v1.0_scaffold00136.4	-53,03052	59	17,8	18	-	11	6	VTEDKTQEEI K NDFTPEEEEE LVEYDGR LYMDGSVKPFT K
205	2	P19036	HSP17.4 (class I small heat shock protein family)	<i>Arabidopsis thaliana</i>	AT3G46230	06 Protein destination and storage	06.01 Folding and stability	1E-52	60	evm_27.model.AmTr_v1.0_scaffold00165.36	-11,88606	15	18,1	2	-	2	0,5	LDTEQQEIFK K
205	2	Q8GWR2	Uncharacterized protein	<i>Arabidopsis thaliana</i>	AT2G31985	13 Unclassified	13 Unclassified	5,00E-50	68	evm_27.model.AmTr_v1.0_scaffold00071.199	-23,66397	25	28,7	6	-	4	0,63636	
206	1	P29448	Thioredoxin	<i>Arabidopsis thaliana</i>	AT3G51030	06 Protein destination and storage	06.01 Folding and stability	0	60	evm_27.model.AmTr_v1.0_scaffold00002.333	-31,90572	62	13,4	10	-	7	1,375	
207	2	P29448	Thioredoxin	<i>Arabidopsis thaliana</i>	AT3G51030	06 Protein destination and storage	06.01 Folding and stability	0	60	evm_27.model.AmTr_v1.0_scaffold00002.333	-22,13214	49	13,4	8	-	6	1	
207	2	O04005	1-Cys peroxiredoxin	<i>Arabidopsis thaliana</i>	AT1G48130	11 Disease/defence	11.05 Stress responses	0	69	evm_27.model.AmTr_v1.0_scaffold00045.37	-36,07572	24	24,2	4	-	3	0,36364	
208	2	P31265	Translationally-controlled tumor protein homolog	<i>Arabidopsis thaliana</i>	AT3G16640	03 Cell growth/division	03.26 Growth regulators	0	79	evm_27.model.AmTr_v1.0_scaffold00045.319	-23,38824	29	16,2	6	-	6	0,75	
208	2	Q9FHW7	S-phase kinase-associated protein	<i>Arabidopsis thaliana</i>	AT5G42190	06 Protein destination and storage	06.13 Proteolysis	0	62	evm_27.model.AmTr_v1.0_scaffold00029.181	-9,440453	15	17,9	2	-	2	0,22222	
209	1	Q9XI01	Protein disulfide isomerase	<i>Arabidopsis thaliana</i>	AT1G21750	06 Protein destination and storage	06.01 Folding and stability	e-178	60	evm_27.model.AmTr_v1.0_scaffold00186.14	-48,17175	21	57,4	9	-	8	0,34483	
210	1	P31265	Translationally-controlled tumor protein homolog	<i>Arabidopsis thaliana</i>	AT3G16640	03 Cell growth/division	03.26 Growth regulators	2,00E-75	79,00	evm_27.model.AmTr_v1.0_scaffold00045.319	-8,335359	13	16,2	2	-	2	0,25	

112b	3	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	4e-53	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-100,0012	48	43,5	23	-	18	1,08696	KGDTATIPAGK IEMACPHVSG GR
112b	3	F4HWR0	Dessication-related protein	<i>Arabidopsis thaliana</i>	AT1G47980	11 Disease/defence	11.05 Stress responses	e-106	70	evm_27.model.AmTr_v1.0_scaffold00016.315	-20,19536	26	33,4	7	-	7	0,61538	KVDPYPH GGPPPIGATK TILYEQANK
112b	3	Q941A4	Uncharacterized protein	<i>Arabidopsis thaliana</i>	AT5G45690	13 Unclassified	13 Unclassified	5,00E-74	55	evm_27.model.AmTr_v1.0_scaffold00162.9	-82,03373	63	28,9	23	-	16	1,41176	CAVYDSDSSD AR LYSHDI TR
113b	5	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5e-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-31,41357	27	43,5	8	-	7	0,3913	EVSFNVP SR PSSEQLQLI H GCSGGGK
113b	5	Q9SF20	MD-2-related lipid recognition domain-containing protein	<i>Arabidopsis thaliana</i>	AT3G11780	11 Disease/defence	11.02 Defence-regulated	0	59	evm_27.model.AmTr_v1.0_scaffold00004.191	-13,75885	26	16,4	4	-	3	0,83333	VSGMEVDPDP VER SISASTEAP I S
113b	5	F4HWR0	Dessication-related protein	<i>Arabidopsis thaliana</i>	AT1G47980	11 Disease/defence	11.05 Stress responses	e-106	70	evm_27.model.AmTr_v1.0_scaffold00016.315	-41,07906	35	33,4	9	-	8	0,76923	TILYEQANK TPQEIL R ANLDPL TR
113b	5	O65398	Glyoxalase I (Lactoylglutathione lyase)	<i>Arabidopsis thaliana</i>	AT1G11840	11 Disease/defence	11.06 Detoxification	e-130	78	evm_27.model.AmTr_v1.0_scaffold00037.106	-39,55994	23	33,2	8	-	7	0,64286	LVTQELGGK AIATEDVYK YTLAMMGYAE
113b	5	Q941A4	Uncharacterized protein	<i>Arabidopsis thaliana</i>	AT5G45690	13 Unclassified	13 Unclassified	5,00E-74	55	evm_27.model.AmTr_v1.0_scaffold00162.9	-129,5669	75	28,9	38	-	25	2,41176	VYDSDSSDAR AVYDSDSSDAR
123b	5	Q9S9P4	S-adenosyl-L-methionine-dependent methyltransferase (7-	<i>Arabidopsis thaliana</i>	AT1G30550	04 Transcription	04.22 mRNA processing	2e-79	68	evm_27.model.AmTr_v1.0_scaffold00019.57	-67,87152	15	122	16	-	13	0,3913	FGLDEAHGK GTSVMLK VEGAVESL SR
123b	5	Q9LUM3	Subtilase family protein	<i>Arabidopsis thaliana</i>	AT3G14240	06 Protein destination and storage	06.13 Proteolysis	0	55	evm_27.model.AmTr_v1.0_scaffold00003.107	-23,87339	11	61	6	-	4	0,38889	DTDGHGHTHTA STAAGNMVPR DTDGHGHTHTA
123b	5	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-62,28012	36	43,5	15	-	12	0,73913	ARIEMACPHV SGG R MACPHVSGG
123b	5	F4HWR0	Dessication-related protein	<i>Arabidopsis thaliana</i>	AT1G47980	11 Disease/defence	11.05 Stress responses	e-106	70	evm_27.model.AmTr_v1.0_scaffold00016.315	-11,48082	16	33,4	5	-	5	0,38462	TILYEQANK TPQEIL R ANLDPL TR
123b	5	O65398	Glyoxalase I (Lactoylglutathione lyase)	<i>Arabidopsis thaliana</i>	AT1G11840	11 Disease/defence	11.06 Detoxification	e-130	78	evm_27.model.AmTr_v1.0_scaffold00037.106	-41,93043	29	33,2	6	-	6	0,5	LVTQELGGK GP TPEPLCHV MLR
155b	3	Q9XF7	protein MOTHER of FT and TF 1	<i>Arabidopsis thaliana</i>	AT1G18100	03 Cell growth/division	03.26 Growth regulators	1e-62	62	evm_27.model.AmTr_v1.0_scaffold00003.462	-23,34102	34	24,5	6	-	5	0,6	QVANGCELKP SGTAEPR QOQPLGSVAR RLSDAQQR
155b	3	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr_v1.0_scaffold00067.7	-25,25354	11	54,5	6	5	6	0,33333	ISGIRPTR ISNQQAQDIK GYEEECNAR
155b	3	P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	5e-72	32	evm_27.model.AmTr_v1.0_scaffold00067.12	-104,2566	29	53	51	50	28	3,47059	IRQNIDNPR IRQNIDNPR
16b	3	Q9S9P4	S-adenosyl-L-methionine-dependent methyltransferase (7-	<i>Arabidopsis thaliana</i>	AT1G30550	04 Transcription	04.22 mRNA processing	2e-79	68	evm_27.model.AmTr_v1.0_scaffold00019.57	-172,2234	27	122	41	-	29	0,93478	KASDLLQK FGLDEAHGK AYEVA NTPSLK
16b	3	Q9S9N1	HSP70 (heat shock protein)	<i>Arabidopsis thaliana</i>	AT1G16030	06 Protein destination and storage	06.01 Folding and stability	0	80	evm_27.model.AmTr_v1.0_scaffold00137.8	-45,67055	18	71,6	12	-	10	0,57143	LSKEIEK FSDPSVQADM K
16b	3	Q9SX53	Oligopeptidase B	<i>Arabidopsis thaliana</i>	AT1G50380	06 Protein destination and storage	06.13 Proteolysis	0	70	evm_27.model.AmTr_v1.0_scaffold00171.48	-19,08181	9	80,9	6	-	6	0,16667	VEGVDITDVSH R TPNSVYDHDM
184b	1	P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	5e-72	32	evm_27.model.AmTr_v1.0_scaffold00067.12	-12,47952	8	53	3	-	3	0,17647	VGGEGQQQ GIK ESLGVIRPDEE
184b	2	Q96262	plasma-membrane associated cation-binding protein	<i>Arabidopsis thaliana</i>	AT4G20260	10 Signal transduction	10.99 Others	5e-38	55	evm_27.model.AmTr_v1.0_scaffold00068.158	-33,49754	34	23,4	7	-	6	0,9	PVAETSEEP K EQSEAMQAVV K
26b	1	P94078	Alpha-mannosidase	<i>Arabidopsis thaliana</i>	AT3G26720	01 Metabolism	01.05 Sugars and polysaccharides	0	67	evm_27.model.AmTr_v1.0_scaffold00016.68	-77,52573	14	114,9	14	-	12	0,34884	QHVANDYAK IFHEASQSDK
30b	1	Q9SPK5	Formate-tetrahydrofolate ligase	<i>Arabidopsis thaliana</i>	AT1G50480	01 Metabolism	01.01 Amino Acid	0	80	evm_27.model.AmTr_v1.0_scaffold00024.123	-70,87616	23	67,3	19	-	15	0,73077	IFHEASQSDK MHGGGPEVVA
33b	5	Q9LIR4	Dihydroxy-acid dehydratase	<i>Arabidopsis thaliana</i>	AT3G23940	01 Metabolism	01.01 Amino Acid	0	82	evm_27.model.AmTr_v1.0_scaffold00039.45	-87,28139	37	65,6	20	-	18	0,875	YVMEDVHK NMPGTIMAMG R

33b	5	Q9FMP3	Pyrimidine 2 (dihydropyrimidinase)	<i>Arabidopsis thaliana</i>	AT5G12200	01 Metabolism	01.03 Nucleotides	0	78	evm_27.model.AmTr_v1.0_scaffold00095.33	-21,26876	11	55	4	-	4	0,21053	TDTNVYEGK IPNGVNGIEER SLGALAQVHA
33b	5	Q9M9K1	Phosphoglycerate mutase	<i>Arabidopsis thaliana</i>	AT3G08590	02 Energy	02.01 Glycolysis	0	82	evm_27.model.AmTr_v1.0_scaffold00077.211	-12,96646	11	61,3	4	-	4	0,16667	GVDAQIASGG GR VHILTDGR
33b	5	P29197	Chaperonin (Chaperonin-60kD, ch60_CPN60)	<i>Arabidopsis thaliana</i>	AT3G23990	06 Protein destination and storage	06.01 Folding and stability	0	86	evm_27.model.AmTr_v1.0_scaffold00147.48	-88,89916	35	61,1	20	9	15	0,7931	LQTANFDQK AIFSEGCK DDTVVLGDGAG
33b	5	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-49,70048	36	43,5	12	-	10	0,65217	IEMACPH KGD TATIPAGK EVSFINVPSR
46b	3	Q9S9P4	S-adenosyl-L-methionine-dependent methyltransferase (7-	<i>Arabidopsis thaliana</i>	AT1G30550	04 Transcription	04.22 mRNA processing	2e-79	68	evm_27.model.AmTr_v1.0_scaffold00019.57	-138,4913	31	122	31	-	26	0,69565	KASDLLQK FGLDEAHGK DDLATSELK
46b	3	P30184	Leucine aminopeptidase	<i>Arabidopsis thaliana</i>	AT2G24200	06 Protein destination and storage	06.13 Proteolysis	0	68	evm_27.model.AmTr_v1.0_scaffold00065.204	-142,6529	51	54,5	27	-	22	0,96552	ILNEDQCR PGDIVTASNGK LASEISGEK
46b	3	Q9SG80	Alpha-L-arabinofuranosidase	<i>Arabidopsis thaliana</i>	AT3G10740	09 Cell structure	09.01 Cell wall	0	68	evm_27.model.AmTr_v1.0_scaffold00095.148	-26,26068	6	76,5	6	-	5	0,3	VIADSSDVQK YVAIGNEDCG K
47b	2	P94078	Alpha-mannosidase	<i>Arabidopsis thaliana</i>	AT3G26720	01 Metabolism	01.05 Sugars and polysaccharides	0	67	evm_27.model.AmTr_v1.0_scaffold00016.68	-64,52913	10	114,9	20	-	11	0,46512	ITEMSLSANQER R
47b	2	Q9S9P4	S-adenosyl-L-methionine-dependent methyltransferase (7-	<i>Arabidopsis thaliana</i>	AT1G30550	04 Transcription	04.22 mRNA processing	2e-79	68	evm_27.model.AmTr_v1.0_scaffold00019.57	-85,59405	17	122	15	-	14	0,32609	FGLDEAHGK DDLATSELK LFSEHQEME
68b	2	Q1WIQ6	Glyceraldehyde-3-phosphate dehydrogenase	<i>Arabidopsis thaliana</i>	AT2G24270	02 Energy	02.01 Glycolysis	0	87	evm_27.model.AmTr_v1.0_scaffold00065.146	-15,5284	9	54,2	5	-	5	0,22727	VQACTQEEVKN K DSVTEVVR
68b	2	Q9FWA3	6-Phosphogluconate dehydrogenase	<i>Arabidopsis thaliana</i>	AT3G02360	02 Energy	02.07 Pentose phosphate	0	87	evm_27.model.AmTr_v1.0_scaffold00061.203	-160,1375	60	53,8	42	-	25	2,09524	VDETVER VDETVER IASLDSR
72b	3	Q9SJK9	Fructose-bisphosphate aldolase	<i>Arabidopsis thaliana</i>	AT2G36460	02 Energy	02.01 Glycolysis	e-172	86	evm_27.model.AmTr_v1.0_scaffold00040.204	-42,18536	29	37,7	9	-	8	0,58824	MVTPGSDAPK NAAYIGTPGR VLAAYYK
72b	3	Q9SAJ6	Glyceraldehyde-3-phosphate dehydrogenase	<i>Arabidopsis thaliana</i>	AT1G79530	02 Energy	02.01 Glycolysis	e-165	70	evm_27.model.AmTr_v1.0_scaffold00039.188	-8,386792	7	45,2	5	4	4	0,3	TVDGPSMKD WR LTGMAFR
72b	3	Q9FX54	Glyceraldehyde-3-phosphate dehydrogenase	<i>Arabidopsis thaliana</i>	AT1G13440	02 Energy	02.01 Glycolysis	6,00E-94	74	evm_27.model.AmTr_v1.0_scaffold00177.24	-74,28809	56	24,7	16	13	14	2,57143	DAPMFVVGVN EHEYKPDVH DAPMFVVGVN
89b	4	Q9SAJ4	Phosphoglycerate kinase	<i>Arabidopsis thaliana</i>	AT1G79550	02 Energy	02.01 Glycolysis	0	85	evm_27.model.AmTr_v1.0_scaffold00062.199	-48,85005	36	42,4	11	-	10	0,54545	AHASTEGLAK FYKEEKNDP EFSK
89b	4	Q9SJK9	Fructose-bisphosphate aldolase	<i>Arabidopsis thaliana</i>	AT2G36460	02 Energy	02.01 Glycolysis	e-172	86	evm_27.model.AmTr_v1.0_scaffold00040.204	-17,99463	13	37,7	4	-	4	0,29412	PEVIAEHTIR VAPEVIAEHTIR
89b	4	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5e-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-121,4036	44	43,5	36	-	23	1,82609	IEMACPH ARIEMACPH KGD TATIPAGK
89b	4	B9DGL8	Alpha-galactosidase	<i>Arabidopsis thaliana</i>	AT5G08370	09 Cell structure	09.01 Cell wall	e-171	75	evm_27.model.AmTr_v1.0_scaffold00171.32	-49,12088	37	45,1	14	-	12	0,66667	YDNCNNDGV DPR GQLTATVDSH

Supplemental table 4: list of the proteins identified from the globulin fraction of *Amborella trichopoda* whole mature seed by 2-DE

Proteins have been analyzed by two-dimensional electrophoresis and identified by mass spectrometry LC/MS-MS. The protein spots were analysed by LC-MS/MS on the PAPPISO platform (Benoit Valot, Thierry Balliau, Michel Zivy, INRA Moulon, France; <http://pappiso.inra.fr>). Based on the spectrum generated, proteins were identified using the X-Tandem software. "Spot ID" relates to the protein position on the 2DE reference map. "Number of id per spot" reflect the number of single identifications in the same spot. "NCBI accession number" is the accession number in NCBI database. "Protein name", "Organism" relates to the organism from which the identified protein comes from for functional analysis - efforts were focus on *Arabidopsis thaliana* as a plant model. "AGI", "Function category" and "Function description" relate to the functional categories defined according to the ontological classification of Bevan *et al.* (1998) Nature 391:485-488. "log(Evalue) identification" reflects the statistical power of the identification by BLAST (performed on TAIR or BLAST). "Identity" indicates in % the recovery of the *Amborella* protein sequence against the identified protein. "Description" was taken from the Amborella EVM 27 Predicted Proteins (<http://www.amborella.org>). The "log (E value)" is a statistical parameter that represents the number of peptides present at random in the database. It was calculated by the product of the Evalue of unique peptides identified in the protein spot (Valot *et al.*, 2011). "Coverage" refers to the recovery rate of the protein by the identified peptides, expressed in %. "MW" relates to the molecular weight expressed in kDa. "Spectra" corresponds to the number of spectra which allowed the protein identification from 2DE protein single spot. "Specifics" corresponds to the number of specific spectrum corresponding to the identification among the other identifications of the group. "Uniques" refers to the number of unique peptides (different sequences) that led to the protein identification. "PAI" is the protein abundance index in the spot. "Peptide sequences" displays identified peptides for each protein spot.

Functional identification									Mass spec data									
Spot ID	Number of id per spot	NCBI accession number	Protein name	Organism	AGI	Function category	Function description	log (Evalue) identificati	Identity	Description	log(E value)	Coverage	MW	Spectra	Specifics	Uniques	PAI	Peptide sequence
211	2	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-109,1154	55	43,5	30	-	21	1,3913	IEMACPHVSG GR KGDATIPAGK
211	2	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr_v1.0_scaffold00067.7	-12,90149	11	54,5	4	-	4	0,19048	GRQEGEYGE E EQRGEQ GK ILSPFG EERE
212	1	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-135,4795	65	43,5	47	-	30	2,3913	IEMACPHVSG GR MACPHVSGG
213	1	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-171,7717	73	43,5	65	-	38	3,30435	REQEGERGK GQGGEIK GLIHGSGGG
214	1	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-141,554	67	43,5	53	-	27	2,73913	KGDATIPAGK IEMACPHVSG GR
215	1	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-115,5609	60	43,5	41	-	24	2,04348	ARIEMACPHV SGGR IEMACPHVSG
216	2	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-105,1129	60	43,5	29	-	20	1,34783	GR KGDATIPAGK
216	2	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr_v1.0_scaffold00067.7	-8,628563	8	54,5	3	-	3	0,14286	GRQEGEYGE E EQRGEQ GK QFFIAGGQPR
217	2	Q9S9P4	S-adenosyl-L-methionine-dependent methyltransferase (7-	<i>Arabidopsis thaliana</i>	AT1G30550	04 Transcription	04.22 mRNA processing	2e-79	68	evm_27.model.AmTr_v1.0_scaffold00019.57	-102,0282	22	122	22	-	17	0,47826	SSLSDDQK FGLDEAHGK AYEVANTPSLK
217	2	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-16,26321	13	43,5	4	-	4	0,17391	KGDATIPAGK ATEIYVILEGR ASQEENLQIIC
218	3	Q9S9N1	HSC70 (Heat shock cognate 70 kDa protein)	<i>Arabidopsis thaliana</i>	AT1G16030	06 Protein destination and storage	06.01 Folding and stability	0	80	evm_27.model.AmTr_v1.0_scaffold00137.8	-99,36326	39	71,6	23	-	19	1,09524	TKDNNLLGK MYQGGDAGG MPGAGGMPS
218	3	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-30,37082	35	43,5	8	-	7	0,47826	KGDATIPAGK LVTIGEER PSSEQLQLIH QEGEYGE EEO
218	3	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr_v1.0_scaffold00067.7	-12,02457	10	54,5	3	-	3	0,14286	R TVTVDVTS DYN SVAAGMNA MD LR
219	4	P29197	Chaperonin (Chaperonin-60kD, ch60, CPN60)	<i>Arabidopsis thaliana</i>	AT3G23990	06 Protein destination and storage	06.01 Folding and stability	0	86	evm_27.model.AmTr_v1.0_scaffold00003.261	-138,6117	47	61,2	36	-	25	1,26667	SAIEASTSDYD IEMACPHVSG GR
219	4	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-42,28413	29	43,5	10	-	8	0,43478	IEMACPHVSG GR PSSEQLQLIH

219	4	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr_v1.0_scaffold00067.7	-11,75103	9	54,5	4	-	4	0,19048	QEGEYEEEE R ISNQAQDIK RGQEEGQQE QEQEQEER ESLGVIRPDEE
219	4	P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	5e-72	32	evm_27.model.AmTr_v1.0_scaffold00067.12	-16,10779	13	53	4	-	4	0,23529	KGDTATIPAGK MACPHVSGG R
220	2	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-102,907	53	43,5	35	-	20	1,86957	GEGQIIQITN GQK TVTDVTSQYN KKGDTATIPAG K GKGQQGQEK
220	2	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr_v1.0_scaffold00067.7	-12,67668	8	54,5	3	-	3	0,14286	RGQEEGQQE QEQEQEER VGGEGQQQQ
221	2	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-173,5958	70	43,5	67	-	38	3,30435	YVANGDAR ARIEMACPH GLIHGGSGGG QEGEYEEEE R ISNQAQDIK RGQEEGQQE QEQEQEER VGGEGQQQQ
221	2	P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	5e-72	32	evm_27.model.AmTr_v1.0_scaffold00067.12	-20,9289	20	53	6	-	6	0,35294	YVANGDAR ARIEMACPH GLIHGGSGGG QEGEYEEEE R ISNQAQDIK RGQEEGQQE QEQEQEER VGGEGQQQQ
222	3	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-196,2082	65	43,5	66	-	39	3,56522	YVANGDAR ARIEMACPH GLIHGGSGGG QEGEYEEEE R ISNQAQDIK RGQEEGQQE QEQEQEER VGGEGQQQQ
222	3	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr_v1.0_scaffold00067.7	-24,73812	17	54,5	5	-	5	0,2381	YVANGDAR ARIEMACPH GLIHGGSGGG QEGEYEEEE R ISNQAQDIK RGQEEGQQE QEQEQEER VGGEGQQQQ
222	3	P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	5e-72	32	evm_27.model.AmTr_v1.0_scaffold00067.12	-15,38863	13	53	4	-	4	0,23529	YVANGDAR ARIEMACPH GLIHGGSGGG QEGEYEEEE R ISNQAQDIK RGQEEGQQE QEQEQEER VGGEGQQQQ
223	1	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-215,282	74	43,5	72	-	45	3,6087	YVANGDAR ARIEMACPH GLIHGGSGGG QEGEYEEEE R ISNQAQDIK RGQEEGQQE QEQEQEER VGGEGQQQQ
224	1	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-243,5827	68	43,5	95	-	48	4,6087	YVANGDAR ARIEMACPH GLIHGGSGGG QEGEYEEEE R ISNQAQDIK RGQEEGQQE QEQEQEER VGGEGQQQQ
225	1	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-209,3419	68	43,5	79	-	38	3,91304	YVANGDAR ARIEMACPH GLIHGGSGGG QEGEYEEEE R ISNQAQDIK RGQEEGQQE QEQEQEER VGGEGQQQQ
226	3	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-209,5653	76	43,5	90	-	41	4,69565	YVANGDAR ARIEMACPH GLIHGGSGGG QEGEYEEEE R ISNQAQDIK RGQEEGQQE QEQEQEER VGGEGQQQQ
226	3	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr_v1.0_scaffold00067.7	-45,05528	33	54,5	10	-	10	0,52381	YVANGDAR ARIEMACPH GLIHGGSGGG QEGEYEEEE R ISNQAQDIK RGQEEGQQE QEQEQEER VGGEGQQQQ
226	3	P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	5e-72	32	evm_27.model.AmTr_v1.0_scaffold00067.12	-20,28565	14	53	5	-	5	0,35294	YVANGDAR ARIEMACPH GLIHGGSGGG QEGEYEEEE R ISNQAQDIK RGQEEGQQE QEQEQEER VGGEGQQQQ
227	2	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr_v1.0_scaffold00067.7	-151,0261	59	54,5	49	-	35	2,66667	YVANGDAR ARIEMACPH GLIHGGSGGG QEGEYEEEE R ISNQAQDIK RGQEEGQQE QEQEQEER VGGEGQQQQ
227	2	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-131,8473	68	43,5	41	-	26	2,17391	YVANGDAR ARIEMACPH GLIHGGSGGG QEGEYEEEE R ISNQAQDIK RGQEEGQQE QEQEQEER VGGEGQQQQ
228	2	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-170,8281	65	43,5	69	-	34	3,21739	YVANGDAR ARIEMACPH GLIHGGSGGG QEGEYEEEE R ISNQAQDIK RGQEEGQQE QEQEQEER VGGEGQQQQ
228	2	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr_v1.0_scaffold00067.7	-83,28143	44	54,5	17	-	16	0,80952	YVANGDAR ARIEMACPH GLIHGGSGGG QEGEYEEEE R ISNQAQDIK RGQEEGQQE QEQEQEER VGGEGQQQQ
229	3	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-150,6976	60	43,5	50	-	29	2,69565	YVANGDAR ARIEMACPH GLIHGGSGGG QEGEYEEEE R ISNQAQDIK RGQEEGQQE QEQEQEER VGGEGQQQQ
229	3	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr_v1.0_scaffold00067.7	-53,76226	36	54,5	13	-	13	0,66667	YVANGDAR ARIEMACPH GLIHGGSGGG QEGEYEEEE R ISNQAQDIK RGQEEGQQE QEQEQEER VGGEGQQQQ
229	3	P48641	Glutathione reductase	<i>Arabidopsis thaliana</i>	AT3G24170	11 Disease/defence	11.06 Detoxification	0	69	evm_27.model.AmTr_v1.0_scaffold00067.136	-14,23599	14	57,5	5	-	5	0,20833	YVANGDAR ARIEMACPH GLIHGGSGGG QEGEYEEEE R ISNQAQDIK RGQEEGQQE QEQEQEER VGGEGQQQQ
230	2	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-135,7838	68	43,5	47	-	27	2,3913	YVANGDAR ARIEMACPH GLIHGGSGGG QEGEYEEEE R ISNQAQDIK RGQEEGQQE QEQEQEER VGGEGQQQQ
230	2	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr_v1.0_scaffold00067.7	-20,89239	16	54,5	5	-	5	0,28571	YVANGDAR ARIEMACPH GLIHGGSGGG QEGEYEEEE R ISNQAQDIK RGQEEGQQE QEQEQEER VGGEGQQQQ

231	3	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr.v1.0_scaffold00002.657	-116,028	49	43,5	37	-	24	1,69565	KGDTATIPAGK IEMACPHVSG GR
231	3	P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	5e-72	32	evm_27.model.AmTr.v1.0_scaffold00067.12	-18,37925	17	53	5	-	5	0,29412	RGQEEGQQE QEQQEQER VGGEGQQQQ
231	3	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr.v1.0_scaffold00067.7	-9,581566	5	54,5	3	-	3	0,14286	LSDAQQCR QGEYGEEEQR
232	3	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr.v1.0_scaffold00002.657	-102,7915	52	43,5	38	-	19	2	KGDTATIPAGK IEMACPHVSG GR
232	3	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr.v1.0_scaffold00067.7	-26,54579	19	54,5	7	-	7	0,38095	GRQEGEYEEE EQRGEQ GK QGEYGEEEQR
232	3	P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	5e-72	32	evm_27.model.AmTr.v1.0_scaffold00067.12	-13,77617	13	53	4	-	4	0,23529	RGQEEGQQE QEQQEQER VGGEGQQQQ
233	1	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr.v1.0_scaffold00002.657	-163,2949	64	43,5	57	-	34	2,73913	SDLNPEDLFVA PPSHPAIR ASQENLQIIC
234	2	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr.v1.0_scaffold00002.657	-107,5683	54	43,5	31	-	20	1,47826	IEMACPHVSG GR KGDTATIPAGK
234	2	P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	5e-72	32	evm_27.model.AmTr.v1.0_scaffold00067.12	-35,06539	26	53	9	-	9	0,52941	RGQEEGQQE QEQQEQER VGGEGQQQQ
235	2	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr.v1.0_scaffold00002.657	-170,1058	62	43,5	60	-	34	2,91304	AFSDEILEASF NVDR IEMACPH
235	2	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr.v1.0_scaffold00067.7	-18,36588	9	54,5	4	-	4	0,19048	GRQEGEYEEE EQRGEQ GK QGEYGEEEQR
236	3	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr.v1.0_scaffold00002.657	-141,8851	65	43,5	61	-	30	3,17391	NSILNQIER AQSDSVFVVG PR
236	3	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr.v1.0_scaffold00067.7	-27,10146	17	54,5	7	-	7	0,33333	GRQEGEYEEE EQRGEQ GK ISNQAQDIK
236	3	P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	5e-72	32	evm_27.model.AmTr.v1.0_scaffold00067.12	-9,631527	8	53	3	-	3	0,17647	RGQEEGQQE QEQQEQER QGDAIAPAGA
237	3	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr.v1.0_scaffold00002.657	-192,0959	65	43,5	82	-	41	3,95652	KGDTATIPAGK SDLNPEDLFVA PPSHPAIR
237	3	P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	5e-72	32	evm_27.model.AmTr.v1.0_scaffold00067.12	-16,69071	12	53	4	-	4	0,35294	RGQEEGQQE QEQQEQER VGGEGQQQQ
237	3	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr.v1.0_scaffold00067.7	-11,95798	9	54,5	4	-	4	0,19048	LSDAQQCR ISNQAQDIK ILSPEGEERE
238	2	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr.v1.0_scaffold00002.657	-187,6107	64	43,5	68	-	38	3,30435	GSLEVPFYNS R AQSDSVFVVG
238	2	P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	5e-72	32	evm_27.model.AmTr.v1.0_scaffold00067.12	-16,80107	9	53	3	-	3	0,17647	RGQEEGQQE QEQQEQER VGGEGQQQQ
239	1	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr.v1.0_scaffold00002.657	-194,9685	59	43,5	70	-	40	3,56522	IEMACPH ARIEMACPH KGDTATIPAGK
240	1	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr.v1.0_scaffold00002.657	-175,454	64	43,5	66	-	40	3,21739	ACPHVSGGR GQGEQEGSR ARIEMACPH
241	4	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr.v1.0_scaffold00002.657	-184,8978	65	43,5	70	-	38	3,17391	KGDTATIPAGK MACPHVSGG R
241	4	P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	5e-72	32	evm_27.model.AmTr.v1.0_scaffold00067.12	-14,9216	13	53	4	-	4	0,29412	RGQEEGQQE QEQQEQER SPILGHASAIK
241	4	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr.v1.0_scaffold00067.7	-7,292089	9	54,5	2	-	2	0,14286	GRQEGEYEEE EQRGEQ GK LIQTLPQIDTR

241	4	Q39649	2S albumin	<i>Cucurbita maxima</i>		06 Protein destination and storage	06.20 Storage proteins	1,00E-13	35	evm_27.model.AmTr.v1.0_scaffold00005.2	-17,59176	20	16,8	2	-	2	0,2857	SLMSEAGQGE QQQIER AEQLPQICGIS
242	1	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr.v1.0_scaffold00002.6	-185,0129	66	43,5	65	-	37	3,3043	IEMACPH KGDATIPAGK IEMACPHVSG
243	3	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr.v1.0_scaffold00002.6	-162,5721	61	43,5	49	-	32	2,6087	ARIEMACPH ARIEMACPH ACPHVSGGR
243	3	P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	5e-72	32	evm_27.model.AmTr.v1.0_scaffold00002.6	-20,60638	17	53	6	-	6	0,4118	RGQEEGQQE QEQQEQEQR QGDAIAPAGA
243	3	Q39649	2S albumin	<i>Cucurbita maxima</i>		06 Protein destination and storage	06.20 Storage proteins	1,00E-13	35	evm_27.model.AmTr.v1.0_scaffold00005.2	-13,73993	20	16,8	4	-	2	0,5714	SLMSEAGQGE QQQIER SLMSEAGQGE
244	3	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr.v1.0_scaffold00002.6	-175,7565	62	43,5	62	-	37	2,9130	ACPHVSGGR KGDATIPAGK IEMACPHVSG
244	3	Q39649	2S albumin	<i>Cucurbita maxima</i>		06 Protein destination and storage	06.20 Storage proteins	1,00E-13	35	evm_27.model.AmTr.v1.0_scaffold00005.2	-9,89279	14	16,8	2	-	2	0,2857	FIQTGRPE AEQLPQICGIS QQR
244	3	Q39649	2S albumin	<i>Cucurbita maxima</i>		06 Protein destination and storage	06.20 Storage proteins	5,00E-16	37	evm_27.model.AmTr.v1.0_scaffold00005.2	-9,89279	14	16,8	2	-	2	0,2500	FIQTGRPE AEQLPQICGIS QQR
245	4	Q9T0G0	Hydroxysteroid dehydrogenase (Steroleosin-B)	<i>Arabidopsis thaliana</i>	AT4G10020	01 Metabolism	01.06 Lipid and sterol	2,00E-86	66	evm_27.model.AmTr.v1.0_scaffold00099.1	-16,29255	19	24,8	3	-	3	0,5000	AADVKEEDCR VVIVTGASSGI
245	4	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr.v1.0_scaffold00002.6	-138,9511	57	43,5	49	-	30	2,5217	MACPHVSGR KGDATIPAGK RGQEEGQQE QEQQEQEQR SPILGHASAIK
245	4	P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	5e-72	32	evm_27.model.AmTr.v1.0_scaffold00002.6	-12,78873	12	53	4	-	4	0,2353	SLMSEAGQGE QQQIER SLMSEAGQGE
245	4	Q39649	2S albumin	<i>Cucurbita maxima</i>		06 Protein destination and storage	06.20 Storage proteins	1,00E-13	35	evm_27.model.AmTr.v1.0_scaffold00005.2	-14,29585	20	16,8	3	-	2	0,4286	SLMSEAGQGE QQQIER SLMSEAGQGE
246	1	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr.v1.0_scaffold00067.7	-172,7552	40	54,5	53	-	37	2,9048	LSDAQCCR GRQEYGEER EORGEQCK
247	1	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr.v1.0_scaffold00067.7	-206,8835	40	54,5	83	-	46	4,2857	RLSDAQCCR GRQEYGEER EORGEQCKE RLSDAQCCR GRQEYGEER EORGEQCKE
248	1	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr.v1.0_scaffold00067.7	-244,8778	40	54,5	89	-	55	4,8095	RLSDAQCCR GRQEYGEER EORGEQCKE LSDAQCCR GRQEYGEER EORGEQCKE
249	2	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr.v1.0_scaffold00067.7	-239,9372	37	54,5	97	-	48	5,0952	LSDAQCCR GRQEYGEER EORGEQCKE IVALQITSTPG QYEIFFGATGQ NPPSYLR
249	2	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr.v1.0_scaffold00002.6	-33,86225	40	43,5	10	-	9	0,4348	EEREERER LSDAQCCR RLSDAQCCR
250	2	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr.v1.0_scaffold00067.7	-299,8078	46	54,5	107	-	62	5,7143	ISNDHGYEL DETEYSPLR SDLNPEDLFVA
250	2	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr.v1.0_scaffold00002.6	-13,14709	19	43,5	5	-	4	0,2609	LSDAQCCR SEGGITELWD EDRDEFQACAG
251	4	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr.v1.0_scaffold00067.7	-33,38869	25	54,5	7	3	7	0,3810	LVTIGEEER ATEIYVILEGR AFSDEILEASE GQEEGQEEQ EQEQEQEQR VGGEGQQQQ VGEGGQQQQ
251	4	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr.v1.0_scaffold00002.6	-21,72978	26	43,5	9	-	6	0,3913	GKDRHQK RGQEEGQQE GQGPVIRPSS EQLQLIHGG SGGGK
251	4	P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	5e-72	32	evm_27.model.AmTr.v1.0_scaffold00067.1	-33,30704	15	53	8	-	7	0,4706	
252	2	P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	5e-72	32	evm_27.model.AmTr.v1.0_scaffold00067.1	-196,2594	45	53	92	-	41	6,2941	
252	2	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr.v1.0_scaffold00002.6	-22,71686	15	43,5	5	-	4	0,2174	

253	3	P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	5e-72	32	evm_27.model.AmTr.v1.0_scaffold00067.12	-125,9256	44	53	53	-	27	3,5882	RGQEEGQQE QEQQ RGQEEGQQE
253	3	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr.v1.0_scaffold00002.657	-44,73332	32	43,5	11	-	10	0,6087	ARIEMACPHV SGGR IEMACPHVSG
253	3	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr.v1.0_scaffold00067.7	-27,80453	20	54,5	9	-	9	0,5238	GRQEGEYGE EQR GEYGEFEQR
254	3	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr.v1.0_scaffold00002.657	-75,97305	50	43,5	26	-	15	1,3478	ACPHVSGGR KGDATIPAGK ARIEMACPHV
254	3	P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	5e-72	32	evm_27.model.AmTr.v1.0_scaffold00067.12	-57,56915	31	53	18	-	11	1,0588	RGQEEGQQE QEQQEQEQR SLOKPDER
254	3	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr.v1.0_scaffold00067.7	-16,50585	15	54,5	4	-	4	0,2381	RGQEEGQQE R GEGQIQIGTN
255	4	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr.v1.0_scaffold00002.657	-121,2288	45	43,5	57	-	28	2,6957	ATEIYVLEGR ACPHVSGGR IEMACPH
255	4	P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	5e-72	32	evm_27.model.AmTr.v1.0_scaffold00067.12	-43,67015	27	53	11	-	9	0,6471	RGQEEGQQE QEQQEQEQR VGGEGQQQQ
255	4	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr.v1.0_scaffold00067.7	-21,1119	14	54,5	6	5	6	0,3333	ROEGEYGE QRGEQK GROEGEYGE
256	3	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr.v1.0_scaffold00002.657	-131,1185	48	43,5	58	-	26	2,7391	ACPHVSGGR ARIEMACPHV SGGR
256	3	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr.v1.0_scaffold00067.7	-13,90981	12	54,5	5	-	5	0,3333	LSDAQQCR GRQEGEYGE EQRGEQK
256	3	P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	5e-72	32	evm_27.model.AmTr.v1.0_scaffold00067.12	-22,81379	15	53	5	-	5	0,2941	RGQEEGQQE QEQQEQEQR VGGEGQQQQ
257	2	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr.v1.0_scaffold00002.657	-98,64301	50	43,5	40	-	20	2,0435	KGDATIPAGK IEMACPHVSG GR
257	2	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr.v1.0_scaffold00067.7	-15,0678	16	54,5	5	-	5	0,2857	FLAALDPIEL AQK LSDAQQCR
258	1	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr.v1.0_scaffold00002.657	-98,37663	35	43,5	26	-	20	1,3043	KGDATIPAGK QGQPIVRPSS EQ
259	2	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr.v1.0_scaffold00002.657	-113,1392	41	43,5	36	-	23	1,7826	KGDATIPAGK QGQPIVRPSS KGDATIPAGK
259	2	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr.v1.0_scaffold00067.7	-37,40088	25	54,5	21	-	8	1,0476	FLAALDPIEL AQK LIQTILPQIDTR
260	2	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr.v1.0_scaffold00002.657	-130,5525	47	43,5	43	-	28	2,1304	KGDATIPAGK QDSHNLKKGD TATIPAGK
260	2	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr.v1.0_scaffold00067.7	-46,03372	29	54,5	25	-	9	1,4286	FLAALDPIEL AQK LIQTILPQIDTR
261	2	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr.v1.0_scaffold00002.657	-90,40794	31	43,5	30	-	22	1,3913	KGDATIPAGK AFVLPCHK TGNPPSYLR
261	2	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr.v1.0_scaffold00067.7	-57,84689	33	54,5	25	-	13	1,1905	FLAALDPIEL AQK LIQTILPQIDTR
262	1	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr.v1.0_scaffold00002.657	-47,66602	24	43,5	10	-	9	0,5652	KGDATIPAGK QGQPIVRPSS IYYVANGDAR
263	4	P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	5e-72	32	evm_27.model.AmTr.v1.0_scaffold00067.12	-41,16557	34	53	15	-	9	0,9412	VGGEGQQQQ GK RGQEEGQQE
263	4	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr.v1.0_scaffold00002.657	-52,52599	27	43,5	15	-	11	0,6957	KGDATIPAGK QGQPIVRPSS PSSEQLQGLIH

263	4	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr_v1.0_scaffold00067.7	-9,198939	6	54,5	3	-	3	0,1429	GRQEGYEGEE EQR ISNQAQDDIK
263	4	Q9ZV34	Thaumatococin putative	<i>Arabidopsis thaliana</i>	AT2G28790	11 Disease/defence	11.01 Resistance genes	2,00E-97	72	evm_27.model.AmTr_v1.0_scaffold00012.9	-20,23329	29	26,5	6	-	6	0,7000	FHCETGDCGR TGCTYSTGR GLCPVWVGR
264	6	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.6	-101,9621	43	43,5	34	-	25	1,6522	KGDTATIPAGK KGDTATIPAGK GQGPVIRPSS
264	6	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr_v1.0_scaffold00067.7	-35,96075	20	54,5	8	-	8	0,4286	GRQEGYEGEE EQR GRQEGYEGEE
264	6	P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	5e-72	32	evm_27.model.AmTr_v1.0_scaffold00067.1	-16,95861	16	53	4	-	4	0,2353	RGQEEGQQE QEQQEQEQR VGGEGQQQQ
264	6	Q39649	2S albumin	<i>Cucurbita maxima</i>		06 Protein destination and storage	06.20 Storage proteins	1,00E-13	35	evm_27.model.AmTr_v1.0_scaffold00005.2	-18,29243	26	16,8	4	-	2	0,7143	SLMSEAGQGE QQQIER SLMSEAGQGE
264	6	Q9SK09	Cupin family protein (Vicilin)	<i>Arabidopsis thaliana</i>	AT2G28490	06 Protein destination and storage	06.20 Storage proteins	e-115	50	evm_27.model.AmTr_v1.0_scaffold00080.8	-9,58203	8	43,1	3	-	3	0,1875	YFPFCQIASR EGDAFWIPR GPPELATAFNLS
264	6	O04005	1-Cys peroxidase	<i>Arabidopsis thaliana</i>	AT1G48130	11 Disease/defence	11.05 Stress responses	9,00E-89	69	evm_27.model.AmTr_v1.0_scaffold00045.3	-11,65131	19	24,2	3	-	3	0,3636	DNQKPLPSR LSFLYPGTGR ALDSLILAAK
265	3	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.6	-43,48357	29	43,5	12	-	9	0,5652	GQGPVIRPSS EQQL ESVILPETIHAP
265	3	Q9SK09	Cupin family protein (Vicilin)	<i>Arabidopsis thaliana</i>	AT2G28490	06 Protein destination and storage	06.20 Storage proteins	e-115	50	evm_27.model.AmTr_v1.0_scaffold00080.8	-26,31966	18	43,1	6	-	5	0,3750	ESVILPETIHAP PHG ESVILPETIHAP
265	3	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr_v1.0_scaffold00067.7	-19,22629	12	54,5	4	-	4	0,1905	ISNQAQDDIK TVTVDVTSYDN QLDTK
266	4	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.6	-54,0337	41	43,5	16	-	11	0,7826	KGDTATIPAGK AQSDSVFVVG PR
266	4	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr_v1.0_scaffold00067.7	-53,84566	28	54,5	12	-	12	0,6190	LSDAQQCR GRQEGYEGEE SDYNQLDTK
266	4	Q9SK09	Cupin family protein (Vicilin)	<i>Arabidopsis thaliana</i>	AT2G28490	06 Protein destination and storage	06.20 Storage proteins	e-115	50	evm_27.model.AmTr_v1.0_scaffold00080.8	-44,097	23	43,1	11	-	9	0,8125	ESVILPETIHAP PHG ESVILPETIHAP
266	4	Q39649	2S albumin	<i>Cucurbita maxima</i>		06 Protein destination and storage	06.20 Storage proteins	1,00E-13	35	evm_27.model.AmTr_v1.0_scaffold00005.2	-16,5938	26	16,8	3	-	2	0,5714	SLMSEAGQGE QQQIER SLMSEAGQGE
267	5	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.6	-24,69562	26	43,5	8	-	6	0,3478	GQGPVIRPSS EQQLQLIHGG SDLNPFDLFVA
267	5	Q39649	2S albumin	<i>Cucurbita maxima</i>		06 Protein destination and storage	06.20 Storage proteins	1,00E-13	35	evm_27.model.AmTr_v1.0_scaffold00005.2	-14,22416	26	16,8	4	-	3	0,5714	FIQTGRPE SLMSEAGQGE QQQIER
267	5	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr_v1.0_scaffold00067.7	-8,205317	11	54,5	3	-	3	0,2381	ISNQAQDDIK GQGIQIITGN GQK
267	5	Q9SK09	Cupin family protein (Vicilin)	<i>Arabidopsis thaliana</i>	AT2G28490	06 Protein destination and storage	06.20 Storage proteins	e-115	50	evm_27.model.AmTr_v1.0_scaffold00080.8	-7,378824	6	43,1	2	-	2	0,1250	YFPFCQIASR GPPELATAFNLS PDEL
267	5	Q9ZV34	Thaumatococin putative	<i>Arabidopsis thaliana</i>	AT2G28790	11 Disease/defence	11.01 Resistance genes	2,00E-97	72	evm_27.model.AmTr_v1.0_scaffold00012.9	-79,24223	68	26,5	24	-	17	2,9000	FHCETGDCGR TGCTYSTGR FHCETGDCGR
268	2	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr_v1.0_scaffold00067.7	-84,91544	41	54,5	26	-	18	1,2857	GRQEGYEGEE GRQEGYEGEE ISNQAQDDIK
268	2	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.6	-55,10893	38	43,5	14	-	12	0,7391	KGDTATIPAGK GQGPVIRPSS EQQLQLIHGG
269	4	P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	5e-72	32	evm_27.model.AmTr_v1.0_scaffold00067.1	-43,21776	22	53	21	20	13	1,6471	IRQNIIDNPR IRQNIIDNPR QAGHQIVNR
269	4	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr_v1.0_scaffold00067.7	-62,5927	29	54,5	12	9	12	0,6190	LSDAQQCR DEFQACGVAA TR

269	4	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr.v1.0_scaffold00002.657	-27,96675	17	43,5	10	-	5	0,4348	ATEIYVILEGR KGDATIPAGK DADIYYVANG
270	2	Q9SK09	Cupin family protein (Vicilin)	<i>Arabidopsis thaliana</i>	AT2G28490	06 Protein destination and storage	06.20 Storage proteins	e-115	50	evm_27.model.AmTr.v1.0_scaffold00080.82	-35,5591	18	43,1	11	-	7	0,8750	SVLNLMR ESVLPETIHAP PHG
270	2	P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	5e-72	32	evm_27.model.AmTr.v1.0_scaffold00067.12	-11,58127	9	53	5	-	4	0,2941	IRQNIDNPR IRQNIDNPR QAGHIQVNR
271	3	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr.v1.0_scaffold00067.7	-87,58012	42	54,5	38	-	21	2,1429	ISNQAQDIK READIYSR YNREDQIM
271	3	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr.v1.0_scaffold00002.657	-26,19777	21	43,5	8	-	5	0,3478	KGDATIPAGK AQSDSVFVVG PR
271	3	Q9SK09	Cupin family protein (Vicilin)	<i>Arabidopsis thaliana</i>	AT2G28490	06 Protein destination and storage	06.20 Storage proteins	e-115	50	evm_27.model.AmTr.v1.0_scaffold00080.82	-20,94954	18	43,1	4	-	4	0,2500	ESVLPETIHAP PH YFPFCQIASR
272	3	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr.v1.0_scaffold00067.7	-104,9099	44	54,5	39	23	24	2,0476	GRQGEYGE EQRGEQ GK HGGHLKTNR
272	3	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr.v1.0_scaffold00002.657	-27,79718	22	43,5	8	-	6	0,3913	KGDATIPAGK GQGPVIRPSS EQLQGLIHGG
273	1	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr.v1.0_scaffold00067.7	-131,874	50	54,5	54	-	30	2,9048	GRQGEYGE EQRGEQ GK ISNQAQDIK
274	3	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr.v1.0_scaffold00067.7	-76,12221	28	54,5	25	18	16	1,2857	YNREDQIMFP SSSR YNREDQIMFP
274	3	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr.v1.0_scaffold00002.657	-9,840433	7	43,5	3	-	2	0,1304	DADIYYVANG DAR AFSDEILEASF
275	3	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr.v1.0_scaffold00067.7	-56,13203	26	54,5	21	9	13	1,0476	TVTDTVSDYN QLDTK NSPLVGYTSAI
275	3	P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	5e-72	32	evm_27.model.AmTr.v1.0_scaffold00067.12	-32,91145	32	53	9	-	9	0,7647	VGEGGQQQ GIK SPILGHAS
276	3	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr.v1.0_scaffold00067.7	-49,33782	25	54,5	14	5	10	0,7619	YNREDQIMFP SSSR QFFIAGGQPR
276	3	P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	5e-72	32	evm_27.model.AmTr.v1.0_scaffold00067.12	-23,49608	10	53	4	-	4	0,2941	SPILGHASAIK GEGNIQVIGTN GR
277	4	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr.v1.0_scaffold00067.7	-73,83707	32	54,5	24	8	17	1,1905	YNREDQIMFP SSSR VGGEGQQQPR
277	4	P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	5e-72	32	evm_27.model.AmTr.v1.0_scaffold00067.12	-28,16292	14	53	7	-	7	0,4706	VGGEGQQQ GIK IRQNIDNPR
277	4	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr.v1.0_scaffold00002.657	-18,72531	14	43,5	4	-	4	0,1739	KGDATIPAGK AQSDSVFVVG PR
278	3	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr.v1.0_scaffold00067.7	-95,1066	37	54,5	41	23	21	2,0476	LSDAQCCR YNREDQIMFP TVTDTVSDYN
278	3	P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	5e-72	32	evm_27.model.AmTr.v1.0_scaffold00067.12	-72,0257	31	53	31	-	21	2,1176	IRQNIDNPR VGEGGQQQ GIK
279	4	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr.v1.0_scaffold00067.7	-101,2754	43	54,5	34	20	22	1,6667	GIGLSAPGCS ESFHSGESGS QHR
279	4	P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	5e-72	32	evm_27.model.AmTr.v1.0_scaffold00067.12	-40,49422	25	53	15	14	14	1,0588	VGGEGQQQ GIK IRQNIDNPR
279	4	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr.v1.0_scaffold00002.657	-13,93085	13	43,5	3	-	3	0,1304	ISNDHGLYEL DETEYSPLR ASQENLQIIC
280	3	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr.v1.0_scaffold00067.7	-78,8131	42	54,5	23	14	15	1,1429	TVTDTVSDYN QLDTK GIGLSAPGCS

280	3	P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	5e-72	32	evm_27.model.AmTr.v1.0_scaffold00067.12	-29,20238	19	53	7	-	7	0,5294	QAGHIQVNR SPILGHAS GHLHPNALYA
281	3	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr.v1.0_scaffold00067.7	-108,7062	46	54,5	24	17	20	1,2857	ISGIRPTR DEFQCGAVAA TR
281	3	P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	5e-72	32	evm_27.model.AmTr.v1.0_scaffold00067.12	-38,27846	20	53	11	-	10	0,8235	SPILGHAS GHLHPNALYA PH
282	3	P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	5e-72	32	evm_27.model.AmTr.v1.0_scaffold00067.12	-96,53345	35	53	42	-	24	3,0588	GYEEREENAR IRQNDNPR RADIYSR
282	3	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr.v1.0_scaffold00067.7	-91,37351	44	54,5	22	-	17	1,1905	LSDAQCCR ISGIRPTR ISNQQAQDIK
282	3	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr.v1.0_scaffold00067.11	-16,75543	16	12,1	6	-	4	1,5000	SLSLPNFSPAP R PNFSPAPR
283	3	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr.v1.0_scaffold00067.7	-94,09697	49	54,5	31	20	21	1,5238	LSDAQCCR ISGIRPTR ILSPGEEEREE
283	3	P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	5e-72	32	evm_27.model.AmTr.v1.0_scaffold00067.12	-47,99188	22	53	19	18	13	1,3529	GHIQIVNR IRQNDNPR SPILGHASAIK
284	3	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr.v1.0_scaffold00067.7	-38,81295	32	54,5	11	-	10	0,6667	GROGEYGEE EQR QEGEYGFEEQ
284	3	Q9SK09	Cupin family protein (Vicilin)	<i>Arabidopsis thaliana</i>	AT2G28490	06 Protein destination and storage	06.20 Storage proteins	e-115	50	evm_27.model.AmTr.v1.0_scaffold00080.82	-29,07367	15	43,1	8	-	7	0,5000	YLVNIGEGQR LQIICSIDTSE GSVLSGFNLK
284	3	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr.v1.0_scaffold00002.657	-11,71309	16	43,5	4	-	3	0,2174	AFSDEILEASF NVDR KGDATIPAGK
285	2	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr.v1.0_scaffold00067.7	-75,15559	43	54,5	26	-	18	1,2857	NLPILDLDMS AAK NLPILDLDMS
285	2	Q9SK09	Cupin family protein (Vicilin)	<i>Arabidopsis thaliana</i>	AT2G28490	06 Protein destination and storage	06.20 Storage proteins	e-115	50	evm_27.model.AmTr.v1.0_scaffold00080.82	-32,34969	22	43,1	12	-	9	0,7500	LVNIGEGQR PSAGPIYMTG AHEPPK
286	3	Q9SK09	Cupin family protein (Vicilin)	<i>Arabidopsis thaliana</i>	AT2G28490	06 Protein destination and storage	06.20 Storage proteins	e-115	50	evm_27.model.AmTr.v1.0_scaffold00080.82	-46,94532	19	43,1	13	-	8	0,9375	LVNIGEGQR PSAGPIYMTG AHEPPK
286	3	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr.v1.0_scaffold00067.7	-36,60592	21	54,5	9	-	9	0,4286	NLPILDLDMS AAK GROGEYGEE
286	3	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr.v1.0_scaffold00002.657	-9,830208	10	43,5	3	-	3	0,1304	LVTIGEEER ASQENLQIIC FEINAR
287	3	P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	5e-72	32	evm_27.model.AmTr.v1.0_scaffold00067.12	-19,70468	23	53	6	-	6	0,5294	VGEGQQQQ GIK ESLGVIRPDEE
287	3	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr.v1.0_scaffold00002.657	-8,89963	14	43,5	3	-	3	0,2174	KGDATIPAGK PSSEQLQGLIH GSGGGK
287	3	Q9SK09	Cupin family protein (Vicilin)	<i>Arabidopsis thaliana</i>	AT2G28490	06 Protein destination and storage	06.20 Storage proteins	e-115	50	evm_27.model.AmTr.v1.0_scaffold00080.82	-8,937418	9	43,1	3	-	3	0,1875	YLVNIGEGQR LQIICSIDTSE IGHQPFQSFIL
288	1	P49206	40S ribosomal protein S26	<i>Arabidopsis thaliana</i>	AT2G40590	05 Protein synthesis	05.01 Ribosomal proteins	2e-31	75	evm_27.model.AmTr.v1.0_scaffold00077.25	-15,95327	12	42,6	4	-	3	0,3077	NLAPVNEGGG EPPK NLAPVNEGGG
289	1	P49206	40S ribosomal protein S26	<i>Arabidopsis thaliana</i>	AT2G40590	05 Protein synthesis	05.01 Ribosomal proteins	2e-31	75	evm_27.model.AmTr.v1.0_scaffold00077.25	-21,16257	18	42,6	5	-	5	0,3846	NLAPVNEGGG EPPK GDASSTVQLQ
290	3	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr.v1.0_scaffold00067.7	-42,4252	22	54,5	16	9	10	0,8571	SINHTIAYITR YNRDQIMIFP SSSR
290	3	P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	5e-72	32	evm_27.model.AmTr.v1.0_scaffold00067.12	-26,97858	22	53	6	-	6	0,4118	VGEGQQQQ GIK SPILGHASAIK
291	2	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr.v1.0_scaffold00002.657	-71,67849	50	43,5	16	-	14	0,7391	ITEMACPHVSG GR PSSEQLQGLIH

291	2	P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	5e-72	32	evm_27.model.AmTr.v1.0_scaffold00067.12	-10,53859	8	53	3	-	3	0,1765	RGQEEGQQE QEQEQEER VGGEGQQQ
292	1	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr.v1.0_scaffold00002.657	-56,02645	38	43,5	14	-	10	0,6522	IEMACPHVSGR ARIEACPHV IEMACPHVSGR
293	1	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr.v1.0_scaffold00002.657	-79,67419	53	43,5	21	-	13	1,0435	KGDTATIPAGK MACPHVSGR KGDATIPAGK
294	2	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr.v1.0_scaffold00002.657	-94,00911	57	43,5	23	-	17	1,1304	MACPHVSGR KGDATIPAGK QEGEYGEER
294	2	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr.v1.0_scaffold00067.757	-26,98573	20	54,5	6	-	6	0,2857	TVTVDVTSQYD KGDATIPAGK IEMACPHVSGR
295	2	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr.v1.0_scaffold00002.657	-107,0359	68	43,5	30	-	21	1,5217	QEGEYGEER KGDATIPAGK IEMACPHVSGR
295	2	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr.v1.0_scaffold00067.757	-31,74412	20	54,5	7	-	6	0,3333	QEGEYGEER TVTVDVTSQYD KGDATIPAGK
296	1	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr.v1.0_scaffold00002.657	-70,05572	50	43,5	19	-	13	0,8696	IEMACPHVSGR PSSEQLQLIH GGSGGK
297	2	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr.v1.0_scaffold00002.657	-44,38897	32	43,5	11	-	9	0,5217	AAKEVSNVNP GROEGEYGEER EQRGEQK
297	2	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr.v1.0_scaffold00067.757	-13,34104	11	54,5	4	-	3	0,1905	LIQTLPOIDTR AEVLDGSEAK GK
298	2	F4JVN6	Tripeptidyl-peptidase II	<i>Arabidopsis thaliana</i>	AT4G20850	06 Protein destination and storage	06.13 Proteolysis	0	65	evm_27.model.AmTr.v1.0_scaffold00009.258	-11,6096	2	143,8	3	-	3	0,0492	NQEAISEALK KGDATIPAGK IEMACPHVSGR
298	2	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr.v1.0_scaffold00002.657	-60,69852	53	43,5	16	-	13	0,7826	IEMACPHVSGR AHEYIQGSK AEDGCIDGASGTR
299	3	F4JVN6	Tripeptidyl-peptidase II	<i>Arabidopsis thaliana</i>	AT4G20850	06 Protein destination and storage	06.13 Proteolysis	0	65	evm_27.model.AmTr.v1.0_scaffold00009.258	-44,35351	9	143,8	9	-	9	0,1639	GGQNSQACP KGDATIPAGK AQSDSVFVVGPR
299	3	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr.v1.0_scaffold00002.657	-41,60591	35	43,5	10	-	9	0,5652	IEMACPHVSGR KGDATIPAGK KGDATIPAGK
299	3	P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	5e-72	32	evm_27.model.AmTr.v1.0_scaffold00067.12	-11,07325	15	53	4	-	4	0,2353	ESLGVIRPDEE RSDLNPEDLFVA AHEYIQGSK
300	1	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr.v1.0_scaffold00002.657	-15,26331	14	43,5	3	-	3	0,1739	EVSNVPSR AEDGCIDGASGTR IEMACPHVSGR
301	2	F4JVN6	Tripeptidyl-peptidase II	<i>Arabidopsis thaliana</i>	AT4G20850	06 Protein destination and storage	06.13 Proteolysis	0	65	evm_27.model.AmTr.v1.0_scaffold00009.258	-40,38381	9	143,8	9	-	9	0,1803	GGQNSQACP KGDATIPAGK KGDATIPAGK
301	2	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr.v1.0_scaffold00002.657	-14,41466	10	43,5	4	-	4	0,1739	EVSNVPSR AEDGCIDGASGTR GGQNSQACP
302	2	F4JVN6	Tripeptidyl-peptidase II	<i>Arabidopsis thaliana</i>	AT4G20850	06 Protein destination and storage	06.13 Proteolysis	0	65	evm_27.model.AmTr.v1.0_scaffold00009.258	-57,88726	11	143,8	12	-	12	0,1967	GGQNSQACP KGDATIPAGK AQSDSVFVVGPR
302	2	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr.v1.0_scaffold00002.657	-15,02326	12	43,5	4	-	4	0,1739	IEMACPHVSGR KGDATIPAGK KGDATIPAGK
303	2	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr.v1.0_scaffold00002.657	-65,74984	52	43,5	20	-	14	0,9565	ARIEACPHV QEGEYGEER ISNQQAQDIK
303	2	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr.v1.0_scaffold00067.757	-19,77358	17	54,5	6	-	6	0,2857	ARIEACPHV SGGR IEMACPHVSGR
304	2	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr.v1.0_scaffold00002.657	-46,59997	50	43,5	12	-	11	0,6957	IEMACPHVSGR LSDAQQR QEGEYGEER
304	2	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr.v1.0_scaffold00067.757	-10,03066	9	54,5	4	-	4	0,1905	QEGEYGEER

305	2	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-71,39986	55	43,5	17	-	13	1,0000	ARIEMACPHV SGGR ARIEMACPHV GRQEGYGEE EQRGEQOK ILSPEGEERE
305	2	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr_v1.0_scaffold00067.7	-28,29747	24	54,5	7	-	7	0,3333	ARIEMACPHV SGGR KGDATIPAGK GRQEGYGEE EQRGEQOK QEYGEYEEQ
306	2	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-97,74711	62	43,5	30	-	22	1,3913	ARIEMACPHV SGGR KGDATIPAGK GRQEGYGEE EQRGEQOK QEYGEYEEQ
306	2	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr_v1.0_scaffold00067.7	-22,25251	16	54,5	5	-	5	0,2381	ARIEMACPHV SGGR KGDATIPAGK GRQEGYGEE EQRGEQOK QEYGEYEEQ
307	1	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-96,93983	60	43,5	26	-	19	1,2609	ARIEMACPHV SGGR KGDATIPAGK GRQEGYGEE EQRGEQOK QEYGEYEEQ
308	3	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-103,3335	55	43,5	27	-	18	1,3478	ARIEMACPHV SGGR KGDATIPAGK GRQEGYGEE EQRGEQOK QEYGEYEEQ
308	3	Q39649	2S albumin	<i>Cucurbita maxima</i>		06 Protein destination and storage	06.20 Storage proteins	1,00E-13	35	evm_27.model.AmTr_v1.0_scaffold00005.212	-15,13371	20	16,8	5	-	2	0,7143	SLMSEAGQGE QQQIER SLMSEAGQGE QEYGEYEEQ R TVTDVTSFDYN
308	3	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr_v1.0_scaffold00067.7	-22,50654	16	54,5	5	-	5	0,2857	ARIEMACPHV SGGR KGDATIPAGK GRQEGYGEE EQRGEQOK QEYGEYEEQ
309	3	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-114,6359	58	43,5	38	-	21	1,9130	ARIEMACPHV SGGR KGDATIPAGK GRQEGYGEE EQRGEQOK QEYGEYEEQ
309	3	Q39649	2S albumin	<i>Cucurbita maxima</i>		06 Protein destination and storage	06.20 Storage proteins	1,00E-13	35	evm_27.model.AmTr_v1.0_scaffold00005.212	-15,02136	20	16,8	5	-	2	0,7143	SLMSEAGQGE QQQIER SLMSEAGQGE
309	3	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr_v1.0_scaffold00067.7	-4,468521	3	54,5	2	-	2	0,0952	LSDAQCCR QFFIAGQPR
310	2	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-44,44918	39	43,5	12	-	11	0,5217	KGDATIPAGK ARIEMACPHV SGGR DEFQACGVA TR GEGQIQIGTN
310	2	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr_v1.0_scaffold00067.7	-14,62155	7	54,5	3	-	3	0,1429	KGDATIPAGK ARIEMACPHV SGGR DEFQACGVA TR GEGQIQIGTN
311	3	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-69,34831	45	43,5	16	-	14	0,7391	KGDATIPAGK GDTATIPAGK IEMACPHVSG GRQEGYGEE EQRGEQOK QEYGEYEEQ
311	3	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr_v1.0_scaffold00067.7	-31,04301	19	54,5	8	5	7	0,4286	ARIEMACPHV SGGR KGDATIPAGK GRQEGYGEE EQRGEQOK QEYGEYEEQ
312	2	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-23,50973	14	43,5	4	-	4	0,2174	ARIEMACPHV SGGR KGDATIPAGK GRQEGYGEE EQRGEQOK QEYGEYEEQ
312	2	P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	5e-72	32	evm_27.model.AmTr_v1.0_scaffold00067.12	-9,96111	12	53	3	-	3	0,1765	SLMSEAGQGE QQQIER SLMSEAGQGE QEYGEYEEQ R TVTDVTSFDYN
313	3	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-52,78958	43	43,5	14	-	11	0,7391	KGDATIPAGK GDTATIPAGK PSSEQLQGLI H LSDAQCCR QEYGEYEEQ R
313	3	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr_v1.0_scaffold00067.7	-28,13613	18	54,5	8	5	8	0,4286	ARIEMACPHV SGGR KGDATIPAGK GRQEGYGEE EQRGEQOK QEYGEYEEQ
314	2	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-76,77163	48	43,5	20	-	13	1,0435	KGDATIPAGK KGDATIPAGK IEMACPHVSG GRQEGYGEE EQRGEQOK QEYGEYEEQ
314	2	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr_v1.0_scaffold00067.7	-20,46771	15	54,5	5	-	5	0,2857	ARIEMACPHV SGGR KGDATIPAGK GRQEGYGEE EQRGEQOK QEYGEYEEQ
315	2	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-58,08045	43	43,5	16	-	12	0,6957	KGDATIPAGK GDTATIPAGK IEMACPHVSG GRQEGYGEE EQRGEQOK QEYGEYEEQ
315	2	P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	5e-72	32	evm_27.model.AmTr_v1.0_scaffold00067.12	-26,30268	19	53	7	-	6	0,4118	SLMSEAGQGE QQQIER SLMSEAGQGE QEYGEYEEQ R TVTDVTSFDYN
316	2	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-71,79536	46	43,5	18	-	13	0,7826	KGDATIPAGK ARIEMACPHV SGGR DEFQACGVA TR GEGQIQIGTN

316	2	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr_v1.0_scaffold00067.7	-19,50242	14	54,5	6	-	6	0,2857	LSDAQCCR ISNQAQDIK QEGEYGEFFQ
317	4	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-37,46281	26	43,5	9	-	7	0,4348	KGDATIPAGK IEMACPHVSG GR
317	4	P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	5e-72	32	evm_27.model.AmTr_v1.0_scaffold00067.12	-24,64141	21	53	7	-	7	0,4118	RGQEEGQQE QEQEQEQR VGGEGQQQQ
317	4	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr_v1.0_scaffold00067.7	-15,50693	12	54,5	4	-	4	0,1905	GEGQIIGTN GQK QFFIAGGQPR
317	4	Q39649	2S albumin	<i>Cucurbita maxima</i>		06 Protein destination and storage	06.20 Storage proteins	1,00E-13	35	evm_27.model.AmTr_v1.0_scaffold00005.212	-16,37675	20	16,8	3	-	2	0,4286	SLMSEAGGQE QQQIER SLMSEAGGQE
318	3	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-73,63341	47	43,5	18	-	13	0,9565	IEMACPHVSG GR ARIEMACPHV
318	3	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr_v1.0_scaffold00067.7	-14,71399	16	54,5	4	-	4	0,2381	GEGQIIGTN GQK EQQIMFPSSS
318	3	P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	5e-72	32	evm_27.model.AmTr_v1.0_scaffold00067.12	-16,0856	11	53	3	-	3	0,2353	RGQEEGQQE QEQEQEQR VGGEGQQQQ
319	4	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-88,75625	56	43,5	24	-	16	1,2174	KGDATIPAGK IEMACPHVSG GR
319	4	P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	5e-72	32	evm_27.model.AmTr_v1.0_scaffold00067.12	-11,00274	15	53	4	-	4	0,2353	RGQEEGQQE QEQEQEQR ESLGVIRPDEE
319	4	Q39649	2S albumin	<i>Cucurbita maxima</i>		06 Protein destination and storage	06.20 Storage proteins	1,00E-13	35	evm_27.model.AmTr_v1.0_scaffold00005.212	-16,54638	20	16,8	4	-	2	0,5714	SLMSEAGGQE QQQIER SLMSEAGGQE
319	4	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr_v1.0_scaffold00067.7	-12,16115	7	54,5	3	-	3	0,1429	QEGEYGEFFQ R GEGQIIGTN
320	3	P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	5e-72	32	evm_27.model.AmTr_v1.0_scaffold00067.12	-106,5646	59	53	38	-	24	2,5882	RGQEEGQQE QEQEQEQR RGQEEGQQE
320	3	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-103,8355	61	43,5	36	-	21	1,9565	GKGGQGEIK KGDATIPAGK IEMACPHVSG
320	3	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr_v1.0_scaffold00067.7	-66,37756	37	54,5	16	-	15	0,8571	LSDAQCCR ISNQAQDIK QEGEYGEFFQ
321	2	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-222,5808	55	43,5	87	-	48	4,0000	CPHVSGGR QGLIHGSGG GK
321	2	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr_v1.0_scaffold00067.7	-7,805208	9	54,5	3	-	3	0,1905	ANVIGVGER QFFIAGGQPR LIQTILPOIDTR
322	2	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-184,688	52	43,5	69	-	40	3,1304	KGDATIPAGK TIPAGK IEMACPHVSG
322	2	P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	5e-72	32	evm_27.model.AmTr_v1.0_scaffold00067.12	-13,42112	15	53	4	-	4	0,2353	RGQEEGQQE QEQEQEQR VGGEGQQQQ
323	2	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-156,0177	49	43,5	60	-	32	3,0870	ACPHVSGGR IEMACPH GLIHGSGGG
323	2	P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	5e-72	32	evm_27.model.AmTr_v1.0_scaffold00067.12	-14,5986	12	53	3	-	3	0,2353	RGQEEGQQE QEQEQEQR SPILGHASAIK
324	2	Q8S9N1	HSC70 (Heat shock cognate 70 kDa protein)	<i>Arabidopsis thaliana</i>	AT1G16030	06 Protein destination and storage	06.01 Folding and stability	0	80	evm_27.model.AmTr_v1.0_scaffold00137.8	-72,79314	28	71,6	18	-	15	0,9524	FSDPSVQADM K ATAGDTHLGG
324	2	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr_v1.0_scaffold00002.657	-20,64738	16	43,5	4	-	4	0,2174	KGDATIPAGK PSSEQLQLIH GSGGGGK
325	2	Q9FX54	Glyceraldehyde-3-phosphate dehydrogenase	<i>Arabidopsis thaliana</i>	AT1G13440	02 Energy	02.01 Glycolysis	6,00E-94	82,00	evm_27.model.AmTr_v1.0_scaffold00177.24	-10,18046	13	24,7	3	-	2	0,4286	AAGFNIIPSS T TLLFGEKPVTV

325	2	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr.v1.0_scaffold00002.657	-27,61741	28	43,5	6	-	6	0,3478	IEMACPHVSG GR PSSEQLQLIHKVVISAPSK
326	2	Q9FX54	Glyceraldehyde-3-phosphate dehydrogenase	<i>Arabidopsis thaliana</i>	AT1G13440	02 Energy	02.01 Glycolysis	6,00E-94	82,00	evm_27.model.AmTr.v1.0_scaffold00177.24	-21,42355	31	24,7	5	-	5	0,8571	AAGFNIPSST GAACK
326	2	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr.v1.0_scaffold00002.657	-46,93636	37	43,5	12	-	10	0,5652	KGDTATIPAGK IEMACPHVSG GR
327	3	Q9FX54	Glyceraldehyde-3-phosphate dehydrogenase	<i>Arabidopsis thaliana</i>	AT1G13440	02 Energy	02.01 Glycolysis	6,00E-94	82,00	evm_27.model.AmTr.v1.0_scaffold00177.24	-28,06334	36	24,7	8	-	6	1,1429	KVVISAPSK AAGFNIPSST GAACK
327	3	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr.v1.0_scaffold00002.657	-18,50076	14	43,5	4	-	4	0,1739	KGDTATIPAGK PSSEQLQLIHKVVISAPSK
327	3	Q9SCV3	Beta-galactosidase	<i>Arabidopsis thaliana</i>	AT2G32810	09 Cell structure	09.01 Cell wall	0	68	evm_27.model.AmTr.v1.0_scaffold00117.17	-29,64166	14	74,6	8	-	6	0,3000	MLVSAGLHYPR MLVSAGLHYPR
328	2	O65390	Aspartic proteinase	<i>Arabidopsis thaliana</i>	AT1G11910	06 Protein destination and storage	06.13 Proteolysis	0	68,00	evm_27.model.AmTr.v1.0_scaffold00106.48	-63,45126	25	55	12	-	12	0,7059	DQVFIATK SCEIHYGTGS VSGY
328	2	P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	5e-72	32	evm_27.model.AmTr.v1.0_scaffold00067.12	-25,73825	16	53	7	-	6	0,4118	RGQEEGQQE QEQEQEQR VGGEGQQQQ
329	2	Q38814	Thiamine thiazole synthase	<i>Arabidopsis thaliana</i>	AT5G54770	01 Metabolism	01.07 Cofactors	E-133	82	evm_27.model.AmTr.v1.0_scaffold00005.125	-36,84054	33	37,5	10	-	8	1,3000	AAHLALK NIGMIESVPGMK
329	2	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr.v1.0_scaffold00002.657	-33,94699	32	43,5	11	-	10	0,5217	IEMACPHVSG GR
330	4	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr.v1.0_scaffold00002.657	-39,42167	35	43,5	10	-	9	0,5217	ARIEMACPHV GR
330	4	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr.v1.0_scaffold00067.7	-17,26041	12	54,5	4	-	4	0,1905	REGYEGEEQR GEGQIQIIGTN
330	4	P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	5e-72	32	evm_27.model.AmTr.v1.0_scaffold00067.12	-10,84869	12	53	3	-	3	0,1765	RGQEEGQQE QEQEQEQR VGGEGQQQQ
330	4	F4HWR0	Dessication-related protein	<i>Arabidopsis thaliana</i>	AT1G47980	11 Disease/defence	11.05 Stress responses	e-106	70	evm_27.model.AmTr.v1.0_scaffold00016.315	-32,18086	27	33,4	11	-	8	1,0769	GGPPPIGATK TILYEQANK TILYEQANK
331	4	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr.v1.0_scaffold00002.657	-45,05148	41	43,5	11	-	10	0,6957	IEMACPHVSG GR
331	4	P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	5e-72	32	evm_27.model.AmTr.v1.0_scaffold00067.12	-15,9824	15	53	4	-	4	0,2941	AQSDSVFVVG VGGEGQQQQ GIK
331	4	Q39649	2S albumin	<i>Cucurbita maxima</i>		06 Protein destination and storage	06.20 Storage proteins	1,00E-13	35	evm_27.model.AmTr.v1.0_scaffold00005.212	-15,72354	20	16,8	3	-	2	0,4286	SEYLAGGQPR SLMSEAGQGE QQEIQR
331	4	F4HWR0	Dessication-related protein	<i>Arabidopsis thaliana</i>	AT1G47980	11 Disease/defence	11.05 Stress responses	e-106	70	evm_27.model.AmTr.v1.0_scaffold00016.315	-48,72667	44	33,4	12	-	12	1,0769	AEQLPOICGIS IVYSSGNEK GPPIGATK TILYEQANK
332	6	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr.v1.0_scaffold00002.657	-44,4781	39	43,5	14	-	12	0,6957	ARIEMACPHV SGR
332	6	P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	5e-72	32	evm_27.model.AmTr.v1.0_scaffold00067.12	-35,73885	30	53	8	-	8	0,5294	LVITIGEEER RGQEEGQQE QEQEQEQR VGGEGQQQQ
332	6	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr.v1.0_scaffold00067.7	-7,713993	10	54,5	3	-	3	0,1905	ISNQQAQDIK REGYEGEEQR
332	6	Q39649	2S albumin	<i>Cucurbita maxima</i>		06 Protein destination and storage	06.20 Storage proteins	1,00E-13	35	evm_27.model.AmTr.v1.0_scaffold00005.212	-14,49539	26	16,8	3	-	2	0,5714	SLMSEAGQGE QQEIQR SLMSEAGQGE
332	6	F4HWR0	Dessication-related protein	<i>Arabidopsis thaliana</i>	AT1G47980	11 Disease/defence	11.05 Stress responses	e-106	70	evm_27.model.AmTr.v1.0_scaffold00016.315	-63,67746	52	33,4	22	-	17	1,7692	VMNSAFGHK IVYSSGNEK VMNSAFGHK
332	6	O65398	Glyoxalase I (Lactoylglutathione lyase)	<i>Arabidopsis thaliana</i>	AT1G11840	11 Disease/defence	11.06 Detoxification	e-130	78	evm_27.model.AmTr.v1.0_scaffold00037.106	-9,891949	10	33,2	3	-	3	0,2143	LVTQELGGK EPGPIPIGNTK VVFDHSDFL

333	3	Q9SK09	Cupin family protein (Vicilin)	<i>Arabidopsis thaliana</i>	AT2G28490	06 Protein destination and storage	06.20 Storage proteins	e-115	50	evm_27.model.AmTr.v1.0_scaffold00080.82	-29,45175	19	43,1	8	-	6	0,5000	PSAGPIIYMTG AHEPPK LQIICSIDTSE GRQEGYGE EQR QEGEYGEF EQ
333	3	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr.v1.0_scaffold00067.72	-19,83845	12	54,5	6	-	6	0,2857	RGQEEGQQE QEQQ RGQEEGQQE RGQEEGQQE
333	3	P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	5e-72	32	evm_27.model.AmTr.v1.0_scaffold00067.12	-24,89617	16	53	5	-	5	0,4118	RGQEEGQQE QEQQ RGQEEGQQE RGQEEGQQE
334	2	P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	5e-72	32	evm_27.model.AmTr.v1.0_scaffold00067.12	-45,52677	24	53	12	-	8	0,7059	RGQEEGQQE QEQQ RGQEEGQQE RGQEEGQQE
334	2	Q9SK09	Cupin family protein (Vicilin)	<i>Arabidopsis thaliana</i>	AT2G28490	06 Protein destination and storage	06.20 Storage proteins	e-115	50	evm_27.model.AmTr.v1.0_scaffold00080.82	-5,294478	6	43,1	2	-	2	0,1250	LQIICSIDTSE IGHQPFQSFIL GGGR
335	4	P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	5e-72	32	evm_27.model.AmTr.v1.0_scaffold00067.12	-77,37683	28	53	27	-	16	1,7647	VGEGGQQQ GIKDR VGEGGQQQ YNRDQIIFP SSSR
335	4	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr.v1.0_scaffold00067.72	-15,01314	10	54,5	4	2	4	0,1905	QFFIAGGQPR GQGPVIRPSS EQLQLIHGG SGGK
335	4	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr.v1.0_scaffold00002.657	-25,13883	21	43,5	5	-	4	0,3043	VGEGGQQQ GIKDRHOK VGEGGQQQ KGDATIPAGK LVTIGEERDS HNLKK
336	1	P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	5e-72	32	evm_27.model.AmTr.v1.0_scaffold00067.12	-109,5973	32	53	31	-	20	1,9412	VGEGGQQQ GIKDRHOK VGEGGQQQ KGDATIPAGK LVTIGEERDS HNLKK
337	3	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr.v1.0_scaffold00002.657	-35,7267	24	43,5	9	-	8	0,5217	VGEGGQQQ GIKDRHOK VGEGGQQQ KGDATIPAGK LVTIGEERDS HNLKK
337	3	Q39649	2S albumin	<i>Cucurbita maxima</i>		06 Protein destination and storage	06.20 Storage proteins	1,00E-13	35	evm_27.model.AmTr.v1.0_scaffold00005.212	-9,236572	14	16,8	2	-	2	0,2857	FIQTGRPE AEQLPQICGIS QQR
337	3	Q39649	2S albumin	<i>Cucurbita maxima</i>		06 Protein destination and storage	06.20 Storage proteins	5,00E-16	37	evm_27.model.AmTr.v1.0_scaffold00005.215	-9,236572	14	16,8	2	-	2	0,2500	FIQTGRPE AEQLPQICGIS QQR
338	2	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr.v1.0_scaffold00002.657	-15,95001	16	43,5	4	-	3	0,2609	AQSDSVFVVG PR ASQENLQIIC CTTNCGQVTQ R
338	2	Q9SCV3	Beta-galactosidase	<i>Arabidopsis thaliana</i>	AT2G32810	09 Cell structure	09.01 Cell wall	0	68	evm_27.model.AmTr.v1.0_scaffold00117.16	-33,03576	36	27,5	8	-	7	0,6154	GEAWVNGHSI SVAAGMNA MDLR APGFGENR
339	4	P29197	Chaperonin (Chaperonin-60KD, ch60, CPN60)	<i>Arabidopsis thaliana</i>	AT3G23990	06 Protein destination and storage	06.01 Folding and stability	0	86	evm_27.model.AmTr.v1.0_scaffold00003.261	-56,36271	22	61,2	13	-	9	0,4667	ISNQAQDIK GEQIQIGTN GQK
339	4	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr.v1.0_scaffold00067.72	-14,90593	12	54,5	5	-	5	0,2857	RGQEEGQQE QEQQ RGQEEGQQE RGQEEGQQE
339	4	P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	5e-72	32	evm_27.model.AmTr.v1.0_scaffold00067.12	-17,0938	12	53	4	-	4	0,2353	RGQEEGQQE QEQQ RGQEEGQQE RGQEEGQQE
339	4	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr.v1.0_scaffold00002.657	-16,38806	9	43,5	3	-	3	0,1304	LVTIGEER AQSDSVFVVG PR
340	2	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr.v1.0_scaffold00067.72	-74,60673	32	54,5	23	-	15	1,0952	HGGHLKTINR ISNQAQDIK READIYSR
340	2	P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	5e-72	32	evm_27.model.AmTr.v1.0_scaffold00067.12	-16,18923	14	53	4	-	4	0,2353	SFYLAGGQPR SLSLPNFEPAP R
225b	1	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr.v1.0_scaffold00002.657	-223,5644	73	43,5	90	-	44	4,6087	IEMACPHVSG IEMACPH IEMACPH HSGEGSIQH R
246b	3	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	6e-69	31	evm_27.model.AmTr.v1.0_scaffold00067.72	-198,2926	43	54,5	68	-	47	3,7143	RLSDAQCCR SLOKPDFER RGQEEGQQE QEQQ RGQEEGQQE
246b	3	P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	5e-72	32	evm_27.model.AmTr.v1.0_scaffold00067.12	-55,68047	28	53	16	-	12	0,9412	RGQEEGQQE QEQQ RGQEEGQQE RGQEEGQQE
246b	3	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr.v1.0_scaffold00002.657	-59,79795	49	43,5	14	-	11	0,6957	ARIEMACPHV SGGR IEMACPHVSG

256b	2	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	5,00E-54	30	evm_27.model.AmTr.v1.0_scaffold00002.657	-113,5415	45	43,5	46	-	24	2,4783	GKGGGQEIK IEMACPH IEMACPHVSG
256b	2	P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	5e-72	32	evm_27.model.AmTr.v1.0_scaffold00067.12	-48,60043	31	53	11	-	10	0,6471	RGQEEGQQE QEQQEQER RGQEEGQQE

Supplemental table 5: Seed biochemical composition

Percentage are expressed in % of the fresh weight. Starch assay has not been performed as literature reports absence of it (Floyd & Friedman, 2001)

Seed storage type	Protein	Lipid	Hydrosoluble polysaccharides
	18.6	57	2.6
Osborne protein fractions			
Albumin	Globulin	Prolamin	Glutelin
4.35	13.91	0.02	0.36

Supplemental table 6: list of the proteins identified from the albumine fraction of germinating seeds of *Amborella trichopoda* significantly varying during germination

Proteins have been analyzed by two-dimensional electrophoresis and identified by mass spectrometry LC/MS-MS. The protein spots were analysed by LC-MS/MS on the PAPPSO platform (Benoit Valot, Thierry Balliau, Michel Zivy, INRA Moulon, France: <http://pappso.inra.fr>). Based on the spectrum generated, proteins were identified using the X-Tandem software. Image analysis of the scanned 2D gels was carried out with the Progenesis Samespots software (nonlinear dynamics) according to the instruction booklet. After spot detection and background subtraction, 2D gels were aligned and matched and the quantitative determination of the spot volumes was performed. Only spots with an average standardized abundance that varied by a minimum a 1,2 fold (p <0.02) were considered as varying spots. "Samespot ID" relates to the protein identification number automatically attribute to a spot by the software. "Spot ID" relates to the protein position on the 2DE reference map. "Number of id per spot" reflect the number of single identifications in the same spot. "NCBI accession number" is the accession number in NCBI database. "Protein name", "Organism" relates to the organism from which the identified protein comes from for functional analysis - efforts were focus on *Arabidopsis thaliana* as a plant model. "AGI", "Function category" and "Function description" relate to the functional categories defined according to the ontological classification of Bevan et al. [Bevan et al. (1998) Nature 391:485-488]. "log(Evalue) identification" reflects the statistical power of the identification by BLAST (performed on TAIR or BLAST). "Identity" indicates in % the recovery of the *Amborella* protein sequence against the identified protein. "Anova" reflects the power of the statistical test performed by the software to confirm the variation of the spot volume during from the different samples. "Fold" relates to the importance of the variation. "Highest mean" indicates the condition with the higher spot volume. "Lowest mean" indicates the condition with the lower spot volume. "Description" was taken from the *Amborella* EVM 27 Predicted Proteins (<http://www.amborella.org>). The "log (E value)" is a statistical parameter that represents the number of peptides present at random in the database. It was calculated by the product of the Evalue of unique peptides identified in the protein spot (Valot et al., 2011). "Coverage" refers to the recovery rate of the protein by the identified peptides, expressed in %. "MW" relates to the molecular weight expressed in kDa. "Spectra" corresponds to the number of spectra which allowed the protein identification from 2DE protein single spot. "Specifics" corresponds to the number of specific spectrum corresponding to the identification among the other identifications of the group. "Uniques" refers to the number of unique peptides (different sequences) that led to the protein identification. "PAI" is the protein abundance index in the spot. "Peptide sequences" displays identified peptides for each protein spot.

Functional analysis										Samespot @ data				Mass spec data									
Samespot of number	from GMS ?	Number of id per spot	NCBI accession N°	protein name	Organism	AGI	Function category	Function description	log (Evalue) identification	Identity	Anova (p)	Quarta/D MS	GSS/DM S	Quarta/ GSS	Identification	log(Evalue)	Coverage	MW	Spectra	Specifics	Uniques	PAI	Peptide sequences
645		7	A1L4Y4	NADPH:quinone reductase	<i>Arabidopsis thaliana</i>	AT5G61510	11 Disease/defence	11.06 Detoxification	e-136	82	0,000128	1,30225	4,22239	0,30842	evm_27.model.AmTr_v1.0_scaffold00111.28	-4,42E+01	41	40,09999847	14	-	12	0,9333	VGPGLTGR AVGPGLTGR KITNGEVHVV
1036		7	A8MS14	Pathogenesis-related protein	<i>Arabidopsis thaliana</i>	AT1G78780	12 Unclear classification	12 Unclear classification	9,00E-62	67	0,0026609	3,25164	7,27437	0,447	evm_27.model.AmTr_v1.0_scaffold00071.75	-5,77E+00	10	24,70000076	2	-	2	0,1429	HGALPNYD/VN K TMELELYDR YDNCNDNGVD PR DSQGNLVPK
533	126	4	B9DGL8	Alpha-galactosidase	<i>Arabidopsis thaliana</i>	AT5G08370	09 Cell structure	09.01 Cell wall	e-171	75	0,0004666	0,35955	0,17708	2,03047	evm_27.model.AmTr_v1.0_scaffold00171.32	-2,40E+01	16	45,09999847	5	-	5	0,3333	TILYEQANK VDYPYHTISEF TNNISQLR
533	126	4	F4HWR0	Dessication-related protein	<i>Arabidopsis thaliana</i>	AT1G47980	11 Disease/defence	11.05 Stress responses	e-109	82	0,0004666	0,35955	0,17708	2,03047	evm_27.model.AmTr_v1.0_scaffold00016.315	-5,40E+01	34	33,40000153	15	-	8	1,3846	TILYEQANK VDYPYHTISEF TNNISQLR
713	113b	5	F4HWR0	Dessication-related protein	<i>Arabidopsis thaliana</i>	AT1G47980	11 Disease/defence	11.05 Stress responses	e-109	82	0,0019856	0,39246	0,12791	3,06825	evm_27.model.AmTr_v1.0_scaffold00016.315	-4,11E+01	35	33,40000153	9	-	8	0,7692	TILYEQANK VDYPYHTISEF ANLDP LTR
731	124	3	F4HWR0	Dessication-related protein	<i>Arabidopsis thaliana</i>	AT1G47980	11 Disease/defence	11.05 Stress responses	e-109	82	9,55E-05	0,27662	0,17504	1,58028	evm_27.model.AmTr_v1.0_scaffold00016.315	-2,34E+01	21	33,40000153	5	-	4	0,4615	TILYEQANK VDYPYHTISEF TNNISQLR
734	119	3	F4HWR0	Dessication-related protein	<i>Arabidopsis thaliana</i>	AT1G47980	11 Disease/defence	11.05 Stress responses	e-109	82	0,0001252	0,54547	0,15533	3,5117	evm_27.model.AmTr_v1.0_scaffold00016.315	-6,24E+01	43	33,40000153	17	-	14	1,4615	VMNSAFGHK IVYSSGNEK TILYEQANK ANLDP LTR
736	123	6	F4HWR0	Dessication-related protein	<i>Arabidopsis thaliana</i>	AT1G47980	11 Disease/defence	11.05 Stress responses	e-109	82	0,0008994	0,37749	0,30548	1,23571	evm_27.model.AmTr_v1.0_scaffold00016.315	-3,38E+01	27	33,40000153	6	-	6	0,5385	GGPPPIGATK AVQEVGHILR TILYEQANK SPGGFFPK
742	120	5	F4HWR0	Dessication-related protein	<i>Arabidopsis thaliana</i>	AT1G47980	11 Disease/defence	11.05 Stress responses	e-109	82	4,48E-05	0,5563	0,22585	2,46319	evm_27.model.AmTr_v1.0_scaffold00016.315	-3,37E+01	23	33,40000153	7	-	7	0,5385	GGPPPIGATK AVQEVGHILR TILYEQANK VMNSAFGH
757	178	2	F4HWR0	Dessication-related protein	<i>Arabidopsis thaliana</i>	AT1G47980	11 Disease/defence	11.05 Stress responses	e-109	82	0,0050002	0,17494	0,7288	0,24004	evm_27.model.AmTr_v1.0_scaffold00016.315	-5,04E+01	32	33,40000153	17	-	14	1,4615	VMNSAFGH GGPPPIGATK AVQEVGHILR
796	180	2	F4HWR0	Dessication-related protein	<i>Arabidopsis thaliana</i>	AT1G47980	11 Disease/defence	11.05 Stress responses	e-109	82	0,0017072	0,12213	0,24349	0,50157	evm_27.model.AmTr_v1.0_scaffold00016.315	-9,65E+01	37	33,40000153	25	-	20	2,1538	VMNSAFGSHK KVDYPYH PPPIGATK
821	170	4	F4HWR0	Dessication-related protein	<i>Arabidopsis thaliana</i>	AT1G47980	11 Disease/defence	11.05 Stress responses	e-109	82	0,0172238	0,44096	0,44829	0,98364	evm_27.model.AmTr_v1.0_scaffold00016.315	-2,70E+01	13	33,40000153	6	-	3	0,4615	RISGNLLASDQ FSLSFDRTPQ EILR
782		9	F4HWR0	Dessication-related protein	<i>Arabidopsis thaliana</i>	AT1G47980	11 Disease/defence	11.05 Stress responses	e-109	82	0,0006529	0,74675	3,14802	0,23721	evm_27.model.AmTr_v1.0_scaffold00016.315	-1,79E+01	11	33,40000153	3	-	3	0,2308	TILYEQANK PLLDLSENFA K
407		14	F4HWR0	Dessication-related protein	<i>Arabidopsis thaliana</i>	AT1G47980	11 Disease/defence	11.05 Stress responses	e-109	82	0,0092583	1,69181	1,84846	0,91526	evm_27.model.AmTr_v1.0_scaffold00016.315	-7,22E+00	12	33,40000153	3	-	3	0,2308	TILYEQANK LGGIQRQDEGIT VMNSAFGHK
768		6	F4HWR0	Dessication-related protein	<i>Arabidopsis thaliana</i>	AT1G47980	11 Disease/defence	11.05 Stress responses	e-109	82	0,0010332	1,85717	5,783	0,32114	evm_27.model.AmTr_v1.0_scaffold00016.315	-6,66E+01	46	33,40000153	16	-	15	1,3846	VMNSAFGH AVQEVGHILR TILYEQANK
789		7	F4HWR0	Dessication-related protein	<i>Arabidopsis thaliana</i>	AT1G47980	11 Disease/defence	11.05 Stress responses	e-109	82	0,017244	1,64782	1,94	0,84939	evm_27.model.AmTr_v1.0_scaffold00016.315	-7,72E+00	13	33,40000153	3	-	3	0,2308	TILYEQANK VDYPYHTISEF TNNISQLR
790		8	F4HWR0	Dessication-related protein	<i>Arabidopsis thaliana</i>	AT1G47980	11 Disease/defence	11.05 Stress responses	e-109	82	5,26E-05	1,00671	3,80321	0,2647	evm_27.model.AmTr_v1.0_scaffold00016.315	-1,97E+01	17	33,40000153	5	-	5	0,3846	GGPPPIGATK TILYEQANK PLLDLSENFA K
808		9	F4HWR0	Dessication-related protein	<i>Arabidopsis thaliana</i>	AT1G47980	11 Disease/defence	11.05 Stress responses	e-109	82	0,0012118	3,14897	4,15446	0,75797	evm_27.model.AmTr_v1.0_scaffold00016.315	-1,59E+01	11	33,40000153	3	-	3	0,2308	TILYEQANK PLLDLSENFA K
818		7	F4HWR0	Dessication-related protein	<i>Arabidopsis thaliana</i>	AT1G47980	11 Disease/defence	11.05 Stress responses	e-109	82	0,0072403	1,69716	3,47994	0,4877	evm_27.model.AmTr_v1.0_scaffold00016.315	-3,05E+01	20	33,40000153	6	-	6	0,4615	TILYEQANK ANLDP LTR PLLDLSENFA K
828		6	F4HWR0	Dessication-related protein	<i>Arabidopsis thaliana</i>	AT1G47980	11 Disease/defence	11.05 Stress responses	e-109	82	0,014279	0,94689	1,68458	0,56209	evm_27.model.AmTr_v1.0_scaffold00016.315	-1,44E+01	14	33,40000153	4	-	3	0,3077	TILYEQANK VDYPYHTISEF TNNISQLR
68		1	F4I3R2	Peptidase M1 family protein	<i>Arabidopsis thaliana</i>	AT1G63770	06 Protein destination and storage	06.13 Proteolysis	0,00E+00	85	0,0045623	3,8802	2,9084	1,33417	evm_27.model.AmTr_v1.0_scaffold00009.158	-7,11E+01	22	100	15	-	14	0,4146	VTGCHLEADK TAIAQNPGEAR DQFFSSDMGS
145		4	F4I3V3	Protein kinase domain-containing protein	<i>Arabidopsis thaliana</i>	AT1G69910	10 Signal transduction	10.0404 Kinases	1,00E-86	52	0,0018854	2,07447	0,8712	2,38116	evm_27.model.AmTr_v1.0_scaffold00002.280	-4,25E+00	7	64	2	-	2	0,0769	GGPPSPVQAV VHSPSSQH TYRLTQASDV

451	2	F4I529	Calreticulin	<i>Arabidopsis thaliana</i>	AT1G56340	06 Protein destination and storage	06.01 Folding and stability	e-164	89	0,0069263	1,29014	4,40772	0,2927	evm_27.model.AmTr.v1.0_scaffold00003.10	-1,18E+02	57	44,9000153	27	-	25	1,0345	IKNPNYQGK LDCGGGYMK KPEPVIADKK	
1070	4	F4ID64	Peroxioredoxin	<i>Arabidopsis thaliana</i>	AT1G65980	11 Disease/defence	11.06 Detoxification	7,00E-31	72	0,0050128	2,36229	4,83628	0,48858	evm_27.model.AmTr.v1.0_scaffold00109.90	-1,78E+01	28	15,69999981	5	-	4	0,7143	KRVGFIAQEE LK SFFDENNSLQ	
407	14	F4IQK5	Cupin-like protein	<i>Arabidopsis thaliana</i>	AT2G18540	06 Protein destination and storage	06.20 Storage proteins	8,00E-82	62	0,0092583	1,69181	1,84846	0,91526	evm_27.model.AmTr.v1.0_scaffold00059.63	-8,83E+00	7	44,09999847	3	-	3	0,1765	VESVEYDGS EK SGSVEYVQSK ANSYSVHGSA	
145	4	F4IW47	Transketolase (chloroplastic)	<i>Arabidopsis thaliana</i>	AT2G45290	02 Energy	02.07 Pentose phosphate	0,00E+00	87	0,0018854	2,07447	0,8712	2,38116	evm_27.model.AmTr.v1.0_scaffold00009.433	-7,45E+01	23	81,30000305	12	-	11	0,4667	GGYIVSDNSM LQAK	
467	11	F4IW47	Transketolase (chloroplastic)	<i>Arabidopsis thaliana</i>	AT2G45290	02 Energy	02.07 Pentose phosphate	0,00E+00	87	0,0173342	0,83843	2,86452	0,29269	evm_27.model.AmTr.v1.0_scaffold00009.433	-3,57E+01	16	81,30000305	9	-	9	0,3333	KRRPSVLALSR RPSVLALSR HVSEGASLEA	
1002	14	F4IW47	Transketolase (chloroplastic)	<i>Arabidopsis thaliana</i>	AT2G45290	02 Energy	02.07 Pentose phosphate	0,00E+00	87	0,0179685	1,00507	2,65214	0,37896	evm_27.model.AmTr.v1.0_scaffold00009.433	-2,67E+01	9	81,30000305	5	-	5	0,1667	YKEEAEFK ALPVTYAESPA DATR	
675	8	F4J2Z7	Short-chain dehydrogenase reductase	<i>Arabidopsis thaliana</i>	AT3G29250	12 Unclear classification	12 Unclear classification	1,00E-33	50	6,01E-05	4,28718	3,84318	1,11553	evm_27.model.AmTr.v1.0_scaffold00030.217	-1,85E+01	16	22,39999962	5	2	4	0,6250	ALYASDDAK AEDIAQAALYL ASDDAK	
689	9	F4J2Z7	Short-chain dehydrogenase reductase	<i>Arabidopsis thaliana</i>	AT3G29250	12 Unclear classification	12 Unclear classification	1,00E-33	50	3,23E-06	0,86804	4,88286	1,65232	evm_27.model.AmTr.v1.0_scaffold00030.217	-1,44E+01	11	22,39999962	3	2	3	0,5000	AALYLASDDAK AEDIAQAALYL ASDDAK	
1018	9	F4K000	Metal-dependent protein hydrolase	<i>Arabidopsis thaliana</i>	AT5G41970	12 Unclear classification	12 Unclear classification	e-150	79	7,51E-05	2,87435	3,95283	0,72716	evm_27.model.AmTr.v1.0_scaffold00027.80	-7,49E+00	8	40,5	3	-	3	0,1500	FADAEVVR ELQLEEGHPD VDR	
944	8	F4K5S5	SRP/BCC ligand-binding domain-containing protein	<i>Arabidopsis thaliana</i>	AT5G28010	12 Unclear classification	12 Unclear classification	2,20E-02	55	0,003015	0,69549	7,23177	0,09617	evm_27.model.AmTr.v1.0_scaffold00048.12	-1,23E+01	23	17	2	-	2	0,7500	LEIEKPGGIS VVK ISADAWDVY	
407	14	O04005	1-Cys peroxiredoxin	<i>Arabidopsis thaliana</i>	AT1G48130	11 Disease/defence	11.05 Stress responses	1,00E-88	82	0,0092583	1,69181	1,84846	0,91526	evm_27.model.AmTr.v1.0_scaffold00045.37	-1,17E+01	13	24,20000076	2	-	2	0,1818	PGLTGDIPNI EADSSHGR ALPDLIAAK	
926	6	O04005	1-Cys peroxiredoxin	<i>Arabidopsis thaliana</i>	AT1G48130	11 Disease/defence	11.05 Stress responses	1,00E-88	82	0,0110232	2,96598	2,57879	1,15015	evm_27.model.AmTr.v1.0_scaffold00045.37	-1,46E+01	23	24,20000076	3	-	3	0,3636	ALHIVSGFK LSFLYPGTTGR DIEAYTPGSNV	
407	14	O23029	AWPM-19-like family protein	<i>Arabidopsis thaliana</i>	AT1G04560	06 Protein destination and storage	06.01 Folding and stability	5,00E-50	77	0,0092583	1,69181	1,84846	0,91526	evm_27.model.AmTr.v1.0_scaffold00039.123	-1,47E+01	12	18,60000038	2	-	2	0,6667	DPDYGAGAAA DPAAPK NGGVYRDPDY	
740	4	O23255	Adenosylhomocysteine hydrolase	<i>Arabidopsis thaliana</i>	AT4G13940	01 Metabolism	01.01 Amino Acid	0,00E+00	92	0,0009213	1,2946	3,94075	0,32852	evm_27.model.AmTr.v1.0_scaffold00013.277	-4,78E+01	25	53	15	-	11	0,8889	AEEFEFK RLVGSEITTT GVK	
979	3	O23255	Adenosylhomocysteine hydrolase	<i>Arabidopsis thaliana</i>	AT4G13940	01 Metabolism	01.01 Amino Acid	0,00E+00	92	0,0002014	2,38364	3,23999	0,73569	evm_27.model.AmTr.v1.0_scaffold00013.277	-7,86E+00	4	53	2	-	2	0,1111	LIVGSEITTT GVK TEEGSQPEFK	
743	7	O23255	Adenosylhomocysteine hydrolase	<i>Arabidopsis thaliana</i>	AT4G13940	01 Metabolism	01.01 Amino Acid	0,00E+00	92	0,0033999	0,72625	3,326	0,21836	evm_27.model.AmTr.v1.0_scaffold00013.277	-3,21E+01	20	53	7	-	5	0,5000	DMSQADFGR DSAADFVAK GFTLQEVWY	
1037	1	O23443	Fumarylacetoacetate hydrolase-like protein	<i>Arabidopsis thaliana</i>	AT4G15940	01 Metabolism	01.01 Amino Acid	e-100	90	0,0015442	0,56374	3,05468	0,18455	evm_27.model.AmTr.v1.0_scaffold00183.26	-7,37E+01	69	23,79999924	21	-	16	2,7500	DKRFSYSLON ALALDMTAR NYAAHAKELG	
768	6	O48587	Halocacid dehalogenase-like hydrolase	<i>Arabidopsis thaliana</i>	AT5G44730	11 Disease/defence	11.06 Detoxification	e-116	90	0,0010332	1,85717	5,783	0,32114	evm_27.model.AmTr.v1.0_scaffold00032.206	-1,34E+01	9	29,20000076	2	-	2	0,1538	AGYDYDOEIF EK GVNIGVSNAE	
882	187	2	O48646	Glutathione peroxidase	<i>Arabidopsis thaliana</i>	AT4G11600	11 Disease/defence	11.06 Detoxification	4e-78	67	0,000333	0,25229	0,10625	2,37449	evm_27.model.AmTr.v1.0_scaffold00009.277	-2,45E+01	40	18,89999962	6	-	6	0,8889	VEVNSDNATP VYK DOTSVHDETIV
230	25	2	O49299	Phosphoglucomutase	<i>Arabidopsis thaliana</i>	AT1G23190	02 Energy	02.01 Glycolysis	0,00E+00	89	0,0021759	0,24941	0,27765	0,89829	evm_27.model.AmTr.v1.0_scaffold00010.123	-6,85E+01	39	63,70000076	18	-	17	0,6897	LSGTGSEGATI R ETSPIQSOKPG
269	6	O49485	Phosphoglycerate dehydrogenase	<i>Arabidopsis thaliana</i>	AT4G34200	01 Metabolism	01.01 Amino Acid	0,00E+00	82	0,0024029	1,40422	0,8639	1,62545	evm_27.model.AmTr.v1.0_scaffold00051.53	-1,09E+01	3	65,19999695	2	-	2	0,1034	APDLDLDR LAVQLVAGGS GVK	
982	3	O50008	^S -methyltetrahydropteroyl tripartamate-	<i>Arabidopsis thaliana</i>	AT5G17920	01 Metabolism	01.01 Amino Acid	0,00E+00	92	0,0100551	3,05388	2,72367	1,12123	evm_27.model.AmTr.v1.0_scaffold00004.99	-7,78E+01	34	84,5	21	-	21	0,6970	ISODEYVK TSDI/ANETK	
537	95	6	O50008	^S -methyltetrahydropteroyl tripartamate-	<i>Arabidopsis thaliana</i>	AT5G17920	01 Metabolism	01.01 Amino Acid	0,00E+00	92	0,0002003	0,09174	0,1778	0,51598	evm_27.model.AmTr.v1.0_scaffold00004.99	-2,78E+01	7	84,5	5	-	5	0,1515	ASHIVGYPR GNASPLAMEM TK
828	6	O50008	^S -methyltetrahydropteroyl tripartamate-	<i>Arabidopsis thaliana</i>	AT5G17920	01 Metabolism	01.01 Amino Acid	0,00E+00	92	0,014279	0,94689	1,68458	0,56209	evm_27.model.AmTr.v1.0_scaffold00004.99	-8,73E+00	4	84,5	3	-	3	0,0909	IPTDEIADR YGAGIGPGVY DIHSR	
583	10	O64640	Carboxylesterase (probable)	<i>Arabidopsis thaliana</i>	AT2G45600	11 Disease/defence	11.02 Defence-related	1,00E-64	57	0,0182765	1,25654	2,01037	0,62503	evm_27.model.AmTr.v1.0_scaffold00001.438	-1,84E+01	19	32,59999847	4	-	4	0,2500	ALNEDLQAK ATTFDPPC NADGR	
799	8	O65282	Chaperonin (20 kDa, Cpn21)	<i>Arabidopsis thaliana</i>	AT5G20720	06 Protein destination and storage	06.01 Folding and stability	e-102	83	0,0125632	1,10491	2,40277	0,45985	evm_27.model.AmTr.v1.0_scaffold00007.333	-3,57E+01	33	26,39999962	11	-	9	0,9231	SKPGQGEVA VGEK PQGGGEVAWG	
808	9	O65282	Chaperonin (20 kDa, Cpn21)	<i>Arabidopsis thaliana</i>	AT5G20720	06 Protein destination and storage	06.01 Folding and stability	e-102	83	0,0012118	3,14897	4,15446	0,75797	evm_27.model.AmTr.v1.0_scaffold00007.333	-6,64E+01	63	26,39999962	16	-	15	1,3077	RGAGIYSK NKVEISVK SKPGQGEVA	
810	12	O65282	Chaperonin (20 kDa, Cpn21)	<i>Arabidopsis thaliana</i>	AT5G20720	06 Protein destination and storage	06.01 Folding and stability	e-102	83	0,0021851	1,58254	4,0931	0,38864	evm_27.model.AmTr.v1.0_scaffold00007.333	-1,01E+01	17	26,39999962	3	-	3	0,2308	PQGGGEVAWG EGK EGGAILPITA	
1036	7	O65282	Chaperonin (20 kDa, Cpn21)	<i>Arabidopsis thaliana</i>	AT5G20720	06 Protein destination and storage	06.01 Folding and stability	e-102	83	0,0026609	3,25164	7,27437	0,447	evm_27.model.AmTr.v1.0_scaffold00007.333	-1,96E+01	18	26,39999962	4	-	4	0,3077	AGAQVYSK PQGGGEVAWG EGK	
713	113b	5	O65398	Lactylglutathione lyase-like protein	<i>Arabidopsis thaliana</i>	AT1G11840	11 Disease/defence	11.06 Detoxification	e-130	78	0,0019856	0,39246	0,12791	3,06825	evm_27.model.AmTr.v1.0_scaffold00037.106	-3,98E+01	23	33,20000076	8	-	7	0,6429	LVTQELGK AATEQVVK VTLAMMGYAE
734	119	3	O65398	Lactylglutathione lyase-like protein	<i>Arabidopsis thaliana</i>	AT1G11840	11 Disease/defence	11.06 Detoxification	e-130	78	0,0001252	0,54547	0,15533	3,5117	evm_27.model.AmTr.v1.0_scaffold00037.106	-1,06E+02	57	33,20000076	31	29	23	2,4286	ISDNPAVK MGYAEK KDKHREHAV

736	123	6	O65398	Lactoylglutathione lyase-like protein	<i>Arabidopsis thaliana</i>	AT1G11840	11 Disease/defence	11.06 Detoxification	e-130	78	0,000894	0,37749	0,30548	1,23571	evm_27.model.AmTr.v1.0_scaffold00037.106	-2,26E+01	21	33,20000076	6	-	5	0,5714	EPGPPIGINTK FYTECFGMK NTLMMGYAE K
742	120	5	O65398	Lactoylglutathione lyase-like protein	<i>Arabidopsis thaliana</i>	AT1G11840	11 Disease/defence	11.06 Detoxification	e-130	78	4,48E-05	0,5563	0,22585	2,46319	evm_27.model.AmTr.v1.0_scaffold00037.106	-2,33E+01	25	33,20000076	4	-	4	0,5000	ISDNPAYK YGVTEYTK NTLMMGYAE K
661	1	1	O65398	Lactoylglutathione lyase-like protein	<i>Arabidopsis thaliana</i>	AT1G11840	11 Disease/defence	11.06 Detoxification	e-130	78	9,96E-05	1,08968	5,35699	0,20341	evm_27.model.AmTr.v1.0_scaffold00037.106	-7,37E+01	45	37,20000076	16	-	14	1,2000	EPGPPIGINTK FYTECFGMK NTLMMGYAE K
675	8	8	O65398	Lactoylglutathione lyase-like protein	<i>Arabidopsis thaliana</i>	AT1G11840	11 Disease/defence	11.06 Detoxification	e-130	87	6,01E-05	4,28718	3,84318	1,11553	evm_27.model.AmTr.v1.0_scaffold00037.106	-6,84E+01	38	37,20000076	11	-	11	0,7333	EPGPPIGINTK FYTECFGMK NTLMMGYAE K
689	9	9	O65398	Lactoylglutathione lyase-like protein	<i>Arabidopsis thaliana</i>	AT1G11840	11 Disease/defence	11.06 Detoxification	e-130	78	3,23E-06	8,06804	4,88286	1,65232	evm_27.model.AmTr.v1.0_scaffold00037.106	-3,74E+01	21	37,20000076	5	-	5	0,3333	VVFVDHSDFL K FGFHAIATED D
663	2	2	O65423	NADPH quinone oxidoreductase	<i>Arabidopsis thaliana</i>	AT4G21580	02 Energy	02.13 Respiration	e-138	84	0,004841	1,94845	2,43558	0,79989	evm_27.model.AmTr.v1.0_scaffold00003.350	-7,03E+01	52	34,59999847	17	-	13	1,1250	IMESSTHIGK QIOEVEDPK NLDSLNMDGR K
802	8	8	O80889	Dienelactone hydratase domain-containing protein	<i>Arabidopsis thaliana</i>	AT2G32520	11 Disease/defence	11.06 Detoxification	e-109	87	0,0053343	1,5642	3,66597	0,42668	evm_27.model.AmTr.v1.0_scaffold00014.87	-3,25E+01	21	29,5	6	-	6	0,6667	AFMTTSPFV K SSGVPEYVHI V
833	6	6	O81235	Superoxide dismutase (Mn)	<i>Arabidopsis thaliana</i>	AT3G10920	11 Disease/defence	11.06 Detoxification	8,00E-76	79	0,0133914	4,64276	2,00655	2,31381	evm_27.model.AmTr.v1.0_scaffold00077.26	-1,33E+01	14	22,39999962	2	-	2	0,2500	GDASSTVLO Q SAIK E TLSNFTTANO K
1039	2	2	O81235	Superoxide dismutase (Mn)	<i>Arabidopsis thaliana</i>	AT3G10920	11 Disease/defence	11.06 Detoxification	8,00E-76	79	4,42E-05	2,22255	5,47811	0,40572	evm_27.model.AmTr.v1.0_scaffold00077.26	-1,38E+01	21	22,39999962	3	-	3	0,3750	EPKK GDASSTVLO Q
97	1	1	O81644	Villin-2	<i>Arabidopsis thaliana</i>	AT2G41740	09 Cell structure	09.04 Cytoskeleton	0,00E+00	74	0,012987	2,9895	0,7035	4,24968	evm_27.model.AmTr.v1.0_scaffold00025.405	-1,07E+02	26	101,5999985	22	-	20	0,5000	AAAGNSFEK K VTOLEDR K LANTMTNSI K
1039	2	2	O81830	Quinone reductase family protein	<i>Arabidopsis thaliana</i>	AT4G27270	12 Unclear classification	12 Unclear classification	1,00E-94	88	4,42E-05	2,22255	5,47811	0,40572	evm_27.model.AmTr.v1.0_scaffold00043.710	-6,89E+01	58	21,60000038	17	-	12	3,8000	YSMYGHVEK SMYGHVEK EGMMAAQFK K
768	6	6	O81862	Glycosyl hydrolase family protein(chitinase domain)	<i>Arabidopsis thaliana</i>	AT4G19810	11 Disease/defence	11.02 Defence-related	6,00E-03	44	0,0010332	1,85717	5,783	0,32114	evm_27.model.AmTr.v1.0_scaffold00023.130	-5,18E+01	31	35	8	-	8	0,6154	NALSISGGDFV K SDSDTFAECIG K
647	106	3	O81884	L-galactose dehydrogenase	<i>Arabidopsis thaliana</i>	AT4G33670	01 Metabolism	01.05 Sugars and polysaccharides	e-135	75,00	0,0049465	0,22485	0,1798	1,25058	evm_27.model.AmTr.v1.0_scaffold00033.28	-7,19E+00	12	34,5	3	-	3	0,3333	ALQSNVPR ENVSSALEISS AEK
600	6	6	O82399	Malate dehydrogenase	<i>Arabidopsis thaliana</i>	AT2G22780	02 Energy	02.10 TCA pathway	e-161	86	0,0178552	5,14912	4,89334	1,05227	evm_27.model.AmTr.v1.0_scaffold00033.38	-1,58E+01	13	37,29999924	4	1	4	0,3333	IQNGGTEVVE AK
645	7	7	O82399	Malate dehydrogenase	<i>Arabidopsis thaliana</i>	AT2G22780	02 Energy	02.10 TCA pathway	e-161	86	0,000128	1,30225	4,22239	0,30842	evm_27.model.AmTr.v1.0_scaffold00033.38	-1,68E+01	12	37,29999924	3	-	3	0,2000	GGAEFIYPLG K
432	4	4	P05466	3-phosphoshikimate 1-carboxyvinyltransferase (chloroplastic)	<i>Arabidopsis thaliana</i>	AT2G45300	01 Metabolism	01.01 Amino Acid	0,00E+00	83	0,0133909	2,25306	1,32966	1,69447	evm_27.model.AmTr.v1.0_scaffold00069.12	-9,42E+01	39	55,09999847	23	-	20	1,0000	ASALASPSK AIVEGGGHF PVGK
510	9	9	P06525	Alcohol dehydrogenase	<i>Arabidopsis thaliana</i>	AT1G7120	02 Energy	02.16 Fermentation	e-159	71	0,0003295	2,01724	2,58062	0,78169	evm_27.model.AmTr.v1.0_scaffold00071.65	-4,52E+00	7	41,09999847	2	-	2	1,88E-01	GTFFGNYKPR IGVDVNP
1004	77	2	P06525	Alcohol dehydrogenase	<i>Arabidopsis thaliana</i>	AT1G7120	02 Energy	02.16 Fermentation	e-159	71	0,0035325	0,58442	0,31418	1,86015	evm_27.model.AmTr.v1.0_scaffold00071.65	-8,34E+01	52	34,20000076	27	-	17	2,2500	GVMLSDGK GVMLSDGK GVMLSDGK
321	131	5	P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	1,00E-70	52	0,0023794	0,45958	0,32038	1,43448	evm_27.model.AmTr.v1.0_scaffold00067.12	-1,65E+01	8	53	3	-	2	0,1765	RGQEEGQOE QOEQOEQOE QOEQOEQOE GISIVFPGCTE K
424	9	9	P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	1,00E-70	52	0,0156606	1,00376	0,52462	1,91332	evm_27.model.AmTr.v1.0_scaffold00067.12	-5,61E+01	32	53	17	-	15	1,1765	RGQEEGQOE QOEQOEQOE QOEQOEQOE RGQEEGQOE K
742	120	5	P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	1,00E-70	52	4,48E-05	0,5563	0,22585	2,46319	evm_27.model.AmTr.v1.0_scaffold00067.12	-5,14E+01	31	53	9	-	9	0,5294	RGQEEGQOE QOEQOEQOE QOEQOEQOE VGGEGQQQQ K
407	14	14	P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	1,00E-70	52	0,0092583	1,69181	1,84846	0,91526	evm_27.model.AmTr.v1.0_scaffold00067.12	-1,38E+02	48	53	44	-	31	2,9412	GKDRHOK RGQEEGQOE K
675	8	8	P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	1,00E-70	52	6,01E-05	4,28718	3,84318	1,11553	evm_27.model.AmTr.v1.0_scaffold00067.12	-3,25E+01	15	53	6	-	6	0,3529	RGQEEGQOE QOEQOEQOE QOEQOEQOE GOEFGQOFO K
793	12	12	P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	1,00E-70	52	0,0010663	2,43627	6,5698	0,37083	evm_27.model.AmTr.v1.0_scaffold00067.12	-2,23E+01	12	53	4	-	4	0,2353	RGQEEGQOE QOEQOEQOE QOEQOEQOE VGGEGQQQQ K
810	12	12	P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	1,00E-70	52	0,0021851	1,58254	4,0931	0,38664	evm_27.model.AmTr.v1.0_scaffold00067.12	-5,03E+01	24	53	12	-	11	0,7059	RGQEEGQOE QOEQOEQOE QOEQOEQOE VGGEGQQQQ K
1066	4	4	P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	1,00E-70	52	0,0002698	3,70566	10,3468	0,35815	evm_27.model.AmTr.v1.0_scaffold00067.12	-7,66E+00	5	53	2	-	2	0,1176	RGQEEGQOE QOEQOEQOE SEYLAGGQPR K
944	8	8	P15455	12S Globulin (cruciferin 4)	<i>Arabidopsis thaliana</i>	AT5G44120	06 Protein destination and storage	06.20 Storage proteins	1,00E-70	52	0,0003015	0,69549	7,23177	0,09617	evm_27.model.AmTr.v1.0_scaffold00067.12	-7,53E+00	5	53	2	-	2	0,1176	RGQEEGQOE QOEQOEQOE SEYLAGGQPR K
926	6	6	P19036	HSP17.4 (class 1 small heat shock protein)	<i>Arabidopsis thaliana</i>	AT3G46230	06 Protein destination and storage	06.01 Folding and stability	2,00E-48	76	0,0110232	2,96598	2,57879	1,15015	evm_27.model.AmTr.v1.0_scaffold00165.36	-6,65E+01	60	18,10000038	26	24	20	6,5000	LPENKQVDEV K LPENKQVDFV K VLOISGER K
1065	4	4	P19036	HSP17.4 (class 1 small heat shock protein)	<i>Arabidopsis thaliana</i>	AT3G46230	06 Protein destination and storage	06.01 Folding and stability	2,00E-48	76	0,0005017	4,67039	8,73697	0,53455	evm_27.model.AmTr.v1.0_scaffold00165.36	-7,13E+00	13	18,10000038	2	-	2	0,5000	ATMENGLTV TVPK K
926	6	6	P19037	HSP18.1 (small heat shock protein family)	<i>Arabidopsis thaliana</i>	AT5G59720	06 Protein destination and storage	06.01 Folding and stability	2,00E-43	56	0,0110232	2,96598	2,57879	1,15015	evm_27.model.AmTr.v1.0_scaffold00009.199	-1,60E+01	20	18,60000038	5	3	4	1,2500	AAIENGVLTV TVPK ADLPGLKFE K
929	2	2	P19037	HSP18.1 (small heat shock protein family)	<i>Arabidopsis thaliana</i>	AT5G59720	06 Protein destination and storage	06.01 Folding and stability	1,00E-46	77	0,0085309	14,9086	9,38328	1,58885	evm_27.model.AmTr.v1.0_scaffold00136.4	-1,00E+01	16	17,79999924	2	-	2	0,5000	GTDDVAPFV NAR ATMETGVLTV K

331	8	P19171	Pathogenesis-related protein 3 (endochitinase)	<i>Arabidopsis thaliana</i>	AT3G12500	11 Disease/defence	11.02 Defence-related	e-116	75	0,0076661	1,16096	0,33556	3,45981	evm_27.model.AmTr.v1.0_scaffold00001.2.85	-4,15E+01	25	34,20000076	6	-	6	0,5455	DRGGVACAG GLCCSK GGVACAGGLC AIGFDGSIKRF AVATDAVISFK VPGYGVITNIN	
583	10	P19171	Pathogenesis-related protein 3 (endochitinase)	<i>Arabidopsis thaliana</i>	AT3G12500	11 Disease/defence	11.02 Defence-related	e-116	75	0,0182765	1,26554	2,01037	0,62503	evm_27.model.AmTr.v1.0_scaffold00001.2.85	-4,19E+01	32	34,20000076	9	-	7	0,8182	GGVACAGGLC CSK SFFPAGTTGD TATQK VPGYGVITNIN	
689	9	P19171	Pathogenesis-related protein 3 (endochitinase)	<i>Arabidopsis thaliana</i>	AT3G12500	11 Disease/defence	11.02 Defence-related	e-116	75	3,23E-06	8,06804	4,88286	1,65232	evm_27.model.AmTr.v1.0_scaffold00001.2.85	-2,42E+01	26	34,20000076	5	-	5	0,4545	GGVACAGGLC CSK SFFPAGTTGD TATQK VPGYGVITNIN	
740	4	P19171	Pathogenesis-related protein 3 (endochitinase)	<i>Arabidopsis thaliana</i>	AT3G12500	11 Disease/defence	11.02 Defence-related	e-116	75	0,0009213	1,2946	3,94075	0,32852	evm_27.model.AmTr.v1.0_scaffold00001.2.85	-5,82E+00	11	34,20000076	2	-	2	0,1818	WTPSAADR SFFPAGTTGD TATQK VPGYGVITNIN	
810	12	P19171	Pathogenesis-related protein 3 (endochitinase)	<i>Arabidopsis thaliana</i>	AT3G12500	11 Disease/defence	11.02 Defence-related	e-116	75	0,0021851	1,58254	4,0931	0,38664	evm_27.model.AmTr.v1.0_scaffold00001.2.85	-3,13E+01	23	34,20000076	5	-	5	0,4545	WTPSAADR SFFPAGTTGD TATQK	
982	3	P19171	Pathogenesis-related protein 3 (endochitinase)	<i>Arabidopsis thaliana</i>	AT3G12500	11 Disease/defence	11.02 Defence-related	e-116	75	0,0100551	3,05388	2,72367	1,12123	evm_27.model.AmTr.v1.0_scaffold00001.2.85	-1,05E+01	14	34,20000076	3	-	3	0,2727	WTPSAADR GNGFYTYSAFI TAAK	
1028	4	P19171	Pathogenesis-related protein 3 (endochitinase)	<i>Arabidopsis thaliana</i>	AT3G12500	11 Disease/defence	11.02 Defence-related	e-116	75	0,0055659	6,06452	9,66228	0,62765	evm_27.model.AmTr.v1.0_scaffold00001.2.85	-3,36E+02	86	34,20000076	88	65	62	8,3636	CLECGHSSDA R GGLECGHSSD	
1028	4	P19171	Pathogenesis-related protein 3 (endochitinase)	<i>Arabidopsis thaliana</i>	AT3G12500	11 Disease/defence	11.02 Defence-related	2,00E-53	68	0,0055659	6,06452	9,66228	0,62765	evm_27.model.AmTr.v1.0_scaffold00001.2.85	-3,72E+01	20	21,60000038	15	1	9	2,3750	VLAQNCCKDR GGVACAGGLC CSK	
1028	4	P19171	Pathogenesis-related protein 3 (endochitinase)	<i>Arabidopsis thaliana</i>	AT3G12500	11 Disease/defence	11.02 Defence-related	e-112	77	0,0055659	6,06452	9,66228	0,62765	evm_27.model.AmTr.v1.0_scaffold00001.2.82	-5,65E+01	25	35,59999847	15	1	12	1,0667	TTOKKEIAAFL AQTSK	
1028	4	P19171	Pathogenesis-related protein 3 (endochitinase)	<i>Arabidopsis thaliana</i>	AT3G12500	11 Disease/defence	11.02 Defence-related	3,00E-35	66	0,0055659	6,06452	9,66228	0,62765	evm_27.model.AmTr.v1.0_scaffold00001.2.88	-2,48E+01	16	20,79999924	8	1	5	1,4286	SFFPAGTTGD TTTRKR	
1036	7	P19171	Pathogenesis-related protein 3 (endochitinase)	<i>Arabidopsis thaliana</i>	AT3G12500	11 Disease/defence	11.02 Defence-related	e-116	75	0,0026609	3,25164	7,27437	0,447	evm_27.model.AmTr.v1.0_scaffold00001.2.85	-1,57E+01	18	34,20000076	3	-	3	0,3636	DRGGVACAG GLCCSK SFFPAGTTGD EKLLEADIER VGAATELETE DRK	
252	3	P21238	Chaperonin (Chaperonin-60kD, ch60, CPN60)	<i>Arabidopsis thaliana</i>	AT2G28000	06 Protein destination and storage	06.01 Folding and stability	0,00E+00	93	0,0016951	4,19739	3,87379	1,08354	evm_27.model.AmTr.v1.0_scaffold00009.2.7	-1,61E+02	53	61,09999847	38	-	30	1,3793	VGAATELETE DRK	
1066	4	P21238	Chaperonin (Chaperonin-60kD, ch60, CPN60)	<i>Arabidopsis thaliana</i>	AT2G28000	06 Protein destination and storage	06.01 Folding and stability	0,00E+00	93	0,0002698	3,70566	10,3468	0,35815	evm_27.model.AmTr.v1.0_scaffold00009.2.7	-5,92E+00	6	61,09999847	2	-	2	0,0690	VGAATELETE DR DSSRAALQA HAGDLGNVTV GEDGTANF HAGDLGNVTV	
269	6	P24704	Superoxide dismutase (Cu/Zn)	<i>Arabidopsis thaliana</i>	AT1G08830	11 Disease/defence	11.06 Detoxification	2,00E-74	84	0,0024029	1,40422	0,8639	1,62545	evm_27.model.AmTr.v1.0_scaffold00057.1.30	-1,48E+01	20	17,79999924	4	-	4	0,8000	AVVHVADPPD LCK HAGDLGNVTV	
944	8	P24704	Superoxide dismutase (Cu/Zn)	<i>Arabidopsis thaliana</i>	AT1G08830	11 Disease/defence	11.06 Detoxification	2,00E-74	84	0,0003015	0,69549	7,23177	0,09611	evm_27.model.AmTr.v1.0_scaffold00057.1.30	-1,11E+01	27	17,79999924	2	-	2	0,4000	AVVHVADPPD LCK HAGDLGNVTV	
1070	4	P24704	Superoxide dismutase (Cu/Zn)	<i>Arabidopsis thaliana</i>	AT1G08830	11 Disease/defence	11.06 Detoxification	2,00E-74	84	0,0050128	2,3629	4,83628	0,48858	evm_27.model.AmTr.v1.0_scaffold00057.1.30	-8,51E+01	53	17,79999924	23	-	18	4,6000	EHGAPEDENR AVVHVADPPD LCKGGGH	
349	58	3	P25696	Enolase	<i>Arabidopsis thaliana</i>	AT2G36530	02 Energy	02.01 Glycolysis	0,00E+00	93	3,36E-05	0,25222	0,24991	1,00927	evm_27.model.AmTr.v1.0_scaffold00041.3.4	-2,90E+01	12	47,90000153	4	-	4	0,1905	HIANLAGNK VOVGGDLLVT NPK
236	3	P25696	Enolase	<i>Arabidopsis thaliana</i>	AT2G36530	02 Energy	02.01 Glycolysis	0,00E+00	93	0,0074384	1,27937	2,72958	0,46871	evm_27.model.AmTr.v1.0_scaffold00041.3.4	-1,90E+01	6	47,90000153	2	-	2	0,0952	VVIGMDVAAS EFYDSK LGANAILAVSL	
407	14	P25696	Enolase	<i>Arabidopsis thaliana</i>	AT2G36530	02 Energy	02.01 Glycolysis	0,00E+00	93	0,0092583	1,69181	1,84846	0,91526	evm_27.model.AmTr.v1.0_scaffold00041.3.4	-9,19E+01	40	47,90000153	14	-	13	0,7143	HIANLAGNK LTAIEGK DGGSDYLGK	
432	4	P25696	Enolase	<i>Arabidopsis thaliana</i>	AT2G36530	02 Energy	02.01 Glycolysis	0,00E+00	93	0,0133909	2,25306	1,32966	1,69447	evm_27.model.AmTr.v1.0_scaffold00041.3.4	-1,98E+01	14	47,90000153	3	-	3	0,1905	GNPTVEVDVG LSDGTCHR VVIGMDVAAS	
488	10	P25696	Enolase	<i>Arabidopsis thaliana</i>	AT2G36530	02 Energy	02.01 Glycolysis	0,00E+00	93	0,0120942	1,5885	2,29785	0,6913	evm_27.model.AmTr.v1.0_scaffold00041.3.4	-6,86E+01	28	47,90000153	11	-	9	0,5714	HIANLAGNK KPVEPY DGGSDYLGK	
467	11	P25696	Enolase	<i>Arabidopsis thaliana</i>	AT2G36530	02 Energy	02.01 Glycolysis	0,00E+00	93	0,0173342	0,83843	2,86452	0,29269	evm_27.model.AmTr.v1.0_scaffold00041.3.4	-5,21E+01	23	47,90000153	9	-	7	0,4286	HIANLAGNK TYDLNFKKEEN NDGSK	
471	8	P25696	Enolase	<i>Arabidopsis thaliana</i>	AT2G36530	02 Energy	02.01 Glycolysis	0,00E+00	93	0,004315	0,79614	2,56316	0,31061	evm_27.model.AmTr.v1.0_scaffold00041.3.4	-5,42E+01	25	47,90000153	11	-	9	0,5238	HIANLAGNK DGGSDYLGK LGANAILAVSL	
600	6	P25696	Enolase	<i>Arabidopsis thaliana</i>	AT2G36530	02 Energy	02.01 Glycolysis	0,00E+00	93	0,0178552	5,14912	4,89334	1,05227	evm_27.model.AmTr.v1.0_scaffold00041.3.4	-1,25E+01	7	47,90000153	2	-	2	0,0952	GNPTVEVDVG LSDGTCHR VVIGMDVAAS	
638	4	P25696	Enolase	<i>Arabidopsis thaliana</i>	AT2G36530	02 Energy	02.01 Glycolysis	0,00E+00	93	0,0027807	7,4861	4,88871	1,53131	evm_27.model.AmTr.v1.0_scaffold00041.3.4	-1,59E+01	6	47,90000153	2	-	2	0,0952	VVIGMDVAAS EFYDSK LGANAILAVSL	
1002	14	P25696	Enolase	<i>Arabidopsis thaliana</i>	AT2G36530	02 Energy	02.01 Glycolysis	0,00E+00	93	0,0179685	1,00507	2,65214	0,37896	evm_27.model.AmTr.v1.0_scaffold00041.3.4	-1,46E+02	46	47,90000153	29	-	22	1,4762	HIANLAGNK KPVEPY VVIGMDVAAS	
1065	4	P25696	Enolase	<i>Arabidopsis thaliana</i>	AT2G36530	02 Energy	02.01 Glycolysis	0,00E+00	93	0,0005017	4,67039	8,73697	0,53455	evm_27.model.AmTr.v1.0_scaffold00041.3.4	-1,13E+01	6	47,90000153	2	-	2	0,0952	VVIGMDVAAS EFYDSK LGANAILAVSL	
743	7	P25696	Enolase	<i>Arabidopsis thaliana</i>	AT2G36530	02 Energy	02.01 Glycolysis	0,00E+00	93	0,0033999	0,76225	3,326	0,21836	evm_27.model.AmTr.v1.0_scaffold00041.3.4	-1,90E+01	7	47,90000153	2	-	2	0,0952	HEELGAEAVY AGANFR VVIGMDVAAS FEFDLOOLK VDDELK FOYGVIPCHT	
959	1	P29448	Thioredoxin	<i>Arabidopsis thaliana</i>	AT3G51030	06 Protein destination and storage	06.01 Folding and stability	9,00E-37	78	0,0062709	0,12046	1,18719	0,10147	evm_27.model.AmTr.v1.0_scaffold00002.3.33	-2,07E+01	39	13,39999962	8	-	6	1,1250	AEQPKPVTKK AKQYGVTVK	
407	14	P29525	Oleoin type 1	<i>Arabidopsis thaliana</i>	AT4G25140	09 Cell structure	09.99 Others	1,00E-25	82	0,0092583	1,69181	1,84846	0,91526	evm_27.model.AmTr.v1.0_scaffold00056.1.89	-6,01E+00	14	15,39999962	2	-	2	1,0000	PGDIVTASNGK TIEVNTDAEGR	
331	8	P30184	Leucine aminopeptidase	<i>Arabidopsis thaliana</i>	AT2G24200	06 Protein destination and storage	06.13 Proteolysis	0,00E+00	78	0,0076661	1,16096	0,33556	3,45981	evm_27.model.AmTr.v1.0_scaffold00065.2.04	-1,11E+02	65	54,79999924	23	-	20	0,8966		

424	9	P30184	Leucine aminopeptidase	<i>Arabidopsis thaliana</i>	AT2G24200	06 Protein destination and storage	06.13 Proteolysis	0.00E+00	78	0.0156606	1.00376	0.52462	1.91332	evm_27.model.AmTr.v1.0_scaffold00065.204	-2.13E+01	7	54.79999924	3	-	3	0.1034	TIEVNTDAEGR GLTFDSQGYN NYACNCGYFK PGDIVTASNGK TIEVNTDAEGR	
325	2	P30184	Leucine aminopeptidase	<i>Arabidopsis thaliana</i>	AT2G24200	06 Protein destination and storage	06.13 Proteolysis	0.00E+00	78	0.0046381	1.89829	1.01019	1.87914	evm_27.model.AmTr.v1.0_scaffold00065.204	-1.34E+02	43	54.79999924	23	-	21	0.8276	TIEVNTDAEGR GLTFDSQGYN NYACNCGYFK PGDIVTASNGK TIEVNTDAEGR	
782	9	P30184	Leucine aminopeptidase	<i>Arabidopsis thaliana</i>	AT2G24200	06 Protein destination and storage	06.13 Proteolysis	0.00E+00	78	0.0006529	0.74675	3.14802	0.23721	evm_27.model.AmTr.v1.0_scaffold00065.204	-2.04E+01	15	54.79999924	5	-	5	0.2069	TIEVNTDAEGR GLTFDSQGYN NYACNCGYFK PGDIVTASNGK TIEVNTDAEGR	
1058	2	P31265	Transcriptionally-controlled tumor protein homolog	<i>Arabidopsis thaliana</i>	AT3G16640	03 Cell growth/division	03.26 Growth regulators	2.00E-75	79	0.0010558	1.54866	3.87352	0.39981	evm_27.model.AmTr.v1.0_scaffold00045.319	-3.06E+01	36	19	12	-	8	1.7143	GAANVGVLLA RGGVDDQAVK GADEFGQVDD LQVDSMESNGK DLUNDSER	
313	41	2	P34795	Phosphoglucose isomerase	<i>Arabidopsis thaliana</i>	AT5G42740	02 Energy	02.01 Glycolysis	0.00E+00	82	0.0073762	0.55087	0.19939	2.76283	evm_27.model.AmTr.v1.0_scaffold00111.63	-1.80E+02	58	62.40000153	54	-	32	2.0000	IWSEQGOEAL EKS SYGLTGLVLR EAIWCGSTNS TTEETGK DRIILLFK RAASDELIVEE R FAAEDTMLAY
743	7	P42738	Chorismate mutase (chloroplastic)	<i>Arabidopsis thaliana</i>	AT3G29200	01 Metabolism	01.01 Amino Acid	2.00E-85	69	0.0033999	0.72625	3.326	0.21836	evm_27.model.AmTr.v1.0_scaffold00065.198	-1.28E+01	11	33.09999847	3	-	3	0.2727	MYDELPLR AMVFGQEVSL DJK IWSEQGOEAL EKS SYGLTGLVLR	
325	2	P42744	NEDD8-activating enzyme	<i>Arabidopsis thaliana</i>	AT1G05180	10 Signal transduction	10.99 Others	0.00E+00	81	0.0046381	1.89829	1.01019	1.87914	evm_27.model.AmTr.v1.0_scaffold00037.87	-7.87E+00	4	58.59999847	2	-	2	0.0909	IWSEQGOEAL EKS SYGLTGLVLR	
583	10	P46637	Arginase	<i>Arabidopsis thaliana</i>	AT4G08900	01 Metabolism	01.01 Amino acid	e-168	92	0.0182765	1.25654	2.01037	0.62503	evm_27.model.AmTr.v1.0_scaffold00002.256	-1.93E+01	23	36.70000076	5	-	5	0.3571	EAIWCGSTNS TTEETGK DRIILLFK RAASDELIVEE R FAAEDTMLAY	
743	7	P48348	14-3-3-like protein GF14	<i>Arabidopsis thaliana</i>	AT5G65430	04 Transcription	04.1901 General TFs	e-124	93	0.0033999	0.72625	3.326	0.21836	evm_27.model.AmTr.v1.0_scaffold00135.27	-2.23E+01	20	27.89999962	5	-	4	0.4000	FAAEDTMLAY	
768	6	P48491	Triosephosphate isomerase	<i>Arabidopsis thaliana</i>	AT3G55440	02 Energy	02.01 Glycolysis	e-114	87	0.0010332	1.85717	5.783	0.32114	evm_27.model.AmTr.v1.0_scaffold00012.164	-1.34E+01	14	27.29999924	3	-	3	0.2500	IYGGSVNGAN CK VIACVGETLEO R VATPAQAQEV ECSGTMDOVVA K VAVL SR	
774	4	P48491	Triosephosphate isomerase	<i>Arabidopsis thaliana</i>	AT3G55440	02 Energy	02.01 Glycolysis	e-114	87	0.0178635	2.04497	3.67878	0.55688	evm_27.model.AmTr.v1.0_scaffold00012.164	-1.50E+01	22	27.29999924	4	-	4	0.3333	VATPAQAQEV ECSGTMDOVVA K VAVL SR	
789	7	P48491	Triosephosphate isomerase	<i>Arabidopsis thaliana</i>	AT3G55440	02 Energy	02.01 Glycolysis	e-114	87	0.017244	1.64782	1.94	0.84939	evm_27.model.AmTr.v1.0_scaffold00012.164	-1.77E+01	21	27.29999924	5	-	5	0.4167	VATPAQAQEV ECSGTMDOVVA K VAVL SR	
790	8	P48491	Triosephosphate isomerase	<i>Arabidopsis thaliana</i>	AT3G55440	02 Energy	02.01 Glycolysis	e-114	87	5.26E-05	1.00671	3.80321	0.2647	evm_27.model.AmTr.v1.0_scaffold00012.164	-3.02E+01	25	27.29999924	5	-	5	0.4167	ECSGTMDOVVA K VAVL SR	
782	9	P48491	Triosephosphate isomerase	<i>Arabidopsis thaliana</i>	AT3G55440	02 Energy	02.01 Glycolysis	e-114	87	0.0006529	0.74675	3.14802	0.23721	evm_27.model.AmTr.v1.0_scaffold00012.164	-6.66E+01	45	27.29999924	16	-	14	1.4167	CNGETVEVK VSPAFASTR CNGETVEVKK ECSGTMDOVVA K VAVL SR	
796	180	2	P48491	Triosephosphate isomerase	<i>Arabidopsis thaliana</i>	AT3G55440	02 Energy	02.01 Glycolysis	e-114	87	0.0017072	0.12213	0.24349	0.50155	evm_27.model.AmTr.v1.0_scaffold00012.164	-1.21E+01	15	27.29999924	3	-	3	0.2500	ECSGTMDOVVA K VAVL SR
355	66	3	P48641	Glutathione reductase	<i>Arabidopsis thaliana</i>	AT3G24170	11 Disease/defence	11.06 Detoxification	0.00E+00	69	0.0027293	0.30401	0.15949	1.90621	evm_27.model.AmTr.v1.0_scaffold00067.136	-5.62E+01	30	57.5	11	-	11	0.4583	NTISGRPEK SEQOAVEQAK LVNHSHTVEVT FAGDDAPR VGMGQKDAYV GDEAQS K
235	19	6	P53492	Actin 7	<i>Arabidopsis thaliana</i>	AT5G09810	09 Cell structure	09.04 Cytoskeleton	0.00E+00	99	0.0059659	0.70174	0.26816	2.61681	evm_27.model.AmTr.v1.0_scaffold00018.104	-2.18E+01	14	41.59999847	6	-	6	0.4000	FAGDDAPR VGMGQKDAYV GDEAQS K
235	19	6	P53496	Actin 11	<i>Arabidopsis thaliana</i>	AT3G12110	09 Cell structure	09.04 Cytoskeleton	0.00E+00	98	0.0059659	0.70174	0.26816	2.61681	evm_27.model.AmTr.v1.0_scaffold00044.6	-2.18E+01	14	43.90000153	6	-	6	0.3750	FAGDDAPR VGMGQKDAYV GDEAQS K
235	19	6	P53496	Actin 11	<i>Arabidopsis thaliana</i>	AT3G12110	09 Cell structure	09.04 Cytoskeleton	0.00E+00	99	0.0059659	0.70174	0.26816	2.61681	evm_27.model.AmTr.v1.0_scaffold00062.182	-2.18E+01	14	41.5	6	-	6	0.4000	FAGDDAPR VGMGQKDAYV GDEAQS K
564	8	P57106	Malate dehydrogenase	<i>Arabidopsis thaliana</i>	AT5G43330	02 Energy	02.10 TCA pathway	6.00E-49	84	0.011869	1.54894	2.36483	0.65499	evm_27.model.AmTr.v1.0_scaffold01428.1	-2.25E+01	40	12.30000019	5	-	3	1.0000	KLDATADELSE EK KLDATADELSE EK	
583	10	P57106	Malate dehydrogenase	<i>Arabidopsis thaliana</i>	AT5G43330	02 Energy	02.10 TCA pathway	6.00E-49	84	0.0182765	1.25654	2.01037	0.62503	evm_27.model.AmTr.v1.0_scaffold01428.1	-1.49E+01	26	12.30000019	3	-	3	0.6000	KLDATADELSE EK KLDATADELSE EK	
346	51	3	P57751	UDP-glucose pyrophosphorylase	<i>Arabidopsis thaliana</i>	AT5G17310	01 Metabolism	01.05 Sugars and polysaccharides	0.00E+00	78	0.0001011	0.18479	0.17894	1.03268	evm_27.model.AmTr.v1.0_scaffold00044.42	-4.20E+01	16	52.20000076	6	-	6	0.2308	AAVATKPASSE SEK LOSVAAGLNQI AAVATKPASSE SEK FFDQAIGNVP
349	58	3	P57751	UDP-glucose pyrophosphorylase	<i>Arabidopsis thaliana</i>	AT5G17310	01 Metabolism	01.05 Sugars and polysaccharides	0.00E+00	78	3.36E-05	0.25222	0.24991	1.00927	evm_27.model.AmTr.v1.0_scaffold00044.42	-4.50E+01	27	52.20000076	9	-	9	0.3462	AAVATKPASSE SEK LOSVAAGLNQI AAVATKPASSE SEK FFDQAIGNVP
402	3	P57751	UDP-glucose pyrophosphorylase	<i>Arabidopsis thaliana</i>	AT5G17310	01 Metabolism	01.05 Sugars and polysaccharides	0.00E+00	78	0.0116642	0.72452	4.74682	0.15263	evm_27.model.AmTr.v1.0_scaffold00044.42	-6.85E+00	5	52.20000076	2	-	2	0.0769	AAVATKPASSE SEK LOSVAAGLNQI AAVATKPASSE SEK FFDQAIGNVP	
833	6	P92963	Ras-related protein	<i>Arabidopsis thaliana</i>	AT4G17170	08 Intracellular traffic	08.07 Vesicular	e-108	90	0.0133914	4.64276	2.00655	2.31381	evm_27.model.AmTr.v1.0_scaffold00166.2	-2.02E+01	32	23.20000076	4	-	4	0.3571	AVSTEEOGFK NYIIGDITGVGK SSQNPGVITIA K LDQFCVADNY REQDSQIENG AR ESLPHIPDER	
799	8	P92999	Germin-like protein	<i>Arabidopsis thaliana</i>	AT5G39160	12 Unclear classification	12 Unclear classification	2.00E-72	77	0.0125632	1.10491	2.40277	0.45985	evm_27.model.AmTr.v1.0_scaffold00089.68	-1.53E+01	18	23.39999962	3	-	3	0.6000	LDQFCVADNY REQDSQIENG AR ESLPHIPDER	
459	86	4	P93026	Vacuolar sorting receptor	<i>Arabidopsis thaliana</i>	AT3G52850	08 Intracellular traffic	08.13 Vacuolar	0.00E+00	73	0.0037057	0.46074	0.36244	1.27121	evm_27.model.AmTr.v1.0_scaffold00077.78	-7.61E+01	26	69.40000153	20	-	15	0.7333	LDQFCVADNY REQDSQIENG AR ESLPHIPDER
302	38	2	P94078	Alpha-mannosidase	<i>Arabidopsis thaliana</i>	AT3G26720	01 Metabolism	01.05 Sugars and polysaccharides	0.00E+00	81	0.000944	0.59421	0.2155	2.75736	evm_27.model.AmTr.v1.0_scaffold00016.68	-3.03E+01	6	114.90000015	7	-	6	0.1628	IDYQDR VMSGYMAAR ECSGFMANV ITEMSLSANDE R LAHLYEAGED
424	9	P94078	Alpha-mannosidase	<i>Arabidopsis thaliana</i>	AT3G26720	01 Metabolism	01.05 Sugars and polysaccharides	0.00E+00	81	0.0156606	1.00376	0.52462	1.91332	evm_27.model.AmTr.v1.0_scaffold00016.68	-1.35E+01	4	114.90000015	3	-	3	0.0698	IDYQDR VMSGYMAAR ECSGFMANV ITEMSLSANDE R LAHLYEAGED	
291	2	Q05758	Ketol-acid reductoisomerase	<i>Arabidopsis thaliana</i>	AT3G58610	01 Metabolism	01.01 Amino Acid	0.00E+00	80	0.0003834	2.93432	2.88705	1.01637	evm_27.model.AmTr.v1.0_scaffold00021.42	-1.17E+02	30	63.40000153	23	-	19	1.2632	MVNDNSTIAR GSGQPAQAK VSMPAVKPEK ISDAAQADTYE K	
294	8	Q05758	Ketol-acid reductoisomerase	<i>Arabidopsis thaliana</i>	AT3G58610	01 Metabolism	01.01 Amino Acid	0.00E+00	80	0.0070497	3.75653	4.0454	0.92859	evm_27.model.AmTr.v1.0_scaffold00021.42	-9.11E+01	28	63.40000153	18	-	13	1.0526	MVNDNSTIAR GSGQPAQAK VSMPAVKPEK ISDAAQADTYE K	

743	7	Q1PER6	Ascorbate peroxidase	<i>Arabidopsis thaliana</i>	AT3G09640	11 Disease/defence	11.06 Detoxification	3,00E-99	79	0,0033999	0,2625	3,326	0,21836	evm_27.model.AmTr.v1.0_scaffold00023.236	-1,87E+01	19	27,79999924	5	-	5	0,4167	NCAPLMVR GANAGLDIAVR AGLDIAVR
740	4	Q1PER6	Ascorbate peroxidase	<i>Arabidopsis thaliana</i>	AT3G09640	11 Disease/defence	11.06 Detoxification	3,00E-99	79	0,0009213	1,2946	3,94075	0,32852	evm_27.model.AmTr.v1.0_scaffold00023.236	-4,31E+01	24	27,79999924	8	-	7	0,6667	DVALSGAHL GANAGLDIAVR DVALSGAHL
774	4	Q1PER6	Ascorbate peroxidase	<i>Arabidopsis thaliana</i>	AT3G09640	11 Disease/defence	11.06 Detoxification	3,00E-99	79	0,0178635	2,04497	3,67878	0,55588	evm_27.model.AmTr.v1.0_scaffold00023.236	-8,04E+01	52	27,79999924	16	-	14	1,3333	LPDTRKGDPH LR GVEYCEVEYO GANAGLDIAVR AGLDIAVR
789	7	Q1PER6	Ascorbate peroxidase	<i>Arabidopsis thaliana</i>	AT3G09640	11 Disease/defence	11.06 Detoxification	3,00E-99	79	0,017244	1,64782	1,94	0,84939	evm_27.model.AmTr.v1.0_scaffold00023.236	-1,46E+01	17	27,79999924	5	-	5	0,4167	ALIDPAFHBY GANAGLDIAVR DVALSGAHL
790	8	Q1PER6	Ascorbate peroxidase	<i>Arabidopsis thaliana</i>	AT3G09640	11 Disease/defence	11.06 Detoxification	3,00E-99	79	5,26E-05	1,00671	3,80321	0,2647	evm_27.model.AmTr.v1.0_scaffold00023.236	-7,35E+00	13	27,79999924	2	-	2	0,2500	GANAGLDIAVR DVALSGAHL
802	8	Q1PER6	Ascorbate peroxidase	<i>Arabidopsis thaliana</i>	AT3G09640	11 Disease/defence	11.06 Detoxification	3,00E-99	79	0,0053343	1,5642	3,66597	0,42668	evm_27.model.AmTr.v1.0_scaffold00023.236	-1,10E+01	15	27,79999924	3	-	3	0,2500	AGLDIAVR DVALSGAHL GR
810	12	Q1PER6	Ascorbate peroxidase	<i>Arabidopsis thaliana</i>	AT3G09640	11 Disease/defence	11.06 Detoxification	3,00E-99	79	0,0021851	1,58254	4,0931	0,38664	evm_27.model.AmTr.v1.0_scaffold00023.236	-7,78E+00	9	27,79999924	2	-	2	0,1667	DVALSGAHL GR EGLIOLPSDK
638	4	Q29Q34	Rossmann-fold NAD(P) binding domain-containing protein	<i>Arabidopsis thaliana</i>	AT5G19440	12 Unclear classification	12 Unclear classification	e-139	86	0,0027807	7,4861	4,88871	1,53131	evm_27.model.AmTr.v1.0_scaffold00025.367	-5,53E+01	46	35,20000076	12	10	12	0,8000	VVHFSELVK CVDENPPPPK DVALSGAHL LAVYVPSASG
638	4	Q29Q34	Rossmann-fold NAD(P) binding domain-containing protein	<i>Arabidopsis thaliana</i>	AT5G19440	12 Unclear classification	12 Unclear classification	e-111	75	0,0027807	7,4861	4,88871	1,53131	evm_27.model.AmTr.v1.0_scaffold00025.366	-1,93E+01	10	37,90000153	5	3	4	0,3333	R DVAEFAHLYE
1018	9	Q29Q34	Rossmann-fold NAD(P) binding domain-containing protein	<i>Arabidopsis thaliana</i>	AT5G19440	12 Unclear classification	12 Unclear classification	e-139	86	7,51E-05	2,87435	3,95283	0,72716	evm_27.model.AmTr.v1.0_scaffold00025.367	-8,04E+00	6	35,20000076	2	-	2	0,1333	GYTVGATVR LAEAAWDF AK
220	4	Q38931	Rotamase	<i>Arabidopsis thaliana</i>	AT3G25230	06 Protein destination and storage	06.01 Folding and stability	0,00E+00	75	0,0013779	2,6839	2,52121	1,06453	evm_27.model.AmTr.v1.0_scaffold00087.200	-1,58E+01	10	65,90000153	5	-	5	0,3158	LGQGVQIK LEEDTIVSK YFYDTSESEE
252	3	Q38950	Semithreonine-protein phosphatase 2A (subunit A beta)	<i>Arabidopsis thaliana</i>	AT3G25800	10 Signal transduction	10.0407 Phosphatases	0,00E+00	96	0,0016951	4,19739	3,87379	1,08354	evm_27.model.AmTr.v1.0_scaffold00048.400	-6,00E+00	3	65,40000153	2	-	2	0,0769	FAATVPEPNYK LASGEWFTAR
467	11	Q39043	HSP70 (Luminal binding protein 2)	<i>Arabidopsis thaliana</i>	AT5G42020	06 Protein destination and storage	06.01 Folding and stability	0,00E+00	88	0,0173342	0,83843	2,86452	0,29269	evm_27.model.AmTr.v1.0_scaffold00009.363	-8,20E+00	5	73,19999695	2	-	2	0,1200	VEIANDQGNR FEELNDLFR
471	8	Q39043	HSP70 (Luminal binding protein 2)	<i>Arabidopsis thaliana</i>	AT5G42020	06 Protein destination and storage	06.01 Folding and stability	0,00E+00	88	0,004315	0,79614	2,56316	0,31061	evm_27.model.AmTr.v1.0_scaffold00009.363	-1,24E+01	3	73,19999695	2	1	2	0,0800	NEIEIIVLGG STR
1002	14	Q39043	HSP70 (Luminal binding protein 2)	<i>Arabidopsis thaliana</i>	AT5G42020	06 Protein destination and storage	06.01 Folding and stability	0,00E+00	88	0,0179685	1,00507	2,65214	0,37896	evm_27.model.AmTr.v1.0_scaffold00009.363	-8,28E+00	3	73,19999695	2	-	2	0,0800	VEIANDQGNR FEELNDLFR
600	6	Q39173	NADP-dependent alkenal double bond reductase	<i>Arabidopsis thaliana</i>	AT5G16990	11 Disease/defence	11.06 Detoxification	3,00E-86	85	0,0178552	5,14912	4,89334	1,05227	evm_27.model.AmTr.v1.0_scaffold00013.620	-5,05E+01	40	23	9	-	8	0,9000	VVVEVARE SIGCYVVGSA GSK
790	8	Q39173	NADP-dependent alkenal double bond reductase	<i>Arabidopsis thaliana</i>	AT5G16990	11 Disease/defence	11.06 Detoxification	3,00E-86	85	5,26E-05	1,00671	3,80321	0,2647	evm_27.model.AmTr.v1.0_scaffold00013.620	-2,92E+01	23	23	5	-	5	0,5000	ISEYNQEEPAG VR SIGCYVVGSA
1013	6	Q39173	NADP-dependent alkenal double bond reductase	<i>Arabidopsis thaliana</i>	AT5G16990	11 Disease/defence	11.06 Detoxification	3,00E-86	85	2,22E-05	1,46601	3,04975	0,4807	evm_27.model.AmTr.v1.0_scaffold00013.620	-2,13E+01	22	23	5	-	5	0,5000	ISEYNQEEPAG VR VAVCGMISEVNI VAVEMETIDR
808	9	Q42539	Protein-L-isoaspartate O-methyltransferase	<i>Arabidopsis thaliana</i>	AT3G48330	11 Disease/defence	11.06 Detoxification	4,00E-94	85	0,0012118	3,14897	4,15446	0,75797	evm_27.model.AmTr.v1.0_scaffold00166.104	-6,54E+00	11	29	2	-	2	0,2000	SPAAPLLOEG SLOIHYGDGR
979	3	Q42560	Aconitase	<i>Arabidopsis thaliana</i>	AT4G35830	02 Energy	02.10 TCA pathway	0,00E+00	84	0,0002014	2,38364	3,23999	0,73569	evm_27.model.AmTr.v1.0_scaffold00115.100	-1,46E+02	40	93,19999695	32	14	27	1,2222	NCDNFQVTK PGODISVTD SGK
980	2	Q42560	Aconitase	<i>Arabidopsis thaliana</i>	AT4G35830	02 Energy	02.10 TCA pathway	0,00E+00	84	0,0158731	2,68389	3,4203	0,7847	evm_27.model.AmTr.v1.0_scaffold00115.100	-1,61E+02	44	93,19999695	48	17	36	1,8519	FSFHGK NCDNFQVTK FSFHGKPAIK
591	1	Q43729	Peroxidase	<i>Arabidopsis thaliana</i>	AT5G17820	11 Disease/defence	11.06 Detoxification	3,00E-97	71	0,0062419	0,95562	10,215	0,09355	evm_27.model.AmTr.v1.0_scaffold00018.806	-3,45E+01	22	35,59999847	6	-	6	0,3158	DAGPNEIVR LCGSSSLPTV R
608	1	Q43729	Peroxidase	<i>Arabidopsis thaliana</i>	AT5G17820	11 Disease/defence	11.06 Detoxification	3,00E-97	71	0,0051106	1,18249	11,3794	0,10392	evm_27.model.AmTr.v1.0_scaffold00018.806	-1,35E+01	11	35,59999847	3	-	3	0,1579	DAGPNEIVR DAVALSGGPS YPIETGR
1015	1	Q43729	Peroxidase	<i>Arabidopsis thaliana</i>	AT5G17820	11 Disease/defence	11.06 Detoxification	3,00E-97	71	0,003793	0,59093	6,4544	0,09155	evm_27.model.AmTr.v1.0_scaffold00018.806	-3,82E+01	31	35,59999847	8	-	8	0,4737	DAGPNEIVR LNFQGTGKP DPSMDTALVS
1017	2	Q43729	Peroxidase	<i>Arabidopsis thaliana</i>	AT5G17820	11 Disease/defence	11.06 Detoxification	3,00E-97	71	0,0066763	0,84286	12,0481	0,06996	evm_27.model.AmTr.v1.0_scaffold00018.806	-2,48E+01	18	35,59999847	5	-	5	0,2632	DAGPNEIVR DAVALSGGPS YPIETGR
331	8	Q56YU0	Aldehyde dehydrogenase	<i>Arabidopsis thaliana</i>	AT3G24503	20 Secondary metabolism	20.1 Phenylpropanoids/phenolics	e-146	79	0,0076661	1,16096	0,33556	3,45981	evm_27.model.AmTr.v1.0_scaffold00078.104	-5,52E+01	41	42,29999924	11	-	10	0,5238	GEICVAGSR VAFGTSTEVG R
467	11	Q68015	Glutathione hydrolase	<i>Arabidopsis thaliana</i>	AT4G39650	11 Disease/defence	11.06 Detoxification	e-176	69	0,0173342	0,83843	2,86452	0,29269	evm_27.model.AmTr.v1.0_scaffold00002.800	-9,81E+00	5	62,90000153	2	-	2	0,0952	EVITEHGSVA ADDGR ISPYLYQMTD
471	8	Q68015	Glutathione hydrolase	<i>Arabidopsis thaliana</i>	AT4G39650	11 Disease/defence	11.06 Detoxification	e-176	69	0,004315	0,79614	2,56316	0,31061	evm_27.model.AmTr.v1.0_scaffold00002.800	-8,19E+01	27	62,90000153	22	13	16	1,0476	DMYANDPSAK YQMTQTEAII R
471	8	Q68015	Glutathione hydrolase	<i>Arabidopsis thaliana</i>	AT4G39650	11 Disease/defence	11.06 Detoxification	e-106	72	0,004315	0,79614	2,56316	0,31061	evm_27.model.AmTr.v1.0_scaffold00002.800	-3,11E+01	23	38,79999924	10	1	7	0,9091	SANGLVDAYD MR
488	10	Q68015	Glutathione hydrolase	<i>Arabidopsis thaliana</i>	AT4G39650	11 Disease/defence	11.06 Detoxification	e-176	69	0,0120942	1,5885	2,29785	0,6913	evm_27.model.AmTr.v1.0_scaffold00002.800	-3,52E+01	15	62,90000153	7	-	6	0,3810	ETAPAAASR DMYANDPSAK EVITEHGSVA
1002	14	Q68015	Glutathione hydrolase	<i>Arabidopsis thaliana</i>	AT4G39650	11 Disease/defence	11.06 Detoxification	e-176	69	0,0179685	1,00507	2,65214	0,37896	evm_27.model.AmTr.v1.0_scaffold00002.800	-2,11E+01	10	62,90000153	5	-	4	0,2381	DMYANDPSAK EVITEHGSVA ADDGR

799	8	Q7DLS1	20S proteasome (beta subunit B-2)	<i>Arabidopsis thaliana</i>	AT5G40580	06 Protein destination and storage	06.13 Proteolysis	e-135	93	0,0125632	1,10491	2,40277	0,45985	evm_27.model.AmTr_v1.0_scaffold00088.126	-8,08E+00	9	29,39999962	3	-	3	0,3750	NHQLPNPR ATEGPVCDK TTIVGVLFK NPLHTVY LHDLVIAEKP AVPVSEAK	
895	4	Q84TH6	Dirigent protein 23	<i>Arabidopsis thaliana</i>	AT2G21100	20 Secondary metabolism	20.1 Phenylpropanoids/phenolics	1,00E-33	64	0,0015653	1,69054	10,4031	0,1625	evm_27.model.AmTr_v1.0_scaffold00041.133	-7,02E+01	52	20,5	12	-	10	1,6250	AVDQIYVATC SPAR	
740	4	Q84WW2	6-Phosphogluconolactonase	<i>Arabidopsis thaliana</i>	AT5G24400	02 Energy	02.07 Pentose phosphate	2,00E-80	80	0,0009213	1,2946	3,94075	0,32852	evm_27.model.AmTr_v1.0_scaffold00027.27	-6,41E+00	11	29,60000038	2	-	2	0,2222	GAFITVVLSSG SLIK LAVNEEELM DLKPOLR TDQYGGSLER	
488	10	Q8GYB8	12-oxophytodieneoate reductase	<i>Arabidopsis thaliana</i>	AT1G76690	01 Metabolism	01.06 Lipid and sterol	e-166	87	0,0120942	1,5885	2,29785	0,6913	evm_27.model.AmTr_v1.0_scaffold00071.207	-1,22E+02	61	38,79999924	30	15	25	2,0000	TDHYGGSLE R QLSPOVDANO GNFISTGGHT K	
488	10	Q8GYB8	12-oxophytodieneoate reductase	<i>Arabidopsis thaliana</i>	AT1G76690	01 Metabolism	01.06 Lipid and sterol	e-169	76	0,0120942	1,5885	2,29785	0,6913	evm_27.model.AmTr_v1.0_scaffold00071.206	-1,26E+02	56	41,90000153	26	12	23	1,4444	TDHYGGSLE R QLSPOVDANO GNFISTGGHT K	
488	10	Q8GYB8	12-oxophytodieneoate reductase	<i>Arabidopsis thaliana</i>	AT1G76690	01 Metabolism	01.06 Lipid and sterol	e-163	85	0,0120942	1,5885	2,29785	0,6913	evm_27.model.AmTr_v1.0_scaffold00071.208	-5,57E+01	40	41,40000153	14	8	13	0,7778	TDHYGGSLE R QLSPOVDANO GNFISTGGHT K	
510	9	Q8GYB8	12-oxophytodieneoate reductase	<i>Arabidopsis thaliana</i>	AT1G76690	01 Metabolism	01.06 Lipid and sterol	e-169	76	0,0003295	2,01724	2,58062	0,78169	evm_27.model.AmTr_v1.0_scaffold00071.206	-3,12E+001	24	41,90000153	8	5	8	4,44E-001	TDHYGGSLE R QLSPOVDANO GNFISTGGHT K	
510	9	Q8GYB8	12-oxophytodieneoate reductase	<i>Arabidopsis thaliana</i>	AT1G76690	01 Metabolism	01.06 Lipid and sterol	e-166	87	0,0003295	2,01724	2,58062	0,78169	evm_27.model.AmTr_v1.0_scaffold00071.207	-1,23E+001	11	38,79999924	4	1	4	2,67E-001	TDHYGGSLE R QLSPOVDANO GNFISTGGHT K	
793	12	Q8GYB8	12-oxophytodieneoate reductase	<i>Arabidopsis thaliana</i>	AT1G76690	01 Metabolism	01.06 Lipid and sterol	e-169	76	0,0010663	2,43627	6,5698	0,37083	evm_27.model.AmTr_v1.0_scaffold00071.206	-2,28E+01	22	41,90000153	4	-	4	0,3333	RFELNAPLNK AIAEGATDLAV FGR	
802	8	Q8GYB8	12-oxophytodieneoate reductase	<i>Arabidopsis thaliana</i>	AT1G76690	01 Metabolism	01.06 Lipid and sterol	e-169	76	0,0053343	1,5642	3,66597	0,42668	evm_27.model.AmTr_v1.0_scaffold00071.206	-2,57E+01	18	41,90000153	5	-	5	0,2778	GTFISAGGYTK R RFELNAPLNK NAIDAGEFDGY	
1002	14	Q8GYB8	12-oxophytodieneoate reductase	<i>Arabidopsis thaliana</i>	AT1G76690	01 Metabolism	01.06 Lipid and sterol	e-166	87	0,0179685	1,00507	2,65214	0,37896	evm_27.model.AmTr_v1.0_scaffold00071.207	-5,69E+01	39	38,79999924	12	5	12	0,8000	TDQYGGSLER K VSNYGYOPNG QAPISCTSK	
1002	14	Q8GYB8	12-oxophytodieneoate reductase	<i>Arabidopsis thaliana</i>	AT1G76690	01 Metabolism	01.06 Lipid and sterol	e-169	76	0,0179685	1,00507	2,65214	0,37896	evm_27.model.AmTr_v1.0_scaffold00071.206	-5,15E+01	42	41,90000153	12	6	12	0,7778	TDQYGGSLER K VSNYGYOPNG QAPISCTSK	
1002	14	Q8GYB8	12-oxophytodieneoate reductase	<i>Arabidopsis thaliana</i>	AT1G76690	01 Metabolism	01.06 Lipid and sterol	e-163	85	0,0179685	1,00507	2,65214	0,37896	evm_27.model.AmTr_v1.0_scaffold00071.208	-1,38E+01	11	41,40000153	5	2	5	0,2778	TDQYGGSLER K VSNYGYOPNG QAPISCTSK	
467	11	Q8GYB8	12-oxophytodieneoate reductase	<i>Arabidopsis thaliana</i>	AT1G76690	01 Metabolism	01.06 Lipid and sterol	e-169	76	0,0173342	0,83843	2,86452	0,29269	evm_27.model.AmTr_v1.0_scaffold00071.206	-2,79E+01	16	41,90000153	5	-	5	0,2778	RFELNAPLNK AIAEGATDLAV FGR	
471	8	Q8GYB8	12-oxophytodieneoate reductase	<i>Arabidopsis thaliana</i>	AT1G76690	01 Metabolism	01.06 Lipid and sterol	e-166	87	0,004315	0,79614	2,56316	0,31061	evm_27.model.AmTr_v1.0_scaffold00071.207	-3,14E+01	20	38,79999924	7	5	7	0,4667	VSNYGYOPNG QAPISCTSK GTFISAGGYTK R	
471	8	Q8GYB8	12-oxophytodieneoate reductase	<i>Arabidopsis thaliana</i>	AT1G76690	01 Metabolism	01.06 Lipid and sterol	e-169	76	0,004315	0,79614	2,56316	0,31061	evm_27.model.AmTr_v1.0_scaffold00071.206	-1,68E+01	12	41,90000153	5	3	5	0,2778	QLSPOVDANO GNFISTGGHT K	
321	131	5	Q8H103	Phosphoglucose isomerase	<i>Arabidopsis thaliana</i>	AT4G24620	02 Energy	02.01 Glycolysis	0,00E+00	92	0,0023794	0,45958	0,32038	1,43448	evm_27.model.AmTr_v1.0_scaffold00135.20	-1,44E+02	49	68,40000153	41	-	28	1,1500	VNIVYAEVEFP R DVAHMAANDR GAIANPDEGR SALYANNR
331	8	Q8H103	Phosphoglucose isomerase	<i>Arabidopsis thaliana</i>	AT4G24620	02 Energy	02.01 Glycolysis	0,00E+00	92	0,0076661	1,16096	0,33556	3,45981	evm_27.model.AmTr_v1.0_scaffold00135.20	-4,74E+01	19	68,40000153	11	-	11	0,2750	AMDELER FSEDTVTR ALIAEGSGGSP	
827	166	2	Q8H114	Appr-1-p processing enzyme family protein	<i>Arabidopsis thaliana</i>	AT2G40600	05 Protein synthesis	05.04 Translation factors	3e-63	67	0,0001876	0,06927	0,04685	1,47864	evm_27.model.AmTr_v1.0_scaffold00077.36	-4,50E+00	13	23,20000076	2	-	2	0,3636	DYHPOASLR VPEVQPGVR
235	19	6	Q8L831	Nudix hydrolase	<i>Arabidopsis thaliana</i>	AT1G79690	01 Metabolism	01.03 Nucleotides	0,00E+00	66	0,0059659	0,70174	0,26816	2,61681	evm_27.model.AmTr_v1.0_scaffold00036.8	-1,46E+01	5	88,19999695	4	1	4	0,1290	LQEAESVAVK
145	4	Q8L831	MutT/nudix family protein	<i>Arabidopsis thaliana</i>	AT1G79690	20 Secondary metabolism	20.2 Terpenoids	0,00E+00	79	0,0018854	2,07447	0,8712	2,38116	evm_27.model.AmTr_v1.0_scaffold00019.58	-6,94E+00	3	86	2	-	2	0,0556	ILQPSIDCITEE OK GPOJVAEFLPN R	
331	8	Q8L831	MutT/nudix family protein	<i>Arabidopsis thaliana</i>	AT1G79690	20 Secondary metabolism	20.2 Terpenoids	0,00E+00	79	0,0076661	1,16096	0,33556	3,45981	evm_27.model.AmTr_v1.0_scaffold00019.58	-2,16E+01	7	86	5	-	5	0,1389	ILQPSIDCITEE OK GPOJVAEFLPN R	
424	9	Q8L831	MutT/nudix family protein	<i>Arabidopsis thaliana</i>	AT1G79690	20 Secondary metabolism	20.2 Terpenoids	0,00E+00	79	0,0156606	1,00376	0,52462	1,91332	evm_27.model.AmTr_v1.0_scaffold00019.58	-1,96E+02	39	86	45	-	32	1,3056	KASDLLQK AYEVANTPSLK R	
218	2	Q8L831	MutT/nudix family protein	<i>Arabidopsis thaliana</i>	AT1G79690	20 Secondary metabolism	20.2 Terpenoids	0,00E+00	79	0,0063427	2,43317	2,16763	1,1225	evm_27.model.AmTr_v1.0_scaffold00019.58	-4,09E+01	14	86	8	-	8	0,2500	AFLTADSAAVK APWSSLDENK EILTIOAGGDK	
220	4	Q8L831	MutT/nudix family protein	<i>Arabidopsis thaliana</i>	AT1G79690	20 Secondary metabolism	20.2 Terpenoids	0,00E+00	79	0,0013779	2,6839	2,52121	1,06459	evm_27.model.AmTr_v1.0_scaffold00019.58	-2,49E+01	10	86	6	-	6	0,1667	AFLTADSAAVK QVVDIAPK EILTIOAGGDK	
407	14	Q8L831	MutT/nudix family protein	<i>Arabidopsis thaliana</i>	AT1G79690	20 Secondary metabolism	20.2 Terpenoids	0,00E+00	79	0,0092583	1,69181	1,84846	0,91526	evm_27.model.AmTr_v1.0_scaffold00019.58	-2,50E+01	10	86	6	-	6	0,1667	IQVVPDIAPK EILTIOAGGDK PAAASLLDK	
810	12	Q8L831	MutT/nudix family protein	<i>Arabidopsis thaliana</i>	AT1G79690	20 Secondary metabolism	20.2 Terpenoids	0,00E+00	79	0,0021851	1,58254	4,0931	0,38664	evm_27.model.AmTr_v1.0_scaffold00019.58	-6,27E+00	5	86	3	-	3	0,0833	VEGAVFESLSR EILTIOAGGDK PAAASLLDK	
828	6	Q8LD27	20S proteasome (beta subunit A-1)	<i>Arabidopsis thaliana</i>	AT4G31300	06 Protein destination and storage	06.13 Proteolysis	e-106	88	0,014279	0,94689	1,68458	0,56209	evm_27.model.AmTr_v1.0_scaffold00025.23	-1,19E+01	13	24,70000076	3	-	3	0,3750	GDVVLGADSR AVSLAIAR ITOLTANQILC ATAYKPEEAR AVDNQIYVATC SPAR	
1018	9	Q8RUF8	Omega-amidase	<i>Arabidopsis thaliana</i>	AT5G12040	01 Metabolism	01.01 Amino Acid	e-140	84	7,51E-05	2,87435	3,95283	0,72716	evm_27.model.AmTr_v1.0_scaffold00024.195	-4,34E+01	26	33,70000076	7	-	7	0,6364	AVDQIYVATC SPAR	
1019	4	Q8RUF8	Omega-amidase	<i>Arabidopsis thaliana</i>	AT5G12040	01 Metabolism	01.01 Amino Acid	e-140	84	0,0016868	2,39482	3,51011	0,68226	evm_27.model.AmTr_v1.0_scaffold00024.195	-9,85E+00	8	33,70000076	2	-	2	0,1818	AVDQIYVATC SPAR RGDLVQLYVD T	
790	8	Q8RWQ9	Thiol protease aleurain-like	<i>Arabidopsis thaliana</i>	AT3G45310	06 Protein destination and storage	06.13 Proteolysis	e-116	85	5,26E-05	1,00671	3,80321	0,2647	evm_27.model.AmTr_v1.0_scaffold00024.285	-1,81E+01	12	33,59999847	3	-	3	0,2727	TGTGVAEAYT QATK	

799	8	Q8W4L0	Calmodulin-like protein	<i>Arabidopsis thaliana</i>	AT3G10300	10 Signal transduction	10.04 Mediators	2,00E-29	92	0,0125632	1,10491	2,40277	0,45985	evm_27.model.AmTr.v1.0_scaffold00053.146	-8,40E+00	18	15,8000019	2	-	2	0,5000	GAPSPFPATA GGKPSAH ALSSVNGSFS SYPCYFGGS PYGGQAPY GYAPYAGAGA	
808	9	Q8W4L0	Calmodulin-like protein	<i>Arabidopsis thaliana</i>	AT3G10300	10 Signal transduction	10.04 Mediators	2,00E-29	92	0,0012118	3,14897	4,15446	0,75797	evm_27.model.AmTr.v1.0_scaffold00053.146	-4,91E+00	36	15,8000019	2	-	2	0,5000	HFEVAQFLGA R SIFNTIYAQER AITTAALANK ISAOMLQDAV SR	
451	2	Q8W4Q1	Uncharacterized protein	<i>Arabidopsis thaliana</i>	AT4G35360	13 Unclassified	13 Unclassified	e-170	88	0,0069263	1,29014	4,40772	0,2927	evm_27.model.AmTr.v1.0_scaffold00022.161	-1,10E+01	5	41,70000076	2	-	2	0,1333	ISAOMLQDAV SR	
321	131	5	Q8W4R0	Phosphoglucosaminase family protein	<i>Arabidopsis thaliana</i>	AT5G17530	02 Energy	02.01 Glycolysis	0,00E+00	66	0,0023794	0,45958	0,32038	1,43448	evm_27.model.AmTr.v1.0_scaffold00148.23	-1,52E+01	11	64	4	-	4	0,1852	ISAOMLQDAV SR
734	119	3	Q8W593	Glyoxalase I (Lactoylglutathione lyase)	<i>Arabidopsis thaliana</i>	AT1G67280	11 Disease/defence	11.06 Detoxification	e-151	78	0,0001252	0,54547	0,15533	3,5117	evm_27.model.AmTr.v1.0_scaffold00109.150	-6,63E+00	8	32	3	1	2	0,2143	GPTPEPLCOV MLR
808	9	Q93V62	Aluminum induced protein with YGL and LRDR motif	<i>Arabidopsis thaliana</i>	AT4G27450	13 Unclassified	13 Unclassified	6,00E-91	78	0,0012118	3,14897	4,15446	0,75797	evm_27.model.AmTr.v1.0_scaffold00009.401	-1,78E+01	12	27,79999924	3	-	3	0,2727	ATNEGQLIEA YK GNLNLSSJR K	
510	9	Q93VR3	GDP-mannose 3,5-epimerase	<i>Arabidopsis thaliana</i>	AT5G28840	01 Metabolism	01.07 Cofactors	0,00E+00	95	0,0003295	2,01724	2,58062	0,78169	evm_27.model.AmTr.v1.0_scaffold00002.538	-2,90E+01	19	42,5	6	-	5	3,00E-001	AGSIDLSVYG SSK FATSYGFEYTY	
808	9	Q93VR3	GDP-mannose 3,5-epimerase	<i>Arabidopsis thaliana</i>	AT5G28840	01 Metabolism	01.07 Cofactors	0,00E+00	95	0,0012118	3,14897	4,15446	0,75797	evm_27.model.AmTr.v1.0_scaffold00002.538	-1,22E+01	7	42,5	2	-	2	0,1000	AGSIDLSVYG SSK FATSYGFEYTY	
1065	4	Q93VR3	GDP-mannose 3,5-epimerase	<i>Arabidopsis thaliana</i>	AT5G28840	01 Metabolism	01.07 Cofactors	0,00E+00	95	0,0005017	4,67039	8,73697	0,53455	evm_27.model.AmTr.v1.0_scaffold00002.538	-1,28E+01	8	42,5	2	-	2	0,1000	AGSIDLSVYG SSK FATSYGFEYTY	
782	9	Q93VR3	GDP-mannose 3,5-epimerase	<i>Arabidopsis thaliana</i>	AT5G28840	01 Metabolism	01.07 Cofactors	0,00E+00	95	0,0006529	0,74675	3,14802	0,23721	evm_27.model.AmTr.v1.0_scaffold00002.538	-2,51E+01	13	42,5	4	-	4	0,2000	AGSIDLSVYG SSK FATSYGFEYTY	
1066	4	Q93VR4	MLP-like protein	<i>Arabidopsis thaliana</i>	AT1G24020	11 Disease/defence	11.02 Defence-related	2,00E-05	44	0,0002698	3,70566	10,3468	0,35815	evm_27.model.AmTr.v1.0_scaffold00003.119	-1,78E+02	95	17,89999962	59	-	33	5,8182	FDEAANGGTV AK FDEAANGGTV AK	
1070	4	Q93VR4	MLP-like protein	<i>Arabidopsis thaliana</i>	AT1G24020	11 Disease/defence	11.02 Defence-related	2,00E-05	44	0,0050128	2,3629	4,83628	0,48858	evm_27.model.AmTr.v1.0_scaffold00003.119	-9,76E+00	15	17,89999962	2	-	2	0,1818	FDEAANGGTV AK FDEAANGGTV AK	
944	8	Q93VR4	MLP-like protein	<i>Arabidopsis thaliana</i>	AT1G24020	11 Disease/defence	11.02 Defence-related	8,00E-32	66	0,0003015	0,69549	7,23177	0,09617	evm_27.model.AmTr.v1.0_scaffold00088.49	-5,84E+01	68	16,5	15	-	10	2,0000	ALDDHVMGAA ALDDHVMGAA VIDIEGAPY FDEAANGGTV AK	
944	8	Q93VR4	MLP-like protein	<i>Arabidopsis thaliana</i>	AT1G24020	11 Disease/defence	11.02 Defence-related	2,00E-05	44	0,0003015	0,69549	7,23177	0,09617	evm_27.model.AmTr.v1.0_scaffold00003.119	-1,37E+01	28	17,89999962	4	-	4	0,3636	FDEAANGGTV AK FDEAANGGTV AK	
743	7	Q93Y22	Coatomer (subunit delta)	<i>Arabidopsis thaliana</i>	AT5G05010	08 Intracellular traffic	08.07 Vesicular	0,00E+00	75	0,0033999	0,72625	3,326	0,21836	evm_27.model.AmTr.v1.0_scaffold00049.8	-1,12E+01	7	61,5	4	-	4	0,1538	QVGGESYVP K NSMEEVVR S	
842	169	4	Q93Z51	Isochorismatase family protein	<i>Arabidopsis thaliana</i>	AT3G16190	20 Secondary metabolism	20.3 Alkaloids	1e-64	64	0,0056319	0,80598	0,20929	3,85098	evm_27.model.AmTr.v1.0_scaffold00067.182	-4,61E+01	59	21,10000038	8	-	7	1,6000	HLVGVGK SVTLTDATAA ASPEVHEANI GAEVIEGLVI EGDYK QTVDEVALD
832	3	Q93Z51	Isochorismatase family protein	<i>Arabidopsis thaliana</i>	AT3G16190	20 Secondary metabolism	20.3 Alkaloids	2,00E-65	75	0,0172602	3,88032	2,10717	1,84448	evm_27.model.AmTr.v1.0_scaffold00067.182	-1,23E+01	14	21,10000038	2	-	2	0,4000	HLVGVGK SVTLTDATAA ASPEVHEANI GAEVIEGLVI EGDYK QTVDEVALD	
682	112	2	Q941A4	Uncharacterized protein	<i>Arabidopsis thaliana</i>	AT5G45690	13 Unclassified	13 Unclassified	1,00E-74	70	0,0108656	0,37066	0,18761	1,97568	evm_27.model.AmTr.v1.0_scaffold00162.9	-9,90E+01	71	28,89999962	28	-	20	1,8235	VYDSDSSDAR AVYDSDSSDA R VYDSDSSDAR AVYDSDSSDA R
684	113	2	Q941A4	Uncharacterized protein	<i>Arabidopsis thaliana</i>	AT5G45690	13 Unclassified	13 Unclassified	1,00E-74	70	4,10E-05	0,58962	0,04952	11,9067	evm_27.model.AmTr.v1.0_scaffold00162.9	-1,53E+02	75	28,89999962	49	-	29	3,4118	VYDSDSSDAR AVYDSDSSDA R VYDSDSSDAR AVYDSDSSDA R
713	113b	5	Q941A4	Uncharacterized protein	<i>Arabidopsis thaliana</i>	AT5G45690	13 Unclassified	13 Unclassified	1,00E-74	70	0,0019856	0,39246	0,12791	3,06825	evm_27.model.AmTr.v1.0_scaffold00162.9	-1,30E+02	75	28,89999962	38	-	25	2,4118	VYDSDSSDAR AVYDSDSSDA R VYDSDSSDAR AVYDSDSSDA R
821	170	4	Q941A4	Uncharacterized protein	<i>Arabidopsis thaliana</i>	AT5G45690	13 Unclassified	13 Unclassified	1,00E-74	70	0,0172238	0,44096	0,44829	0,98364	evm_27.model.AmTr.v1.0_scaffold00162.9	-1,32E+01	21	28,89999962	4	-	4	0,2353	IFESLPDEEKK QIQHVCSFR LIGVEYVSDR VYDSDSSDAR AVYDSDSSDA R
843	4	Q941A4	Uncharacterized protein	<i>Arabidopsis thaliana</i>	AT5G45690	13 Unclassified	13 Unclassified	1,00E-74	70	0,0054464	1,06921	0,166	6,44124	evm_27.model.AmTr.v1.0_scaffold00162.9	-1,21E+01	14	28,89999962	2	-	2	0,1765	VYDSDSSDAR AVYDSDSSDA R LIGVEYVSDR VYDSDSSDAR AVYDSDSSDA R	
294	8	Q949W8	Xylose kinase	<i>Arabidopsis thaliana</i>	AT5G49650	02 Energy	02.07 Pentose phosphate	0,00E+00	84	0,0070497	3,75653	4,0454	0,92859	evm_27.model.AmTr.v1.0_scaffold00109.157	-2,75E+01	15	61	6	-	6	0,2500	LYGTQPEVYE K VLEQTAFLNG K QVGSAGPDC K QYQDLSNLVK	
346	51	3	Q94CC6	Serine carboxypeptidase	<i>Arabidopsis thaliana</i>	AT4G36195	06 Protein destination and storage	06.13 Proteolysis	0,00E+00	84	0,0001011	0,18479	0,17894	1,03268	evm_27.model.AmTr.v1.0_scaffold00182.29	-1,24E+01	9	54,29999924	4	-	4	0,2667	QVGSAGPDC K QYQDLSNLVK
539	93	4	Q94CC6	Serine carboxypeptidase	<i>Arabidopsis thaliana</i>	AT4G36195	06 Protein destination and storage	06.13 Proteolysis	0,00E+00	84	0,0017522	0,13283	0,24423	0,54388	evm_27.model.AmTr.v1.0_scaffold00182.29	-2,66E+01	15	54,29999924	7	-	7	0,5333	QVGSAGPDC K GALQEITR K
583	10	Q94CC6	Serine carboxypeptidase	<i>Arabidopsis thaliana</i>	AT4G36195	06 Protein destination and storage	06.13 Proteolysis	0,00E+00	84	0,0182765	1,25654	2,01037	0,62503	evm_27.model.AmTr.v1.0_scaffold00182.29	-6,84E+00	4	54,29999924	2	-	2	0,1333	LLDNEIAVK YYINTPGOLET YDR	
675	8	Q94K41	Short-chain dehydrogenase reductase	<i>Arabidopsis thaliana</i>	AT2G47140	12 Unclear classification	12 Unclear classification	3,00E-63	67	6,01E-05	4,28718	3,84318	1,11553	evm_27.model.AmTr.v1.0_scaffold00030.220	-4,00E+01	47	28,79999924	14	11	13	1,8750	VTNEDDVCK VYDSDSSDAR AVYDSDSSDA R VYDSDSSDAR AVYDSDSSDA R	
689	9	Q94K41	Short-chain dehydrogenase reductase	<i>Arabidopsis thaliana</i>	AT2G47140	12 Unclear classification	12 Unclear classification	3,00E-63	67	3,23E-06	8,06804	4,88286	1,65232	evm_27.model.AmTr.v1.0_scaffold00030.220	-3,38E+01	39	28,79999924	12	11	11	1,7500	VMIIPAGK STPAPSPVNA K GOVPAFEDGD LK LHGSWMSTAT	
799	8	Q96266	Glutathione S-transferase	<i>Arabidopsis thaliana</i>	AT2G47730	11 Disease/defence	11.06 Detoxification	3,00E-52	62	0,0125632	1,10491	2,40277	0,45985	evm_27.model.AmTr.v1.0_scaffold00057.261	-7,36E+00	11	22,39999962	2	-	2	0,1818	AAALSDAIPK LHGSWMSTAT LR	
808	9	Q96266	Glutathione S-transferase	<i>Arabidopsis thaliana</i>	AT2G47730	11 Disease/defence	11.06 Detoxification	3,00E-52	62	0,0012118	3,14897	4,15446	0,75797	evm_27.model.AmTr.v1.0_scaffold00057.261	-6,28E+00	17	22,39999962	3	-	3	0,2727	AAALSDAIPK LHGSWMSTAT LR	
1019	4	Q9ASR1	Translation elongation factor 2	<i>Arabidopsis thaliana</i>	AT1G56070	05 Protein synthesis	05.04 Translation factors	0,00E+00	93	0,0016868	2,39482	3,51011	0,68226	evm_27.model.AmTr.v1.0_scaffold00032.93	-6,70E+00	3	93,90000153	2	-	2	0,0667	VYASQLTATP R PLFEGLPFAID	

1017		2	Q9C966	GDSL esterase/lipase	<i>Arabidopsis thaliana</i>	AT1G71120	01 Metabolism	01.06 Lipid and sterol	1,00E-78	73	0,0066763	0,84286	12,0481	0,06996	evm_27.model.AmTr.v1.0_scaffold00105.8	-9,22E+00	11	32,59999847	2	-	2	0,1667	TGINFASAGSGLLOEITSRVAALGJGPFVGCATAGVPDAKIQEHPVIRCGGAPITAMM
230	25	2	Q9C9K3	Pyrophosphate-fructose 6-phosphate 1-phosphotransferase	<i>Arabidopsis thaliana</i>	AT1G76550	02 Energy	02.01 Glycolysis	0	79	0,0021759	0,24941	0,27765	0,89829	evm_27.model.AmTr.v1.0_scaffold00022.14	-4,39E+01	24	73,80000305	15	-	12	0,6071	IPVLLHKEMLLESSKAMVTSGEVRSFVLLQPNPIHRGJSYVYLEFDL
790		8	Q9CA57	Glutathione S-transferase	<i>Arabidopsis thaliana</i>	AT1G74590	11 Disease/defence	11.06 Detoxification	5,00E-49	61	5,26E-05	1,00671	3,80321	0,2647	evm_27.model.AmTr.v1.0_scaffold00033.121	-4,20E+01	40	26,39999962	10	-	10	1,2222	AMVTSGEVKTIFFVEGEEQEK
793		12	Q9CA57	Glutathione S-transferase	<i>Arabidopsis thaliana</i>	AT1G74590	11 Disease/defence	11.06 Detoxification	5,00E-49	61	0,0010663	2,43627	6,5698	0,37083	evm_27.model.AmTr.v1.0_scaffold00033.121	-1,07E+01	11	26,39999962	2	-	2	0,2222	AMVTSGEVKTIFFVEGEEQEK
810		12	Q9CA57	Glutathione S-transferase	<i>Arabidopsis thaliana</i>	AT1G74590	11 Disease/defence	11.06 Detoxification	5,00E-49	61	0,0021851	1,58254	4,0931	0,38664	evm_27.model.AmTr.v1.0_scaffold00033.121	-1,71E+01	18	26,39999962	4	-	4	0,4444	AMVTSGEVKTIFFVEGEEQEK
1036		7	Q9CA57	Glutathione S-transferase	<i>Arabidopsis thaliana</i>	AT1G74590	11 Disease/defence	11.06 Detoxification	5,00E-49	61	0,0026609	3,25164	7,27437	0,447	evm_27.model.AmTr.v1.0_scaffold00033.121	-1,23E+01	10	26,39999962	2	-	2	0,2222	AMVTSGEVKTIFFVEGEEQEK
221		2	Q9CA83	Malate dehydrogenase	<i>Arabidopsis thaliana</i>	AT1G79750	02 Energy	02.10 TCA pathway	0,00E+00	87	0,0011093	3,70339	0,98016	3,77835	evm_27.model.AmTr.v1.0_scaffold00056.87	-1,98E+02	39	71,90000153	45	-	33	1,5517	ISAHIAANVATKISAHIAANVATK
424		9	Q9FF40	2S albumin	<i>Arabidopsis thaliana</i>	AT5G38160	06 Protein destination and storage	06.20 Storage proteins	2,70E+00	36	0,0156606	1,00376	0,52462	1,91332	evm_27.model.AmTr.v1.0_scaffold00005.212	-2,71E+01	31	16,79999924	9	7	5	1,2857	FIOTGRPEQQQIERSLMSEAGQEQEQQIER
407		14	Q9FF40	2S albumin	<i>Arabidopsis thaliana</i>	AT5G38160	06 Protein destination and storage	06.20 Storage proteins	2,70E+00	36	0,0092583	1,69181	1,84846	0,91526	evm_27.model.AmTr.v1.0_scaffold00005.212	-2,13E+01	20	16,79999924	8	7	3	1,2857	FIOTGRPEQQQIERSLMSEAGQEQEQQIER
768		6	Q9FF40	2S albumin	<i>Arabidopsis thaliana</i>	AT5G38160	06 Protein destination and storage	06.20 Storage proteins	2,70E+00	36	0,0010332	1,85717	5,783	0,32114	evm_27.model.AmTr.v1.0_scaffold00005.212	-9,20E+00	16	16,79999924	2	-	2	0,2857	FIOTGRPEQQQIERSLMSEAGQEQEQQIER
789		7	Q9FF40	2S albumin	<i>Arabidopsis thaliana</i>	AT5G38160	06 Protein destination and storage	06.20 Storage proteins	2,70E+00	36	0,017244	1,64782	1,94	0,84939	evm_27.model.AmTr.v1.0_scaffold00005.212	-1,23E+01	16	16,79999924	3	-	2	0,4286	FIOTGRPEQQQIERSLMSEAGQEQEQQIER
802		8	Q9FF40	2S albumin	<i>Arabidopsis thaliana</i>	AT5G38160	06 Protein destination and storage	06.20 Storage proteins	2,70E+00	36	0,0053343	1,5642	3,66597	0,42668	evm_27.model.AmTr.v1.0_scaffold00005.212	-1,14E+01	20	16,79999924	2	-	2	0,2857	FIOTGRPEQQQIERSLMSEAGQEQEQQIER
895		4	Q9FF40	2S albumin	<i>Arabidopsis thaliana</i>	AT5G38160	06 Protein destination and storage	06.20 Storage proteins	2,70E+00	36	0,0015653	1,69054	10,4031	0,1625	evm_27.model.AmTr.v1.0_scaffold00005.212	-1,07E+01	16	16,79999924	3	-	2	0,4286	FIOTGRPEQQQIERSLMSEAGQEQEQQIER
1066		4	Q9FF40	2S albumin	<i>Arabidopsis thaliana</i>	AT5G38160	06 Protein destination and storage	06.20 Storage proteins	2,70E+00	36	0,0002698	3,70566	10,3468	0,35815	evm_27.model.AmTr.v1.0_scaffold00005.212	-1,29E+01	20	16,79999924	2	-	2	0,2857	FIOTGRPEQQQIERSLMSEAGQEQEQQIER
944		8	Q9FF40	2S albumin	<i>Arabidopsis thaliana</i>	AT5G38160	06 Protein destination and storage	06.20 Storage proteins	2,70E+00	36	0,0003015	0,69549	7,23177	0,09617	evm_27.model.AmTr.v1.0_scaffold00005.212	-1,22E+01	20	16,79999924	2	-	2	0,2857	FIOTGRPEQQQIERSLMSEAGQEQEQQIER
224		2	Q9FF55	Protein disulfide isomerase	<i>Arabidopsis thaliana</i>	AT5G60640	06 Protein destination and storage	06.01 Folding and stability	0,00E+00	79	0,0007787	6,66879	4,48676	1,48633	evm_27.model.AmTr.v1.0_scaffold00175.37	-3,81E+01	15	63,70000076	6	-	6	0,2308	VDAIEDSLAOKSEFDPITVITERFGYLVYSR
564		8	Q9FFD2	UDP-arabinopyranose mutase	<i>Arabidopsis thaliana</i>	AT5G16510	09 Cell structure	09.01 Cell wall	e-110	70	0,011869	1,54894	2,36483	0,65499	evm_27.model.AmTr.v1.0_scaffold00020.62	-8,20E+00	6	39,09999847	2	-	2	0,1053	TAVTAEDCILEIAK
647	106	3	Q9F8H3	Cinnamoyl-CoA reductase	<i>Arabidopsis thaliana</i>	AT5G58490	20 Secondary metabolism	20.1 Phenylpropanoids/phenolics	e-124	67	0,0049465	0,22485	0,1798	1,25058	evm_27.model.AmTr.v1.0_scaffold00153.35	-1,87E+01	14	24,79999924	4	-	4	0,4444	FLHGLEGAESR
424		9	Q9FH31	2S albumin	<i>Arabidopsis thaliana</i>	AT5G54740	06 Protein destination and storage	06.20 Storage proteins	4,50E-02	55	0,0156606	1,00376	0,52462	1,91332	evm_27.model.AmTr.v1.0_scaffold00005.215	-2,12E+01	25	17,20000076	6	4	3	0,8571	FIOTGRPEQQQIERSLMSEAGQEQEQQIER
407		14	Q9FH31	2S albumin	<i>Arabidopsis thaliana</i>	AT5G54740	06 Protein destination and storage	06.20 Storage proteins	4,50E-02	55	0,0092583	1,69181	1,84846	0,91526	evm_27.model.AmTr.v1.0_scaffold00005.215	-2,11E+01	20	17,20000076	5	4	2	0,7143	FIOTGRPEQQQIERSLMSEAGQEQEQQIER
1058		2	Q9FHW7	S-phase kinase-associated protein	<i>Arabidopsis thaliana</i>	AT5G42190	06 Protein destination and storage	06.13 Proteolysis	2,00E-54	62	0,0010558	1,54866	3,87352	0,39981	evm_27.model.AmTr.v1.0_scaffold00029.181	-7,34E+00	15	17,89999962	2	-	2	0,2222	NDIPTDEFEERAPFPNSAIEIR
432		4	Q9F178	Shikimate O-hydroxycinnamoyltransferase	<i>Arabidopsis thaliana</i>	AT5G48930	20 Secondary metabolism	20.1 Phenylpropanoids/phenolics	3,00E-38	44	0,0133909	2,25306	1,32966	1,69447	evm_27.model.AmTr.v1.0_scaffold00002.43	-3,23E+01	17	48,79999924	6	-	6	0,3333	VAALHAAIAQVNDR
432		4	Q9F178	Shikimate O-hydroxycinnamoyltransferase	<i>Arabidopsis thaliana</i>	AT5G48930	20 Secondary metabolism	20.1 Phenylpropanoids/phenolics	1,00E-44	46	0,0133909	2,25306	1,32966	1,69447	evm_27.model.AmTr.v1.0_scaffold00038.22	-1,10E+01	7	48,29999924	3	-	3	0,1667	GVGEEETSGLR
564		8	Q9FJZ3	Beta-mannanase	<i>Arabidopsis thaliana</i>	AT5G66460	03 Cell growth/division	03.99 Other	e-149	75	0,011869	1,54894	2,36483	0,65499	evm_27.model.AmTr.v1.0_scaffold00003.131	-1,25E+02	40	47,90000153	28	11	22	1,4737	FNHVSVISREQFNPQYKPOYQWAR
564		8	Q9FJZ3	Beta-mannanase	<i>Arabidopsis thaliana</i>	AT5G66460	03 Cell growth/division	03.99 Other	e-149	78	0,011869	1,54894	2,36483	0,65499	evm_27.model.AmTr.v1.0_scaffold00003.124	-1,13E+02	24	47,79999924	21	4	19	1,5714	DLCGRPRPYQWAGDGCAGNOGOSLNS
645		7	Q9FLC0	Peroxidase	<i>Arabidopsis thaliana</i>	AT5G05340	11 Disease/defence	11.06 Detoxification	e-115	82	0,000128	1,30225	4,22239	0,30842	evm_27.model.AmTr.v1.0_scaffold00077.2	-1,46E+01	17	33,20000076	4	-	3	0,5714	MGNISPLTGSSGOVR
645		7	Q9FLC0	Peroxidase	<i>Arabidopsis thaliana</i>	AT5G05340	11 Disease/defence	11.06 Detoxification	3,00E-46	88	0,000128	1,30225	4,22239	0,30842	evm_27.model.AmTr.v1.0_scaffold00077.3	-1,41E+01	34	13,60000038	3	-	3	1,0000	MGNISPLTGSSRAGFNANSVIR
645		7	Q9FLC0	Peroxidase	<i>Arabidopsis thaliana</i>	AT5G05340	11 Disease/defence	11.06 Detoxification	e-108	78	0,000128	1,30225	4,22239	0,30842	evm_27.model.AmTr.v1.0_scaffold00077.150	-1,16E+01	10	32,5	2	-	2	0,1818	DSVVOLGGPSSYSPVPGRSYVSCAPILAIASSIQNLDSSG
269		6	Q9FN41	Bifunctional methylthioribulose-1-phosphate	<i>Arabidopsis thaliana</i>	AT5G53850	01 Metabolism	01.01 Amino Acid	0,00E+00	84	0,0024029	1,40422	0,8639	1,6255	evm_27.model.AmTr.v1.0_scaffold00068.116	-3,34E+01	12	57,40000153	4	-	4	0,1600	GPSRNDLISTYDSEF
743		7	Q9FN41	Bifunctional methylthioribulose-1-phosphate	<i>Arabidopsis thaliana</i>	AT5G53850	01 Metabolism	01.01 Amino Acid	0,00E+00	84	0,0033999	0,72625	3,326	0,21836	evm_27.model.AmTr.v1.0_scaffold00068.116	-1,28E+01	6	57,40000153	3	-	3	0,1200	NLDSSSGPSRAQLEDLKNLISTYDSEF
818		7	Q9FUS8	Glutathione S-transferase	<i>Arabidopsis thaliana</i>	AT1G10370	11 Disease/defence	11.06 Detoxification	7,00E-72	73	0,0072403	1,69716	3,47994	0,4877	evm_27.model.AmTr.v1.0_scaffold00022.188	-2,59E+01	28	25,39999962	5	-	5	0,6667	VPVLLHHWADSFSAEA

564	8	Q9FV1	GDSL esterase/lipase	<i>Arabidopsis thaliana</i>	AT1G71250	12 Unclear classification	12 Unclear classification	e-113	70	0,011869	1,54894	2,36483	0,65499	evm_27.model.AmTr.v1.0_scaffold00099.102	-1,29E+01	9	38	2	-	2	0,2500	NEGQITCLPLA TPCPNR	
627	6	Q9FV1	GDSL esterase/lipase	<i>Arabidopsis thaliana</i>	AT1G71250	12 Unclear classification	12 Unclear classification	e-113	70	0,0003956	3,60946	5,35739	0,67374	evm_27.model.AmTr.v1.0_scaffold00099.102	-3,43E+01	21	38	7	-	5	0,8750	ASAAGILDET GVLCGVNPR NEGQITCLPLA TPCPNR	
639	5	Q9FV1	GDSL esterase/lipase	<i>Arabidopsis thaliana</i>	AT1G71250	12 Unclear classification	12 Unclear classification	e-113	70	0,003018	2,45421	4,50863	0,54434	evm_27.model.AmTr.v1.0_scaffold00099.102	-2,16E+01	21	38	4	-	4	0,5000	NEGQITCLPLA TPCPNR	
1018	9	Q9FV1	GDSL esterase/lipase	<i>Arabidopsis thaliana</i>	AT1G71250	12 Unclear classification	12 Unclear classification	e-113	70	7,51E-05	2,87435	3,95283	0,72716	evm_27.model.AmTr.v1.0_scaffold00099.102	-1,24E+01	10	38	2	-	2	0,2500	ASAAGILDET NEGQITCLPLA TPCPNR	
402	3	Q9FWA3	6-Phosphogluconate dehydrogenase	<i>Arabidopsis thaliana</i>	AT3G02360	02 Energy	02.07 Pentose phosphate	0,00E+00	94	0,0116642	0,72452	4,74682	0,15263	evm_27.model.AmTr.v1.0_scaffold00061.203	-2,08E+02	64	53,79999924	56	45	38	2,6667	VDETVR GNHLR DNKGDGYLD	
731	124	3	Q9FX54	Glyceraldehyde-3-phosphate dehydrogenase	<i>Arabidopsis thaliana</i>	AT1G13440	02 Energy	02.01 Glycolysis	8,00E-95	86	9,55E-05	0,27662	0,17504	1,58028	evm_27.model.AmTr.v1.0_scaffold00177.24	-3,36E+01	42	24,70000076	9	-	6	1,4286	KVVISAPSK KVVISAPSK DAPMFVGVN
736	123	6	Q9FX54	Glyceraldehyde-3-phosphate dehydrogenase	<i>Arabidopsis thaliana</i>	AT1G13440	02 Energy	02.01 Glycolysis	8,00E-95	86	0,0008994	0,37749	0,30548	1,23571	evm_27.model.AmTr.v1.0_scaffold00177.24	-3,42E+01	33	24,70000076	9	-	6	1,4286	KVVISAPSK DAPMFVGVN FHEYKPDVH
742	120	5	Q9FX54	Glyceraldehyde-3-phosphate dehydrogenase	<i>Arabidopsis thaliana</i>	AT1G13440	02 Energy	02.01 Glycolysis	8,00E-95	86	4,48E-05	0,5563	0,22585	2,46319	evm_27.model.AmTr.v1.0_scaffold00177.24	-5,97E+01	42	24,70000076	16	-	13	2,4286	VVESTGVTFD K DAPMFVGVN
1002	14	Q9FXD2	Restriction endonuclease (type II)	<i>Arabidopsis thaliana</i>	AT1G67660	01 Metabolism	01.03 Nucleotides	0,01	55	0,0179685	1,00507	2,65214	0,37896	evm_27.model.AmTr.v1.0_scaffold00045.53	-1,53E+01	12	37,20000076	3	-	3	0,2308	DAPMFVGVN DSPINPSLR GCGVSLDST AGNSAFK	
467	11	Q9FXD2	Restriction endonuclease (type II)	<i>Arabidopsis thaliana</i>	AT1G67660	01 Metabolism	01.03 Nucleotides	0,01	55	0,0173342	0,83843	2,86452	0,29269	evm_27.model.AmTr.v1.0_scaffold00045.53	-7,34E+00	7	37,20000076	2	-	2	0,1538	DSPINPSLR DFTALTGGLNF PVQAGR	
218	2	Q9LDZ0	HSP70 (Heat shock cognate 70 kDa protein)	<i>Arabidopsis thaliana</i>	AT5G09590	06 Protein destination and storage	06.01 Folding and stability	0,00E+00	92	0,0063427	2,43317	2,16763	1,1225	evm_27.model.AmTr.v1.0_scaffold00046.170	-1,34E+02	43	71,90000153	32	-	24	1,0645	NAMGGENAE IK	
220	4	Q9LDZ0	HSP70 (Heat shock cognate 70 kDa protein)	<i>Arabidopsis thaliana</i>	AT5G09590	06 Protein destination and storage	06.01 Folding and stability	0,00E+00	92	0,0013779	2,6839	2,52121	1,06453	evm_27.model.AmTr.v1.0_scaffold00046.170	-1,43E+02	49	71,90000153	41	30	27	1,3226	NPKVWENSEG NAMGGENAE IK	
220	4	Q9LDZ0	HSP70 (Heat shock cognate 70 kDa protein) (mitochondrial)	<i>Arabidopsis thaliana</i>	AT5G09590	06 Protein destination and storage	06.01 Folding and stability	0,00E+00	87	0,0013779	2,6839	2,52121	1,06453	evm_27.model.AmTr.v1.0_scaffold00022.119	-3,81E+01	14	72,5	13	2	10	0,4194	RFDDPQTK HINEPTAAALSY GLNKK	
236	3	Q9LDZ0	HSP70 (Heat shock cognate 70 kDa protein)	<i>Arabidopsis thaliana</i>	AT5G09590	06 Protein destination and storage	06.01 Folding and stability	0,00E+00	92	0,0074384	1,27937	2,72956	0,46871	evm_27.model.AmTr.v1.0_scaffold00046.170	-2,51E+01	13	71,90000153	7	-	6	0,2581	NAMGGENAE IK	
675	8	Q9LE15	Peroxidase	<i>Arabidopsis thaliana</i>	AT1G14540	11 Disease/defence	11.06 Detoxification	3,00E-40	74	6,01E-05	4,28718	3,84318	1,11553	evm_27.model.AmTr.v1.0_scaffold00029.235	-1,46E+01	21	13,89999962	2	1	2	0,6667	SEVESICPGVV SCADILAAVAR	
689	9	Q9LE15	Peroxidase	<i>Arabidopsis thaliana</i>	AT1G14540	11 Disease/defence	11.06 Detoxification	3,00E-40	74	3,23E-06	0,86804	4,88286	1,65233	evm_27.model.AmTr.v1.0_scaffold00029.235	-1,18E+01	37	13,89999962	3	-	3	1,0000	GFEVIDEVK QLSSNFYDSS CPNALSTIR	
264	2	Q9LF46	2-hydroxyacyl-CoA lyase	<i>Arabidopsis thaliana</i>	AT5G17380	01 Metabolism	01.06 Lipid and sterol	0,00E+00	62	8,68E-05	2,8676	2,34851	1,22103	evm_27.model.AmTr.v1.0_scaffold00111.8	-1,37E+02	50	61,29999924	37	-	30	1,7619	HEMLOK RNPEISGPYK LDPYAGTESSG	
459	86	4	Q9LF88	Late embryogenesis abundant protein (LEA)	<i>Arabidopsis thaliana</i>	AT3G53040	11 Disease/defence	11.05 Stress responses	3e-44	37	0,0037057	0,46074	0,36244	1,27121	evm_27.model.AmTr.v1.0_scaffold00002.388	-1,93E+01	13	33,90000153	3	-	3	0,5000	AGEANDSAAD ATR
533	126	4	Q9LF88	Late embryogenesis abundant protein (LEA)	<i>Arabidopsis thaliana</i>	AT3G53040	11 Disease/defence	11.05 Stress responses	3e-44	37	0,0004666	0,35955	0,17708	2,03047	evm_27.model.AmTr.v1.0_scaffold00002.388	-2,17E+01	16	33,90000153	4	-	4	0,7500	REAVFDAGER AGEANDSAAD ATR
467	11	Q9LFA3	Monodehydroascorbate reductase	<i>Arabidopsis thaliana</i>	AT3G52880	11 Disease/defence	11.06 Detoxification	e-175	84	0,0173342	0,83843	2,86452	0,29269	evm_27.model.AmTr.v1.0_scaffold00069.193	-6,93E+01	35	47,09999847	12	-	12	0,6842	VYCVSGSGER EAVAPYERPAL SK	
471	8	Q9LFA3	Monodehydroascorbate reductase	<i>Arabidopsis thaliana</i>	AT3G52880	11 Disease/defence	11.06 Detoxification	e-175	84	0,004315	0,79614	2,56316	0,31061	evm_27.model.AmTr.v1.0_scaffold00069.193	-6,10E+01	32	47,09999847	10	-	10	0,5789	EAVAPYERPAL SK	
488	10	Q9LFA3	Monodehydroascorbate reductase	<i>Arabidopsis thaliana</i>	AT3G52880	11 Disease/defence	11.06 Detoxification	e-175	84	0,0120942	1,5885	2,29785	0,6913	evm_27.model.AmTr.v1.0_scaffold00069.193	-9,15E+01	40	47,09999847	16	-	15	0,9474	GTAVGFSDS EAVAPYERPAL SK	
510	9	Q9LFA3	Monodehydroascorbate reductase	<i>Arabidopsis thaliana</i>	AT3G52880	11 Disease/defence	11.06 Detoxification	e-175	84	0,0003295	2,01724	2,58062	0,78169	evm_27.model.AmTr.v1.0_scaffold00069.193	-2,48E+001	16	47,09999847	6	-	6	3,16E-001	AYLFFPGAAR PLTNLFK YGTLIATGSTV	
645	7	Q9LFA3	Monodehydroascorbate reductase	<i>Arabidopsis thaliana</i>	AT3G52880	11 Disease/defence	11.06 Detoxification	e-175	84	0,000128	1,30225	4,22239	0,30842	evm_27.model.AmTr.v1.0_scaffold00069.193	-2,28E+01	15	47,09999847	4	-	4	0,2105	VIGVFLGPTP EENK YGTLIATGSTV	
1002	14	Q9LFA3	Monodehydroascorbate reductase	<i>Arabidopsis thaliana</i>	AT3G52880	11 Disease/defence	11.06 Detoxification	e-175	84	0,0179685	1,00507	2,65214	0,37896	evm_27.model.AmTr.v1.0_scaffold00069.193	-7,61E+01	33	47,09999847	12	-	11	0,6316	EAVAPYERPAL LSDFGVOGAD	
782	9	Q9LIL3	Aluminum induced protein with YGL and LRR motifs	<i>Arabidopsis thaliana</i>	AT3G22850	13 Unclassified	13 Unclassified	6,00E-99	79	0,0006529	0,74675	3,14802	0,23721	evm_27.model.AmTr.v1.0_scaffold00002.570	-2,06E+01	18	27	4	-	4	0,4000	GPYPDPQVR LVGASMVYT ADK	
799	8	Q9LIP9	Glutamine-fructose-6-phosphate transaminase	<i>Arabidopsis thaliana</i>	AT3G24090	20 Secondary metabolism	20.5 Amines	0,00E+00	84	0,0125632	1,10491	2,40277	0,45985	evm_27.model.AmTr.v1.0_scaffold00095.96	-4,05E+00	5	76,59999847	2	-	2	0,0690	REAVIDGLFDL PNK LSEDSNNGAS	
471	8	Q9LKR3	HSP70 (Luminal binding protein 1)	<i>Arabidopsis thaliana</i>	AT5G28540	06 Protein destination and storage	06.01 Folding and stability	0,00E+00	90	0,004315	0,79614	2,56316	0,31061	evm_27.model.AmTr.v1.0_scaffold00002.574	-1,53E+01	5	74,19999695	3	2	3	0,1111	ALEDASLQK HINEPTAAAIAY GLDK	
488	10	Q9LKR3	HSP70 (Luminal binding protein 1)	<i>Arabidopsis thaliana</i>	AT5G28540	06 Protein destination and storage	06.01 Folding and stability	0,00E+00	90	0,0120942	1,5885	2,29785	0,6913	evm_27.model.AmTr.v1.0_scaffold00002.574	-1,38E+01	4	74,19999695	2	-	2	0,0741	VEIANDQGNR HINEPTAAAIAY GLDK	
510	9	Q9LKR3	HSP70 (Luminal binding protein 1)	<i>Arabidopsis thaliana</i>	AT5G28540	06 Protein destination and storage	06.01 Folding and stability	0,00E+00	90	0,0003295	2,01724	2,58062	0,78169	evm_27.model.AmTr.v1.0_scaffold00002.574	-1,15E+001	4	74,19999695	3	-	3	1,11E-001	HINEPTAAAIAY GLDK DAGVIAGI NVA QVVVGVGDK YAVYIQGK YAVYIQGK	
537	95	6	Q9LQ03	12S Globulin	<i>Arabidopsis thaliana</i>	AT1G07750	06 Protein destination and storage	06.20 Storage proteins	e-129	63	0,0002003	0,09174	0,1778	0,51598	evm_27.model.AmTr.v1.0_scaffold00044.174	-7,18E+01	45	38,40000153	18	-	14	1,6364	

564	8	Q9LQQ3	12S Globulin	<i>Arabidopsis thaliana</i>	AT1G07750	06 Protein destination and storage	06.20 Storage proteins	e-129	63	0,011869	1,54894	2,36483	0,65499	evm_27.model.AmTr.v1.0_scaffold00044.174	-2,58E+01	19	38,40000153	6	-	6	0,5455	TAFNVSPDMEK NCFEATLVDVLD VQVGVGVGKRR STEFVSR STEFVSR	
583	10	Q9LQQ3	12S Globulin	<i>Arabidopsis thaliana</i>	AT1G07750	06 Protein destination and storage	06.20 Storage proteins	e-129	63	0,0182765	1,26554	2,01037	0,62503	evm_27.model.AmTr.v1.0_scaffold00044.174	-5,45E+01	38	38,40000153	20	-	12	1,9091	NGFALPSPSYSD SAK KGDATIPAGK EGEEDPPISSS SSSPSVR VLDQGHVWEK	
1013	6	Q9LQQ3	12S Globulin	<i>Arabidopsis thaliana</i>	AT1G07750	06 Protein destination and storage	06.20 Storage proteins	e-129	63	2,22E-05	1,46601	3,04975	0,4807	evm_27.model.AmTr.v1.0_scaffold00044.174	-9,09E+00	10	38,40000153	3	-	3	0,2727	NGFALPSPSYSD SAK KGDATIPAGK EGEEDPPISSS SSSPSVR VLDQGHVWEK	
583	10	Q9LR75	Coproporphyrinogen-III oxidase (chloroplastic)	<i>Arabidopsis thaliana</i>	AT1G03475	02 Energy	02.30 Photosynthesis	e-165	83	0,0182765	1,26554	2,01037	0,62503	evm_27.model.AmTr.v1.0_scaffold00032.43	-1,87E+01	18	45,09999847	5	-	5	0,2727	YSLDDETVRK SSGSDAALLH PSLVKPEIDISE AVVTGSSDSK R CPJAILGAFIDK	
793	12	Q9LUG8	Dienelactone hydrolase domain-containing protein	<i>Arabidopsis thaliana</i>	AT3G23600	11 Disease/defence	11.06 Detoxification	6,00E-84	77	0,0010663	2,43627	6,5698	0,37083	evm_27.model.AmTr.v1.0_scaffold00025.100	-1,42E+01	30	25,89999962	3	-	3	0,3077	YSLDDETVRK SSGSDAALLH PSLVKPEIDISE AVVTGSSDSK R CPJAILGAFIDK	
802	8	Q9LUG8	Dienelactone hydrolase domain-containing protein	<i>Arabidopsis thaliana</i>	AT3G23600	11 Disease/defence	11.06 Detoxification	6,00E-84	77	0,0053343	1,5642	3,66597	0,42668	evm_27.model.AmTr.v1.0_scaffold00025.100	-8,43E+00	9	25,89999962	2	-	2	0,1538	YSLDDETVRK SSGSDAALLH PSLVKPEIDISE AVVTGSSDSK R CPJAILGAFIDK	
15	2	1	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	4,00E-53	48	0,0068724	0,19404	0,21547	0,90054	evm_27.model.AmTr.v1.0_scaffold00002.657	-1,36E+02	65	43,5	42	-	24	2,0000	MEMACPH KGDATIPAGK KGDATIPAGK
145	4	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	4,00E-53	48	0,0018854	2,07447	0,8712	2,38116	evm_27.model.AmTr.v1.0_scaffold00002.657	-8,45E+00	6	59,79999924	2	-	2	0,0714	ISNDHGLEYLEL DETEYSPFLR KGDATIPAGK ACSDSVFVVG PR ASOFENLQIC	
221	2	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	4,00E-53	48	0,0011093	3,70339	0,98016	3,77835	evm_27.model.AmTr.v1.0_scaffold00002.657	-7,99E+00	5	59,79999924	2	-	2	0,0714	ISNDHGLEYLEL DETEYSPFLR KGDATIPAGK ACSDSVFVVG PR ASOFENLQIC	
269	6	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	4,00E-53	48	0,0024029	1,40422	0,8639	1,62545	evm_27.model.AmTr.v1.0_scaffold00002.657	-2,96E+01	14	59,79999924	5	-	5	0,2143	DISTEHGSFR KGDATIPAGK ACSDSVFVVG PR	
321	131	5	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	4,00E-53	48	0,0023794	0,45958	0,32038	1,43448	evm_27.model.AmTr.v1.0_scaffold00002.657	-8,96E+01	60	43,5	23	-	18	1,0870	MEMACPH KGDATIPAGK MEMACPHVSGG KGDATIPAGK
346	51	3	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	4,00E-53	48	0,0001011	0,18479	0,17894	1,03268	evm_27.model.AmTr.v1.0_scaffold00002.657	-1,93E+02	68	43,5	78	-	39	3,5652	MEMACPH KGDATIPAGK MEMACPHVSGG KGDATIPAGK
347	52	1	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	4,00E-53	48	0,0061084	0,07817	0,16902	0,46245	evm_27.model.AmTr.v1.0_scaffold00002.657	-1,65E+02	57	43,5	57	-	32	2,5217	MEMACPH KGDATIPAGK MEMACPHVSGG KGDATIPAGK
349	58	3	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	4,00E-53	48	3,36E-05	0,25222	0,24991	1,00927	evm_27.model.AmTr.v1.0_scaffold00002.657	-1,62E+02	60	43,5	58	-	28	2,6522	MEMACPH KGDATIPAGK MEMACPHVSGG KGDATIPAGK
355	66	3	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	4,00E-53	48	0,0027293	0,30401	0,15949	1,90621	evm_27.model.AmTr.v1.0_scaffold00002.657	-1,19E+02	60	43,5	38	-	24	1,8261	MEMACPH KGDATIPAGK MEMACPHVSGG KGDATIPAGK
371	57	1	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	4,00E-53	48	0,0011097	0,28952	0,12721	2,27602	evm_27.model.AmTr.v1.0_scaffold00002.657	-1,58E+02	61	43,5	54	-	29	2,4783	MEMACPH KGDATIPAGK MEMACPHVSGG KGDATIPAGK
424	9	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	4,00E-53	48	0,0156606	1,00376	0,52462	1,91332	evm_27.model.AmTr.v1.0_scaffold00002.657	-3,72E+01	18	59,79999924	8	-	8	0,2857	MEMACPH KGDATIPAGK DISTEHGSFR EVSFNVPFR	
459	86	4	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	4,00E-53	48	0,0037057	0,46074	0,36244	1,27121	evm_27.model.AmTr.v1.0_scaffold00002.657	-2,70E+01	15	43,5	6	-	4	0,3043	MEMACPH KGDATIPAGK ATEIYVILEGR ASOFENLQIC ACPHVSGR
523	90	2	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	4,00E-53	48	4,13E-05	0,23029	0,18131	1,27018	evm_27.model.AmTr.v1.0_scaffold00002.657	-2,05E+02	49	43,5	79	-	39	3,6957	MEMACPH KGDATIPAGK TIPAGK
537	95	6	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	4,00E-53	48	0,0002003	0,09174	0,1778	0,51598	evm_27.model.AmTr.v1.0_scaffold00002.657	-9,80E+01	54	43,5	23	-	17	1,1304	MEMACPHVSGG GR MACPHVSGG
539	93	4	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	4,00E-53	48	0,0017522	0,13283	0,24423	0,54388	evm_27.model.AmTr.v1.0_scaffold00002.657	-1,60E+02	57	43,5	57	-	31	2,8696	MEMACPH ARIEMACPH KGDATIPAGK
682	112	2	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	4,00E-53	48	0,0108656	0,37066	0,18761	1,97568	evm_27.model.AmTr.v1.0_scaffold00002.657	-2,07E+01	19	43,5	6	-	6	0,2609	GGQPIVR PSSEQLGGLIH GGSGGK
713	1136	5	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	4,00E-53	48	0,0019856	0,39246	0,12791	3,06829	evm_27.model.AmTr.v1.0_scaffold00002.657	-3,14E+01	27	43,5	8	-	7	0,3913	EVSFNVPFR PSSEQLGGLIH GGSGGK
731	124	3	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	4,00E-53	48	9,55E-05	0,27662	0,17504	1,58028	evm_27.model.AmTr.v1.0_scaffold00002.657	-5,57E+01	35	43,5	14	-	11	0,6522	MEMACPH ARIEMACPHV SGR
736	123	6	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	4,00E-53	48	0,0008994	0,37749	0,30548	1,23571	evm_27.model.AmTr.v1.0_scaffold00002.657	-4,54E+01	28	43,5	11	-	8	0,5217	MEMACPH MEMACPHVSGG GR
264	2	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	4,00E-53	48	8,68E-05	2,8676	2,34851	1,22103	evm_27.model.AmTr.v1.0_scaffold00002.657	-1,93E+01	9	59,79999924	4	-	4	0,1429	KGDATIPAGK DISTEHGSFR DADIIYYANG KGDATIPAGK	
291	2	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	4,00E-53	48	0,0003834	2,93432	2,88705	1,01637	evm_27.model.AmTr.v1.0_scaffold00002.657	-3,24E+01	17	59,79999924	7	-	7	0,2500	DISTEHGSFR GVTGNPYAFE	
742	120	5	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	4,00E-53	48	4,48E-05	0,5563	0,22585	2,46319	evm_27.model.AmTr.v1.0_scaffold00002.657	-3,25E+01	27	43,5	8	-	7	0,3913	MEMACPH AQSDSVFVVG GR ERESESESEGR R KGDATIPAGK
407	14	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	4,00E-53	48	0,0092583	1,69181	1,84846	0,91526	evm_27.model.AmTr.v1.0_scaffold00002.657	-1,11E+02	40	59,79999924	25	-	21	0,9286	MEMACPH KGDATIPAGK	
583	10	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	4,00E-53	48	0,0182765	1,26554	2,01037	0,62503	evm_27.model.AmTr.v1.0_scaffold00002.657	-1,63E+01	8	59,79999924	4	-	4	0,1429	DISTEHGSFR GVTGNPYAFE	
782	9	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	4,00E-53	48	0,0006529	0,74675	3,14802	0,23721	evm_27.model.AmTr.v1.0_scaffold00002.657	-9,56E+00	4	59,79999924	2	-	2	0,0714	GVTGNPYAFER AFSDEILEASF	

627	6	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	4,00E-53	48	0,0003956	3,60946	5,35739	0,67374	evm_27.model.AmTr_v1.0_scaffold00002.6_57	-1,69E+01	15	59,79999924	5	-	5	0,2143	DISTEHGSFR GVGTGNPYAFER	
675	8	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	4,00E-53	48	6,01E-05	4,28718	3,84318	1,11553	evm_27.model.AmTr_v1.0_scaffold00002.6_57	-8,13E+00	7	59,79999924	2	-	2	0,1071	ACSDSVFVVG PRISNDHGELYEL	
689	9	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	4,00E-53	48	3,23E-06	8,06804	4,88286	1,65232	evm_27.model.AmTr_v1.0_scaffold00002.6_57	-6,55E+00	5	59,79999924	2	-	2	0,0714	ISNDHGELYEL DETEYSPRLR ATRYVILEGR ACSDSVFVVG PRNSLNQIFER	
774	4	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	4,00E-53	48	0,0178635	2,04497	3,67878	0,55588	evm_27.model.AmTr_v1.0_scaffold00002.6_57	-2,34E+01	11	59,79999924	5	-	5	0,1786	NSLNQIFER	
810	12	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	4,00E-53	48	0,0021851	1,58254	4,0931	0,38664	evm_27.model.AmTr_v1.0_scaffold00002.6_57	-3,30E+01	16	59,79999924	6	-	6	0,2143	KGDTATIPAGK DISTEHGSFR GGPIVRPSS EQ	
832	3	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	4,00E-53	48	0,0172602	3,88032	2,10717	1,84148	evm_27.model.AmTr_v1.0_scaffold00002.6_57	-4,68E+01	18	59,79999924	13	-	11	0,4643	DISTEHGSFR STEHGSFR LVTIGEER	
833	6	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	4,00E-53	48	0,0133914	4,64276	2,00655	2,31381	evm_27.model.AmTr_v1.0_scaffold00002.6_57	-5,61E+01	21	59,79999924	22	-	15	0,8571	GGPIVRPSS EQ TTYINKDSOR	
1018	9	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	4,00E-53	48	7,51E-05	2,87435	3,95283	0,72716	evm_27.model.AmTr_v1.0_scaffold00002.6_57	-2,13E+01	15	59,79999924	6	-	6	0,2143	IEMACPH IEMACPHVSG GE	
1019	4	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	4,00E-53	48	0,0016868	2,39482	3,51011	0,68226	evm_27.model.AmTr_v1.0_scaffold00002.6_57	-1,33E+01	8	59,79999924	3	-	3	0,1071	PSSEOLOGLIH GGSGGGK ATRYVILEGR	
821	170	4	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	4,00E-53	48	0,0172238	4,04096	0,44829	0,98364	evm_27.model.AmTr_v1.0_scaffold00002.6_57	-2,98E+01	21	43,5	6	-	6	0,3043	KGDTATIPAGK GGPIVRPSS EQ GGSGGGK	
827	166	2	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	4,00E-53	48	0,0001876	0,06927	0,04685	1,47864	evm_27.model.AmTr_v1.0_scaffold00002.6_57	-1,78E+01	14	43,5	5	-	4	0,2174	KGDTATIPAGK GGPIVRPSS EQ	
836	168	2	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	4,00E-53	48	0,0032058	0,61535	0,19061	3,22831	evm_27.model.AmTr_v1.0_scaffold00002.6_57	-2,46E+01	18	43,5	6	-	5	0,3043	KGDTATIPAGK GGPIVRPSS EQ	
842	169	4	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	4,00E-53	48	0,0056319	0,80598	0,20929	3,85098	evm_27.model.AmTr_v1.0_scaffold00002.6_57	-2,22E+01	14	43,5	6	-	6	0,2609	KGDTATIPAGK LVTIGEER GGPIVRPSS EQ	
843	4	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	06.20 Storage proteins	4,00E-53	48	0,0054464	1,06921	0,166	6,44124	evm_27.model.AmTr_v1.0_scaffold00002.6_57	-1,98E+01	6	59,79999924	4	-	4	0,1429	GGPIVRPSS GGPIVRPSS EQ	
871	284	3	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	4,00E-53	48	1,59E-05	0,13357	0,05308	2,51653	evm_27.model.AmTr_v1.0_scaffold00002.6_57	-1,17E+01	16	43,5	4	-	3	0,2174	AFSDEILEAGF NVDI KGDTATIPAGK	
1074	54	1	Q9LUJ7	Cupin family protein (Nutrient reservoir protein)	<i>Arabidopsis thaliana</i>	AT3G22640	06 Protein destination and storage	4,00E-53	48	0,0010006	0,27312	0,21134	1,29238	evm_27.model.AmTr_v1.0_scaffold00002.6_57	-2,17E+02	69	43,5	85	-	42	3,9130	IEMACPH ARIEMACPH KGDTATIPAGK	
736	123	6	Q9LUM3	Subtilase family protein	<i>Arabidopsis thaliana</i>	AT3G14240	06 Protein destination and storage	06.13 Proteolysis	0	55	0,0008994	0,37749	0,30548	1,23571	evm_27.model.AmTr_v1.0_scaffold00003.1_07	-1,82E+01	8	61	6	-	5	0,3333	SVASGMAPLA R ASALGYAR
537	95	6	Q9LVC5	Phosphoglucose isomerase	<i>Arabidopsis thaliana</i>	AT5G57330	02 Energy	02.01 Glycolysis	e-143	76	0,0002003	0,09174	0,1778	0,51598	evm_27.model.AmTr_v1.0_scaffold00019.3_39	-3,96E+01	33	35,20000076	8	-	7	0,6471	I AVLDRHEK QELSAVPSY GGPIVRPSS LFLRPEPSVEG YSTPGGYSK GGDCDLGEV
467	11	Q9LV19	Senescence-related protein dihydroorotate dehydrogenase-like	<i>Arabidopsis thaliana</i>	AT3G17810	12 Unclear classification	12 Unclear classification	0,00E+00	89	0,0173342	0,83843	2,86452	0,29269	evm_27.model.AmTr_v1.0_scaffold00176.8_0	-8,94E+00	11	46,90000153	3	-	3	0,1579	GGPIVRPSS GGPIVRPSS GGPIVRPSS	
467	11	Q9LYE7	Uncharacterized protein	<i>Arabidopsis thaliana</i>	AT5G11420	13 Unclassified	13 Unclassified	e-147	85	0,0173342	0,83843	2,86452	0,29269	evm_27.model.AmTr_v1.0_scaffold00042.5_0	-2,03E+01	22	35,79999924	5	-	5	0,5000	LGNNEAYIR CGDMLLVYPE GACAVR	
502	1	Q9LYR4	Transaldolase	<i>Arabidopsis thaliana</i>	AT5G13420	02 Energy	02.07 Pentose phosphate	e-163	87	0,0032833	3,88104	5,36256	0,72373	evm_27.model.AmTr_v1.0_scaffold00016.4_57	-3,87E+01	22	47,29999924	10	-	8	0,5789	TIDSNVEQAK IGPDTVSTMP DK	
313	41	2	Q9LZC3	Malate synthase	<i>Arabidopsis thaliana</i>	AT5G03860	02 Energy	02.10 TCA pathway	0,00E+00	75	0,0073752	0,55087	0,19939	2,76283	evm_27.model.AmTr_v1.0_scaffold00049.8_6	-6,47E+00	6	64,80000305	3	-	3	0,1111	DHSVGLNCGR HGAVLGDGQV K
828	6	Q9LZG0	Adenosine kinase	<i>Arabidopsis thaliana</i>	AT5G03300	01 Metabolism	01.03 Nucleotides	e-166	91	0,014279	0,94689	1,68458	0,56209	evm_27.model.AmTr_v1.0_scaffold00148.6_2	-1,86E+01	8	37,5	2	-	2	0,1250	AGCYAANEIIQ R I AVITOGADPV VMDEVVSR VESEVLCR ALHDGLEMMIG	
793	12	Q9M1X2	Chalcone-flavanone isomerase family protein	<i>Arabidopsis thaliana</i>	AT3G63170	01 Metabolism	01.06 Lipid and sterol	2,00E-37	61	0,0010663	2,43627	6,5698	0,37083	evm_27.model.AmTr_v1.0_scaffold00061.1_92	-7,34E+01	62	23,20000076	27	-	16	2,0667	VESEVLCR ALHDGLEMMIG	
799	8	Q9M1X2	Chalcone-flavanone isomerase family protein	<i>Arabidopsis thaliana</i>	AT3G63170	01 Metabolism	01.06 Lipid and sterol	2,00E-37	61	0,0125632	1,10491	2,40277	0,45985	evm_27.model.AmTr_v1.0_scaffold00061.1_92	-3,37E+01	39	23,20000076	8	-	6	0,6000	VESEVLCR IFNDNLGASIK LVVYGGGLNM	
802	8	Q9M1X2	Chalcone-flavanone isomerase family protein	<i>Arabidopsis thaliana</i>	AT3G63170	01 Metabolism	01.06 Lipid and sterol	2,00E-37	61	0,0053343	1,5642	3,66597	0,42668	evm_27.model.AmTr_v1.0_scaffold00061.1_92	-5,70E+01	54	23,20000076	14	-	12	1,0000	VMDEVVSR VESEVLCR KIFNDNLGASIK AKFESAPSEPK VMDEVVSR	
808	9	Q9M1X2	Chalcone-flavanone isomerase family protein	<i>Arabidopsis thaliana</i>	AT3G63170	01 Metabolism	01.06 Lipid and sterol	2,00E-37	61	0,0012118	3,14897	4,15446	0,75797	evm_27.model.AmTr_v1.0_scaffold00061.1_92	-7,45E+01	69	23,20000076	21	-	14	1,6000	AKFESAPSEPK VMDEVVSR	
810	12	Q9M1X2	Chalcone-flavanone isomerase family protein	<i>Arabidopsis thaliana</i>	AT3G63170	01 Metabolism	01.06 Lipid and sterol	2,00E-37	61	0,0021851	1,58254	4,0931	0,38664	evm_27.model.AmTr_v1.0_scaffold00061.1_92	-5,90E+01	68	23,20000076	18	-	14	1,4000	FESAPSEPK VESEVLCR LSQGNNDL VMDEVVSR	
818	7	Q9M1X2	Chalcone-flavanone isomerase family protein	<i>Arabidopsis thaliana</i>	AT3G63170	01 Metabolism	01.06 Lipid and sterol	2,00E-37	61	0,0072403	1,69716	3,47994	0,4877	evm_27.model.AmTr_v1.0_scaffold00061.1_92	-3,17E+01	45	23,20000076	8	-	8	0,5333	VESEVLCR LSQGNNDL	
1036	7	Q9M1X2	Chalcone-flavanone isomerase family protein	<i>Arabidopsis thaliana</i>	AT3G63170	01 Metabolism	01.06 Lipid and sterol	2,00E-37	61	0,0026609	3,25164	7,27437	0,447	evm_27.model.AmTr_v1.0_scaffold00061.1_92	-3,13E+01	37	23,20000076	6	-	6	0,4667	LSQGNNDL LOR FNDNLGASIK VMDEVVSR VESEVLCR LSQGNNDL	
782	9	Q9M1X2	Chalcone-flavanone isomerase family protein	<i>Arabidopsis thaliana</i>	AT3G63170	01 Metabolism	01.06 Lipid and sterol	2,00E-37	61	0,0006529	0,74675	3,14802	0,23721	evm_27.model.AmTr_v1.0_scaffold00061.1_92	-4,38E+01	56	23,20000076	10	-	9	0,7333	VMDEVVSR VESEVLCR LSQGNNDL	

944	8	Q9M1X2	Chalcone-flavanone isomerase family protein	<i>Arabidopsis thaliana</i>	AT3G63170	01 Metabolism	01.06 Lipid and sterol	2.00E-37	61	0.0003015	0.69549	7.23177	0.09617	evm_27.model.AmTr.v1.0_scaffold00061.1.92	-9.62E+00	11	23.20000076	2	-	2	0.1333	NLLGLVPLKIY LTVR	
294	8	Q9M5K2	Dihydroipoamide dehydrogenase	<i>Arabidopsis thaliana</i>	AT3G17240	02 Energy	02.10 TCA pathway	0.00E+00	86	0.0070497	3.75653	4.0454	0.92859	evm_27.model.AmTr.v1.0_scaffold00014.1.14	-5.25E+01	36	53.90000153	12	5	10	0.5833	NMVCVDASGS GVR VMGVVASGS	
302	38	2	Q9M5K3	Dihydroipoamide dehydrogenase	<i>Arabidopsis thaliana</i>	AT1G48030	02 Energy	02.10 TCA pathway	0.00E+00	87	0.000944	0.59421	0.2155	2.75736	evm_27.model.AmTr.v1.0_scaffold00064.4.9	-8.25E+01	40	53.79999924	19	2	17	0.8261	AAQLGLR GALGGTCLNV GSPK
459	86	4	Q9M5K3	Dihydroipoamide dehydrogenase	<i>Arabidopsis thaliana</i>	AT1G48030	02 Energy	02.10 TCA pathway	0.00E+00	87	0.0037057	0.46074	0.36244	1.27121	evm_27.model.AmTr.v1.0_scaffold00064.4.9	-1.18E+02	42	53.79999924	30	-	18	1.3478	EAAMATYDR TCHAHPTLSE AVK
294	8	Q9M5K3	Dihydroipoamide dehydrogenase	<i>Arabidopsis thaliana</i>	AT1G48030	02 Energy	02.10 TCA pathway	0.00E+00	87	0.0070497	3.75653	4.0454	0.92859	evm_27.model.AmTr.v1.0_scaffold00064.4.9	-3.62E+01	21	53.79999924	8	1	8	0.3478	VTGVDAQSDSG VR	
342	65	3	Q9M5K5	Dihydroipoamide dehydrogenase	<i>Arabidopsis thaliana</i>	AT3G16950	02 Energy	02.10 TCA pathway	0.00E+00	82	0.0079229	0.26873	0.11466	2.34363	evm_27.model.AmTr.v1.0_scaffold00003.1.6	-1.06E+02	40	57.09999847	22	-	17	1.0952	SNLTNSMK QGVADHANL ASK
355	66	3	Q9M5K5	Dihydroipoamide dehydrogenase	<i>Arabidopsis thaliana</i>	AT3G16950	02 Energy	02.10 TCA pathway	0.00E+00	82	0.0027293	0.30401	0.15949	1.90621	evm_27.model.AmTr.v1.0_scaffold00003.1.6	-1.04E+02	42	57.09999847	26	-	19	1.3333	IMLAHTASAG QGVADHANL ASK
488	10	Q9M8M7	Acetylornithine aminotransferase (chloroplastic/mitochondrial)	<i>Arabidopsis thaliana</i>	AT1G80600	01 Metabolism	01.01 Amino Acid	e-169	82	0.0120942	1.5885	2.29785	0.6913	evm_27.model.AmTr.v1.0_scaffold00032.1.26	-1.39E+01	9	57.20000076	2	-	2	0.1200	LVDSCFADR IFFNSNGTEAN FAAK	
1002	14	Q9M8M7	Acetylornithine aminotransferase (chloroplastic/mitochondrial)	<i>Arabidopsis thaliana</i>	AT1G80600	01 Metabolism	01.01 Amino Acid	e-169	82	0.0179685	1.00507	2.65214	0.37896	evm_27.model.AmTr.v1.0_scaffold00032.1.26	-2.54E+01	12	57.20000076	5	-	5	0.2000	LVDSCFADR ELEQVEILCK IFFNSNGTEAN	
236	3	Q9M9K1	Phosphoglycerate mutase	<i>Arabidopsis thaliana</i>	AT3G08590	02 Energy	02.01 Glycolysis	0.00E+00	82	0.0074384	1.27937	2.72956	0.46871	evm_27.model.AmTr.v1.0_scaffold00077.2.11	-1.70E+02	62	61.29999924	40	-	35	1.6667	SALEAVRK GVDAQIASGG GR	
488	10	Q9M9K1	Phosphoglycerate mutase	<i>Arabidopsis thaliana</i>	AT3G08590	02 Energy	02.01 Glycolysis	0.00E+00	82	0.0120942	1.5885	2.29785	0.6913	evm_27.model.AmTr.v1.0_scaffold00077.2.11	-9.90E+00	4	61.29999924	2	-	2	0.0833	GVDAQIASGG GR TSGEVILVHNGI GVDAQIASGG GR	
510	9	Q9M9K1	Phosphoglycerate mutase	<i>Arabidopsis thaliana</i>	AT3G08590	02 Energy	02.01 Glycolysis	0.00E+00	82	0.0003295	2.01724	2.58062	0.78169	evm_27.model.AmTr.v1.0_scaffold00077.2.11	-1.69E+001	7	61.29999924	4	-	4	1.67E-001	VHLLTDGR	
600	6	Q9M9M7	Zinc-binding dehydrogenase family protein	<i>Arabidopsis thaliana</i>	AT3G03080	13 Unclassified	13 Unclassified	2.00E-17	77	0.0178552	5.14912	4.89334	1.05227	evm_27.model.AmTr.v1.0_scaffold00013.6.3	-9.68E+00	63	8.800000191	3	-	3	0.8000	TPSYSSDSK ETDFEMVPS LKK	
1013	6	Q9M9M7	Zinc-binding dehydrogenase family protein	<i>Arabidopsis thaliana</i>	AT3G03080	13 Unclassified	13 Unclassified	2.00E-17	77	2.22E-05	1.46601	3.04975	0.4807	evm_27.model.AmTr.v1.0_scaffold00013.6.3	-9.66E+00	39	8.800000191	3	-	3	0.6000	TPSYSSDSK ETDFEMVPS LKK	
675	8	Q9M9Q9	Peroxidase	<i>Arabidopsis thaliana</i>	AT1G14550	11 Disease/defence	11.06 Detoxification	e-108	75	6.01E-05	4.28718	3.84318	1.11553	evm_27.model.AmTr.v1.0_scaffold00029.2.31	-3.16E+01	23	33.90000153	7	6	5	1.0000	IHNEANIDSGF ASTR IHNEANIDSGF ASTR	
689	9	Q9M9Q9	Peroxidase	<i>Arabidopsis thaliana</i>	AT1G14550	11 Disease/defence	11.06 Detoxification	e-108	75	3.23E-06	8.06804	4.88286	1.65232	evm_27.model.AmTr.v1.0_scaffold00029.2.31	-1.80E+01	13	33.90000153	3	-	3	0.4286	IHNEANIDSGF ASTR MGDQPI TGS FRKNNLLGK	
150	16	2	Q9S9N1	HSP70 (heat shock protein)	<i>Arabidopsis thaliana</i>	AT1G16030	06 Protein destination and storage	06.01 Folding and stability	0.00E+00	80	0.0011266	0.4233	0.21509	1.96797	evm_27.model.AmTr.v1.0_scaffold00137.8	-7.51E+01	23	71.59999847	15	-	13	0.7619	FRKNNLLGK FSDPSVQADM K
153	16	2	Q9S9N1	HSP70 (heat shock protein)	<i>Arabidopsis thaliana</i>	AT1G16030	06 Protein destination and storage	06.01 Folding and stability	0.00E+00	80	0.0053885	0.52253	0.24434	2.13855	evm_27.model.AmTr.v1.0_scaffold00137.8	-7.51E+01	23	71.59999847	15	-	13	0.7619	FRKNNLLGK FSDPSVQADM K
235	19	6	Q9S9N1	HSP70 (heat shock protein)	<i>Arabidopsis thaliana</i>	AT1G16030	06 Protein destination and storage	06.01 Folding and stability	0.00E+00	80	0.0059659	0.70174	0.26816	2.61681	evm_27.model.AmTr.v1.0_scaffold00137.8	-3.74E+01	14	71.59999847	7	-	7	0.3333	VEIIPNDQGNR ATAGDTHLGG RFSDFPSVQAD MK
1004	77	2	Q9S9N1	HSP70 (heat shock protein)	<i>Arabidopsis thaliana</i>	AT1G16030	06 Protein destination and storage	06.01 Folding and stability	0.00E+00	80	0.0035325	0.58442	0.31418	1.86015	evm_27.model.AmTr.v1.0_scaffold00137.8	-1.50E+02	36	71.59999847	34	-	24	1.7619	ATAGDTHLGG RFSDFPSVQAD MK
143	11	1	Q9S9P4	S-adenosyl-L-methionine-dependent methyltransferase (7-)	<i>Arabidopsis thaliana</i>	AT1G30550	04 Transcription	04.22 mRNA processing	2e-79	68	0.001741	0.5739	0.2859	2.00727	evm_27.model.AmTr.v1.0_scaffold00019.5.7	-1.99E+02	35	122	57	-	35	1.3043	SSLSEDOQK AGVVSAGDK SKGVTAAPIR K
150	16	2	Q9S9P4	S-adenosyl-L-methionine-dependent methyltransferase (7-)	<i>Arabidopsis thaliana</i>	AT1G30550	04 Transcription	04.22 mRNA processing	2e-79	68	0.0011266	0.4233	0.21509	1.96797	evm_27.model.AmTr.v1.0_scaffold00019.5.7	-1.34E+02	24	122	32	-	25	0.7391	SSLSEDOQK KASDLLOK FHSDDSDLDK
153	16	2	Q9S9P4	S-adenosyl-L-methionine-dependent methyltransferase (7-)	<i>Arabidopsis thaliana</i>	AT1G30550	04 Transcription	04.22 mRNA processing	2e-79	68	0.0053885	0.52253	0.24434	2.13855	evm_27.model.AmTr.v1.0_scaffold00019.5.7	-1.34E+02	24	122	32	-	25	0.7391	SSLSEDOQK KASDLLOK FHSDDSDLDK
235	19	6	Q9S9P4	S-adenosyl-L-methionine-dependent methyltransferase (7-)	<i>Arabidopsis thaliana</i>	AT1G30550	04 Transcription	04.22 mRNA processing	2e-79	68	0.0059659	0.70174	0.26816	2.61681	evm_27.model.AmTr.v1.0_scaffold00019.5.7	-1.32E+02	30	122	33	30	26	0.7391	KASDLLOK AYEVANTPSLK FGLDEAH
736	123	6	Q9S9P4	S-adenosyl-L-methionine-dependent methyltransferase (7-)	<i>Arabidopsis thaliana</i>	AT1G30550	04 Transcription	04.22 mRNA processing	2e-79	68	0.0008994	0.37749	0.30548	1.23571	evm_27.model.AmTr.v1.0_scaffold00019.5.7	-5.94E+01	11	122	11	-	11	0.2826	FGLDEAHGK PAASLLDK FELTIOAGDK
757	178	2	Q9S9P4	S-adenosyl-L-methionine-dependent methyltransferase (7-)	<i>Arabidopsis thaliana</i>	AT1G30550	04 Transcription	04.22 mRNA processing	2e-79	68	0.0050002	0.17494	0.7288	0.24004	evm_27.model.AmTr.v1.0_scaffold00019.5.7	-6.91E+00	2	122	3	-	3	0.0652	APWSSLDENK IQVPVDIAPK
523	90	2	Q9SAJ4	Phosphoglycerate kinase	<i>Arabidopsis thaliana</i>	AT1G79550	02 Energy	02.01 Glycolysis	0.00E+00	93	4.13E-05	0.23029	0.18131	1.27018	evm_27.model.AmTr.v1.0_scaffold00062.1.99	-2.43E+01	20	42.40000153	4	-	4	0.2273	RPPAAVGSGR VDLNVPLDDN QK
533	126	4	Q9SAJ4	Phosphoglycerate kinase	<i>Arabidopsis thaliana</i>	AT1G79550	02 Energy	02.01 Glycolysis	0.00E+00	93	0.0004666	0.35955	0.17708	2.03047	evm_27.model.AmTr.v1.0_scaffold00062.1.99	-1.17E+02	63	42.40000153	24	-	19	1.1364	AHASTEGLAK YLMENGAK YILASHIGR LSSPHDEVR
539	93	4	Q9SCX9	Glycerol-3-phosphate dehydrogenase	<i>Arabidopsis thaliana</i>	AT5G40610	01 Metabolism	01.06 Lipid and sterol	e-164	78	0.0017522	0.13283	0.24423	0.54388	evm_27.model.AmTr.v1.0_scaffold00049.11.1	-1.01E+01	15	42.5	3	-	3	0.3125	VRPDAQAISL K
627	6	Q9SD45	Epoxide hydrolase-like protein	<i>Arabidopsis thaliana</i>	AT3G51000	01 Metabolism	01.06 Lipid and sterol	e-116	77	0.0003956	3.60946	5.35739	0.67374	evm_27.model.AmTr.v1.0_scaffold00002.2.76	-1.77E+01	18	36.20000076	5	4	5	0.5000	ATMEVHVHR AFACYDALTIM	
627	6	Q9SD45	Epoxide hydrolase-like protein	<i>Arabidopsis thaliana</i>	AT3G51000	01 Metabolism	01.06 Lipid and sterol	e-117	78	0.0003956	3.60946	5.35739	0.67374	evm_27.model.AmTr.v1.0_scaffold00002.2.74	-8.00E+00	10	36.5	2	1	2	0.2727	FITGNEDIGFE AYR	

639	5	Q9SD45	Epoxide hydrolase-like protein	<i>Arabidopsis thaliana</i>	AT3G51000	01 Metabolism	01.06 Lipid and sterol	e-116	77	0,003018	2,45421	4,50863	0,54434	evm_27.model.AmTr.v1.0_scaffold00002.276	-3,20E+01	23	36,20000076	6	5	6	0,6000	YYVIGPTFK AYGDGFIYINQ FQEPGGR	
639	5	Q9SD45	Epoxide hydrolase-like protein	<i>Arabidopsis thaliana</i>	AT3G51000	01 Metabolism	01.06 Lipid and sterol	e-117	78	0,003018	2,45421	4,50863	0,54434	evm_27.model.AmTr.v1.0_scaffold00002.274	-1,49E+01	12	36,5	4	3	4	0,3636	AGMEVVRH DYVNGAIFK ALVSLSIFYQP	
1018	9	Q9SD45	Epoxide hydrolase-like protein	<i>Arabidopsis thaliana</i>	AT3G51000	01 Metabolism	01.06 Lipid and sterol	e-117	78	7,51E-05	2,87435	3,95283	0,72716	evm_27.model.AmTr.v1.0_scaffold00002.274	-7,91E+01	41	36,5	20	16	18	1,8182	ALGMEVVRH YDILLTVVKK LTOGEPGGR	
1018	9	Q9SD45	Epoxide hydrolase-like protein	<i>Arabidopsis thaliana</i>	AT3G51000	01 Metabolism	01.06 Lipid and sterol	e-116	77	7,51E-05	2,87435	3,95283	0,72716	evm_27.model.AmTr.v1.0_scaffold00002.276	-2,31E+01	16	36,20000076	6	2	6	0,6000	ATMEVVRH FIVGNEDIGFQ SFGTK	
321	131	5	Q9SEE5	Galactokinase	<i>Arabidopsis thaliana</i>	AT3G06580	01 Metabolism	01.05 Sugars and polysaccharides	0,00E+00	83	0,0023794	0,45958	0,32038	1,43448	evm_27.model.AmTr.v1.0_scaffold00003.234	-6,78E+01	38	50,90000153	14	-	14	0,7000	AVTAAINYNN R FAVSSSEI SDE
684	113	2	Q9SF20	MD-2-related lipid recognition domain-containing protein	<i>Arabidopsis thaliana</i>	AT3G11780	11 Disease/defence	11.02 Defence-related	4,00E-46	74	4,10E-05	0,58962	0,04952	11,9067	evm_27.model.AmTr.v1.0_scaffold00004.131	-1,49E+01	26	16,39999962	3	-	3	0,5000	SISASTEAPLS EGK VSGMEVDPDP
713	113b	5	Q9SF20	MD-2-related lipid recognition domain-containing protein	<i>Arabidopsis thaliana</i>	AT3G11780	11 Disease/defence	11.02 Defence-related	4,00E-46	74	0,0019856	0,39246	0,12791	3,06825	evm_27.model.AmTr.v1.0_scaffold00004.131	-1,38E+01	26	16,39999962	4	-	3	0,8333	VSGMEVDPDP VER SISASTEAPLS
331	8	Q9SG80	Alpha-L-arabinofuranosidase	<i>Arabidopsis thaliana</i>	AT3G10740	09 Cell structure	09.01 Cell wall	0,00E+00	68	0,0076661	1,16096	0,33556	3,45981	evm_27.model.AmTr.v1.0_scaffold00095.148	-1,22E+01	4	73,09999847	2	-	2	0,1000	SLATANVIADS SDVQK DFGACVWEGE	
1002	14	Q9SGE0	xylose synthase	<i>Arabidopsis thaliana</i>	AT1G08200	01 Metabolism	01.05 Sugars and polysaccharides	0,00E+00	94	0,0179685	1,00507	2,65214	0,37896	evm_27.model.AmTr.v1.0_scaffold00040.298	-4,86E+01	30	43,70000076	13	-	10	0,5200	AGSSVAAR QLAEMTEVY SK	
467	11	Q9SGE0	xylose synthase	<i>Arabidopsis thaliana</i>	AT1G08200	01 Metabolism	01.05 Sugars and polysaccharides	0,00E+00	94	0,0173342	0,83843	2,86452	0,29269	evm_27.model.AmTr.v1.0_scaffold00040.298	-3,54E+01	30	43,70000076	8	-	7	0,3600	EFYGEGYDSS DK ANGQENFVGN	
402	3	Q9SH69	6-Phosphogluconate dehydrogenase	<i>Arabidopsis thaliana</i>	AT1G64190	02 Energy	02.07 Pentose phosphate	0,00E+00	90	0,0116642	0,72452	4,74682	0,15263	evm_27.model.AmTr.v1.0_scaffold00047.159	-4,94E+01	16	53,79999924	12	1	9	0,6000	ILSAFMEPGD CLIDGNEWY ENTER	
979	3	Q9SIB9	Aconitase	<i>Arabidopsis thaliana</i>	AT2G05710	02 Energy	02.10 TCA pathway	0,00E+00	91	0,0002014	2,38364	3,23999	0,73569	evm_27.model.AmTr.v1.0_scaffold00001.143	-1,75E+02	45	107	39	21	34	1,0833	PGQDVTVVTD SGK FVDYNEPOTE	
980	2	Q9SIB9	Aconitase	<i>Arabidopsis thaliana</i>	AT2G05710	02 Energy	02.10 TCA pathway	0,00E+00	91	0,0158731	2,68389	3,4203	0,7847	evm_27.model.AmTr.v1.0_scaffold00001.143	-2,23E+02	50	107	63	32	46	1,7778	RDFNSYGSR NCDDFEVKK SFHGSARQIK	
982	3	Q9SIB9	Aconitase	<i>Arabidopsis thaliana</i>	AT2G05710	02 Energy	02.10 TCA pathway	0,00E+00	91	0,0100551	3,05388	2,72367	1,12123	evm_27.model.AmTr.v1.0_scaffold00001.143	-1,14E+02	22	107	23	-	18	0,6389	RGNDEVMAR PGQDVTVVTD SGK	
793	12	Q9SIY3	Adenylate cyclase	<i>Arabidopsis thaliana</i>	AT2G11890	10 Signal transduction	10.04 Mediators	e-38	60	0,0010663	2,43627	6,5698	0,37083	evm_27.model.AmTr.v1.0_scaffold00033.138	-1,51E+01	16	22,60000038	2	-	2	0,1538	AEEEEEEFDP SLQR THLOENAFDD	
488	10	Q9SJQ9	Fructose-bisphosphate aldolase	<i>Arabidopsis thaliana</i>	AT2G36460	02 Energy	02.01 Glycolysis	e-178	91	0,0120942	1,5885	2,29785	0,6913	evm_27.model.AmTr.v1.0_scaffold00040.204	-1,53E+01	16	38,20000076	4	-	4	0,2500	NAAYIGTPGR RLSSINVENVE SNR	
510	9	Q9SJQ9	Fructose-bisphosphate aldolase	<i>Arabidopsis thaliana</i>	AT2G36460	02 Energy	02.01 Glycolysis	e-178	91	0,0003295	2,01724	2,58062	0,78169	evm_27.model.AmTr.v1.0_scaffold00040.204	-6,88E+00	9	38,20000076	2	-	2	1,25E-01	USSINVENVES NR IGPTEPSPISIL	
564	8	Q9SJQ9	Fructose-bisphosphate aldolase	<i>Arabidopsis thaliana</i>	AT2G36460	02 Energy	02.01 Glycolysis	e-178	91	0,011869	1,54894	2,36483	0,65499	evm_27.model.AmTr.v1.0_scaffold00040.204	-5,60E+01	36	38,20000076	8	-	8	0,6250	GDAPVGEAS ESLH ANSEATI GTY	
583	10	Q9SJQ9	Fructose-bisphosphate aldolase	<i>Arabidopsis thaliana</i>	AT2G36460	02 Energy	02.01 Glycolysis	e-178	91	0,0182765	1,26554	2,01037	0,62503	evm_27.model.AmTr.v1.0_scaffold00040.204	-4,53E+01	31	38,20000076	8	-	8	0,5000	COQYAAAGAR NAAYIGTPGR ANSEATI GTY	
600	6	Q9SJQ9	Fructose-bisphosphate aldolase	<i>Arabidopsis thaliana</i>	AT2G36460	02 Energy	02.01 Glycolysis	e-178	91	0,0178552	5,14912	4,89334	1,05222	evm_27.model.AmTr.v1.0_scaffold00040.204	-4,38E+01	25	38,20000076	7	-	7	0,4375	GDAPVGEAS ESLH NAAYIGTPGR	
537	95	6	Q9SJQ9	Fructose-bisphosphate aldolase	<i>Arabidopsis thaliana</i>	AT2G36460	02 Energy	02.01 Glycolysis	e-178	91	0,0002003	0,09174	0,1778	0,51598	evm_27.model.AmTr.v1.0_scaffold00040.204	-4,72E+01	33	37,70000076	9	-	9	0,5294	MVTPGSDAPK NAAYIGTPGR ANSEATI GTY
539	93	4	Q9SJQ9	Fructose-bisphosphate aldolase	<i>Arabidopsis thaliana</i>	AT2G36460	02 Energy	02.01 Glycolysis	e-178	91	0,0017522	0,13283	0,24423	0,54388	evm_27.model.AmTr.v1.0_scaffold00040.204	-1,97E+01	12	37,70000076	5	-	4	0,2941	MVTPGSDAPK COQYAAAGAR
1013	6	Q9SJQ9	Fructose-bisphosphate aldolase	<i>Arabidopsis thaliana</i>	AT2G36460	02 Energy	02.01 Glycolysis	e-178	91	2,22E-05	1,46601	3,04975	0,4807	evm_27.model.AmTr.v1.0_scaffold00040.204	-9,94E+01	62	38,20000076	24	-	23	1,6875	COQYAAAGAR TWAGKEENIP AAOK VLOGMGNVO	
407	14	Q9SK09	Cupin family protein (Vicilin)	<i>Arabidopsis thaliana</i>	AT2G28490	06 Protein destination and storage	06.20 Storage proteins	e-118	66	0,0092583	1,69181	1,84846	0,91526	evm_27.model.AmTr.v1.0_scaffold00080.82	-8,63E+00	9	50,40000153	3	-	3	0,1667	VVFPNGSLAM DTNVK	
833	6	Q9SK09	Cupin family protein (Vicilin)	<i>Arabidopsis thaliana</i>	AT2G28490	06 Protein destination and storage	06.20 Storage proteins	e-118	66	0,0133914	4,64276	2,00655	2,31381	evm_27.model.AmTr.v1.0_scaffold00080.82	-7,02E+00	7	50,40000153	2	-	2	0,1667	EGDAPWIPK LPELATAFNLS PDELB	
821	170	4	Q9SK09	Cupin family protein (Vicilin)	<i>Arabidopsis thaliana</i>	AT2G28490	06 Protein destination and storage	06.20 Storage proteins	e-118	66	0,0172239	0,44096	0,44829	0,98364	evm_27.model.AmTr.v1.0_scaffold00080.82	-4,73E+01	17	43,09999847	13	-	9	0,8125	ESVILPETIHAP PHG
836	168	2	Q9SK09	Cupin family protein (Vicilin)	<i>Arabidopsis thaliana</i>	AT2G28490	06 Protein destination and storage	06.20 Storage proteins	e-118	66	0,0032058	0,61535	0,19061	3,22831	evm_27.model.AmTr.v1.0_scaffold00080.82	-1,04E+02	218	43,09999847	26	-	20	1,8125	HTTDSYNLYK PETIHAPHGK LPETHAPPHG
842	169	4	Q9SK09	Cupin family protein (Vicilin)	<i>Arabidopsis thaliana</i>	AT2G28490	06 Protein destination and storage	06.20 Storage proteins	e-118	66	0,0056319	0,80598	0,20929	3,85098	evm_27.model.AmTr.v1.0_scaffold00080.82	-1,64E+02	30	43,09999847	47	-	29	3,1875	LAMD TNVK HTTDSYNLYK HTTDSYNLYK
843	4	Q9SK09	Cupin family protein (Vicilin)	<i>Arabidopsis thaliana</i>	AT2G28490	06 Protein destination and storage	06.20 Storage proteins	e-118	66	0,0054464	1,06921	0,166	6,44124	evm_27.model.AmTr.v1.0_scaffold00080.82	-5,41E+01	17	50,40000153	13	-	10	0,7778	ESVILPETIHAP PH	
871	284	3	Q9SK09	Cupin family protein (Vicilin)	<i>Arabidopsis thaliana</i>	AT2G28490	06 Protein destination and storage	06.20 Storage proteins	e-118	66	1,59E-05	0,13357	0,05308	2,51653	evm_27.model.AmTr.v1.0_scaffold00080.82	-2,91E+01	15	43,09999847	8	-	7	0,5000	VLVNIAGEQR LOICSDTSEK GSLVSGFNLIK
877	186	1	Q9SK09	Cupin family protein (Vicilin)	<i>Arabidopsis thaliana</i>	AT2G28490	06 Protein destination and storage	06.20 Storage proteins	e-118	66	0,0002383	0,19234	0,08471	2,2705	evm_27.model.AmTr.v1.0_scaffold00080.82	-7,79E+01	21	43,09999847	28	-	16	1,8750	TGAHEPPK LVNIGEGOR

882	187	2	Q9SK09	Cupin family protein (Vicilin)	<i>Arabidopsis thaliana</i>	AT2G28490	06 Protein destination and storage	06.20 Storage proteins	e-118	66	0,000333	0,25229	0,10625	2,37449	evm_27.model.AmTr.v1.0_scaffold00080.82	-6,66E+01	22	43,09999847	29	-	14	1,8750	TGAHEPPK INRDDLVEK LVNIGEGQR
888	188	2	Q9SK09	Cupin family protein (Vicilin)	<i>Arabidopsis thaliana</i>	AT2G28490	06 Protein destination and storage	06.20 Storage proteins	e-118	66	0,0066561	0,38386	0,22927	1,67431	evm_27.model.AmTr.v1.0_scaffold00080.82	-5,42E+01	19	43,09999847	13	-	10	0,9375	DDLVEKELR YLVNIGEGQR IGWINRDDLVE
331		8	Q8SKP6	Triosephosphate isomerase (chloroplastic)	<i>Arabidopsis thaliana</i>	AT2G21170	02 Energy	02.01 Glycolysis	2,00E-48	87	0,0076661	1,16096	0,33556	3,45981	evm_27.model.AmTr.v1.0_scaffold00041.261	-1,18E+01	27	12,39999962	2	-	2	0,4000	HIYGGSVNGSN CAELAK GDIQDCFLVG
774		4	Q8SKP6	Triosephosphate isomerase (chloroplastic)	<i>Arabidopsis thaliana</i>	AT2G21170	02 Energy	02.01 Glycolysis	2,00E-48	87	0,0178635	2,04497	3,67878	0,55588	evm_27.model.AmTr.v1.0_scaffold00041.261	-1,52E+01	36	12,39999962	3	-	3	0,6000	WATPQQAQDV H
789		7	Q8SKP6	Triosephosphate isomerase (chloroplastic)	<i>Arabidopsis thaliana</i>	AT2G21170	02 Energy	02.01 Glycolysis	2,00E-48	87	0,017244	1,64782	1,94	0,84939	evm_27.model.AmTr.v1.0_scaffold00041.261	-2,75E+01	52	12,39999962	7	-	5	1,4000	WATPQQAQDV H
790		8	Q8SKP6	Triosephosphate isomerase (chloroplastic)	<i>Arabidopsis thaliana</i>	AT2G21170	02 Energy	02.01 Glycolysis	2,00E-48	87	5,26E-05	1,00671	3,80321	0,2647	evm_27.model.AmTr.v1.0_scaffold00041.261	-9,17E+00	23	12,39999962	2	-	2	0,4000	WATPQQAQDV H
793		12	Q8SKP6	Triosephosphate isomerase (chloroplastic)	<i>Arabidopsis thaliana</i>	AT2G21170	02 Energy	02.01 Glycolysis	2,00E-48	87	0,0010663	2,43627	6,5698	0,37083	evm_27.model.AmTr.v1.0_scaffold00041.261	-6,17E+00	23	12,39999962	2	-	2	0,4000	WATPQQAQDV H
802		8	Q8SKP6	Triosephosphate isomerase (chloroplastic)	<i>Arabidopsis thaliana</i>	AT2G21170	02 Energy	02.01 Glycolysis	2,00E-48	87	0,0053343	1,5642	3,66597	0,42668	evm_27.model.AmTr.v1.0_scaffold00041.261	-1,77E+01	27	12,39999962	2	-	2	0,4000	HIYGGSVNGSN CAELAK GDIQDCFLVG
1002		14	Q8SMT7	Coumarate-CoA ligase	<i>Arabidopsis thaliana</i>	AT3G48990	20 Secondary metabolism	20.1 Phenylpropanoids/phenolics	0,00E+00	78	0,0179685	1,00507	2,65214	0,37896	evm_27.model.AmTr.v1.0_scaffold00009.281	-5,39E+00	5	57,70000076	2	-	2	0,1111	NLAASVENIR GDDVALFLHT SGTTSRPK
627		6	Q8SN86	Malate dehydrogenase	<i>Arabidopsis thaliana</i>	AT3G47520	02 Energy	02.10 TCA pathway	e-151	82	0,0003956	3,60946	5,35739	0,67374	evm_27.model.AmTr.v1.0_scaffold00010.472	-3,97E+01	28	43,70000076	9	-	9	0,5000	IQNAGTEVVEA K
639		5	Q8SN86	Malate dehydrogenase	<i>Arabidopsis thaliana</i>	AT3G47520	02 Energy	02.10 TCA pathway	e-151	82	0,003018	2,45421	4,50863	0,54434	evm_27.model.AmTr.v1.0_scaffold00010.472	-3,76E+01	25	43,70000076	8	-	8	0,4444	GVAADLSHCN TPSK
1018		9	Q8SN86	Malate dehydrogenase	<i>Arabidopsis thaliana</i>	AT3G47520	02 Energy	02.10 TCA pathway	e-151	82	7,51E-05	2,87435	3,95283	0,72716	evm_27.model.AmTr.v1.0_scaffold00010.472	-2,00E+01	12	43,70000076	4	-	4	0,2222	IQNAGTEVVEA K
294		8	Q8SQT8	Bifunctional 3-dehydroquinate dehydratase/shikimate	<i>Arabidopsis thaliana</i>	AT3G06350	01 Metabolism	01.01 Amino Acid	0,00E+00	76	0,0070497	3,75653	4,0454	0,92859	evm_27.model.AmTr.v1.0_scaffold00057.121	-1,79E+01	11	56,70000076	4	-	4	0,1905	SIGAVNTIVR LDHLEAFRPS EDLQF
768		6	Q8SR36	Glutathione S-transferase	<i>Arabidopsis thaliana</i>	AT3G09270	11 Disease/defence	11.06 Detoxification	3,00E-56	67	0,0010332	1,85717	5,783	0,32114	evm_27.model.AmTr.v1.0_scaffold00027.107	-4,45E+01	47	25,70000076	12	-	11	2,3333	NIEHYDAEK AAMIEHYDAEK WYAYSTQGVQ
793		12	Q8SR36	Glutathione S-transferase	<i>Arabidopsis thaliana</i>	AT3G09270	11 Disease/defence	11.06 Detoxification	5,00E-50	65	0,0010663	2,43627	6,5698	0,37083	evm_27.model.AmTr.v1.0_scaffold00019.57	-1,54E+01	27	25,20000076	5	-	5	0,4545	GINYEYKDEDI HNK IPIILHGSK
793		12	Q8SR36	Glutathione S-transferase	<i>Arabidopsis thaliana</i>	AT3G09270	11 Disease/defence	11.06 Detoxification	5,00E-56	67	0,0010663	2,43627	6,5698	0,37083	evm_27.model.AmTr.v1.0_scaffold00027.111	-8,10E+00	16	25,29999924	3	-	3	0,3333	GHLEALHSTS TSS
802		8	Q8SR36	Glutathione S-transferase	<i>Arabidopsis thaliana</i>	AT3G09270	11 Disease/defence	11.06 Detoxification	5,00E-56	67	0,0053343	1,5642	3,66597	0,42668	evm_27.model.AmTr.v1.0_scaffold00027.111	-1,42E+01	20	25,29999924	3	-	3	0,3333	SPHLLFESNPVH HLEGAAGIQY DAEK
810		12	Q8SR36	Glutathione S-transferase	<i>Arabidopsis thaliana</i>	AT3G09270	11 Disease/defence	11.06 Detoxification	5,00E-56	67	0,0021851	1,58254	4,0931	0,38664	evm_27.model.AmTr.v1.0_scaffold00027.111	-4,20E+01	44	25,29999924	8	-	7	0,8889	GHLEALHSTS TSS
810		12	Q8SR36	Glutathione S-transferase	<i>Arabidopsis thaliana</i>	AT3G09270	11 Disease/defence	11.06 Detoxification	5,00E-50	65	0,0021851	1,58254	4,0931	0,38664	evm_27.model.AmTr.v1.0_scaffold00019.57	-3,33E+01	38	25,20000076	6	-	6	0,6364	SPHLLFESNPVH GINYEYKDEDI HNK
818		7	Q8SR36	Glutathione S-transferase	<i>Arabidopsis thaliana</i>	AT3G09270	11 Disease/defence	11.06 Detoxification	5,00E-50	65	0,0072403	1,69716	3,47994	0,4877	evm_27.model.AmTr.v1.0_scaffold00019.57	-1,02E+01	20	25,20000076	3	-	3	0,2727	DPLDHPVIK QGEELVESL
1036		7	Q8SR36	Glutathione S-transferase	<i>Arabidopsis thaliana</i>	AT3G09270	11 Disease/defence	11.06 Detoxification	5,00E-50	65	0,0026609	3,25164	7,27437	0,447	evm_27.model.AmTr.v1.0_scaffold00019.57	-6,45E+01	59	25,20000076	20	-	16	2,0909	LAQCOAVHVR GINYEYKDEDI HNK
1036		7	Q8SR36	Glutathione S-transferase	<i>Arabidopsis thaliana</i>	AT3G09270	11 Disease/defence	11.06 Detoxification	5,00E-56	67	0,0026609	3,25164	7,27437	0,447	evm_27.model.AmTr.v1.0_scaffold00027.111	-5,35E+01	46	25,29999924	11	-	11	1,2222	GHLEALHSTS TSS
818		7	Q8SRL5	Ferritin, chloroplastic	<i>Arabidopsis thaliana</i>	AT3G11050	11 Disease/defence	11.02 Defence-related	2,00E-88	84	0,0072403	1,69716	3,47994	0,4877	evm_27.model.AmTr.v1.0_scaffold00007.7	-8,37E+00	15	28,10000038	3	-	3	0,3000	GISEYVAQLR ELLTLASTPQT SLAR
537	95	6	Q8SRT9	UDP-L-arabinose mutase	<i>Arabidopsis thaliana</i>	AT3G02230	09 Cell structure	09.01 Cell wall	0,00E+00	95	0,0002003	0,09174	0,1778	0,51598	evm_27.model.AmTr.v1.0_scaffold00047.149	-5,91E+01	35	40,90000153	13	-	11	0,5909	DGADFVR HLIVQGDGPT K
782		9	Q8SRY5	Glutathione S-transferase	<i>Arabidopsis thaliana</i>	AT1G02920	11 Disease/defence	11.06 Detoxification	2,00E-37	67	0,0006529	0,74675	3,14802	0,23721	evm_27.model.AmTr.v1.0_scaffold00057.265	-1,64E+01	41	19,39999962	6	-	5	0,8000	AITNYIAHK HNK EQGTFLVGTD
828		6	Q8SRY5	Glutathione S-transferase	<i>Arabidopsis thaliana</i>	AT1G02920	11 Disease/defence	11.06 Detoxification	2,00E-37	67	0,014279	0,94689	1,68458	0,56209	evm_27.model.AmTr.v1.0_scaffold00057.265	-4,92E+00	15	19,39999962	2	-	2	0,2000	AITNYIAHK AMLGIPVDET VEFATGK
790		8	Q8SRY5	Glutathione S-transferase	<i>Arabidopsis thaliana</i>	AT1G02920	11 Disease/defence	11.06 Detoxification	2,00E-37	67	5,26E-05	1,00671	3,80321	0,2647	evm_27.model.AmTr.v1.0_scaffold00057.265	-8,44E+00	16	19,39999962	2	-	2	0,2000	AVALSDAVIK AMLGIPVDET VEFATGK
799		8	Q8SRY5	Glutathione S-transferase	<i>Arabidopsis thaliana</i>	AT1G02920	11 Disease/defence	11.06 Detoxification	2,00E-37	67	0,0125632	1,10491	2,40277	0,45985	evm_27.model.AmTr.v1.0_scaffold00057.265	-1,19E+01	22	19,39999962	4	-	4	0,5000	AITNYIAHK TNYIAHK ESLVDLHLBN
808		9	Q8SRY5	Glutathione S-transferase	<i>Arabidopsis thaliana</i>	AT1G02920	11 Disease/defence	11.06 Detoxification	2,00E-37	67	0,0012118	3,14897	4,15446	0,75797	evm_27.model.AmTr.v1.0_scaffold00057.265	-1,01E+01	14	19,39999962	2	-	2	0,2000	AVALSDAVIK LNEVLVDYES MLAK
269		6	Q8SRZ4	Peroxioredoxin	<i>Arabidopsis thaliana</i>	AT1G65970	11 Disease/defence	11.06 Detoxification	2,00E-34	88	0,0024029	1,40422	0,8639	1,62545	evm_27.model.AmTr.v1.0_scaffold00109.91	-3,28E+01	60	9,5	5	-	4	1,0000	ALGLELDLTK VANLEEGCAF SVSSADEILK
1070		4	Q8SRZ4	Peroxioredoxin	<i>Arabidopsis thaliana</i>	AT1G65970	11 Disease/defence	11.06 Detoxification	2,00E-34	88	0,0050128	2,3629	4,83628	0,48858	evm_27.model.AmTr.v1.0_scaffold00109.91	-6,72E+01	78	9,5	13	-	12	2,6000	WAESYPENK FVADGSASYT H

998	1	Q9SRZ6	Iso citrate dehydrogenase	<i>Arabidopsis thaliana</i>	AT1G65930	02 Energy	02.10 TCA pathway	0.00E+00	92	0.0035458	4.2904	2.75285	1.55853	evm_27.model.AmTr.v1.0_scaffold00071.1.47	-1.27E+02	61	46.70000076	37	-	29	2.0000	SSMTVAYEK HAFGDOYK TIEAFAMHTV	
999	1	Q9SRZ6	Iso citrate dehydrogenase	<i>Arabidopsis thaliana</i>	AT1G65930	02 Energy	02.10 TCA pathway	0.00E+00	92	8.51E-05	3.10103	2.74392	1.13015	evm_27.model.AmTr.v1.0_scaffold00071.1.47	-1.15E+02	58	46.70000076	31	-	24	1.7000	SSMTVAYEK HAFGDOYK HAFGDOYK	
926	6	Q9SSK7	MLP-like protein	<i>Arabidopsis thaliana</i>	AT1G70850	11 Disease/defence	11.02 Defence-related	4.00E-03	51	0.0110232	2.96598	2.57879	1.15015	evm_27.model.AmTr.v1.0_scaffold00003.1.27	-2.08E+01	38	17.60000038	4	-	4	0.5556	FEEGAGGSSV SK AVCYLILQNH SVEVCEGNGG VGVTK ISSVFCVCGN	
929	2	Q9SSK7	MLP-like protein	<i>Arabidopsis thaliana</i>	AT1G70850	11 Disease/defence	11.02 Defence-related	4.00E-03	51	0.0085309	14.9086	9.38328	1.58885	evm_27.model.AmTr.v1.0_scaffold00003.1.27	-9.67E+01	56	17.60000038	22	-	18	2.5556	FEEGAGGSSV SK AVCYLILQNH SVEVCEGNGG VGVTK ISSVFCVCGN	
1065	4	Q9SSK7	MLP-like protein	<i>Arabidopsis thaliana</i>	AT1G70850	11 Disease/defence	11.02 Defence-related	4.00E-03	51	0.0005017	4.67039	8.73697	0.53455	evm_27.model.AmTr.v1.0_scaffold00003.1.27	-1.11E+02	70	17.60000038	26	-	19	3.0000	FEEGAGGSSV SK DKTVALDDEK DLEQCDR SEGATILCGGD RPOHLEK	
269	6	Q9STS1	Betaine aldehyde dehydrogenase	<i>Arabidopsis thaliana</i>	AT3G48170	11 Disease/defence	11.05 Stress responses	0.00E+00	89	0.0024029	1.40422	0.8639	1.62545	evm_27.model.AmTr.v1.0_scaffold00055.1.45	-6.18E+01	37	54.59999847	19	-	15	1.1111	IMSGQTLSDA NK FYHSIAK	
71	1	Q9STX5	HSP90	<i>Arabidopsis thaliana</i>	AT4G24190	06 Protein destination and storage	06.01 Folding and stability	0.00E+00	90	0.0063056	6.1887	0.9314	6.64486	evm_27.model.AmTr.v1.0_scaffold00041.1.14	-9.14E+01	24	93.59999847	22	-	21	0.5789	IVGLQTGR MESQFSSHILR FPMNSVYRHM HIEISPDARVW SVLFAVGTAG OR	
342	65	3	Q9SX53	Oligopeptidase B	<i>Arabidopsis thaliana</i>	AT1G50380	06 Protein destination and storage	06.13 Proteolysis	0.00E+00	85	0.0079229	0.26873	0.11466	2.34363	evm_27.model.AmTr.v1.0_scaffold00171.4.8	-4.41E+01	17	80.90000153	11	-	11	0.3056	VTLVTIIGLNK VGSLLTDLSLK R
294	8	Q9SYG7	Aldehyde dehydrogenase (Turgor responsive)	<i>Arabidopsis thaliana</i>	AT1G54100	11 Disease/defence	11.06 Detoxification	0.00E+00	85	0.0070497	3.75653	4.0454	0.92859	evm_27.model.AmTr.v1.0_scaffold00024.3.06	-2.38E+01	14	54.79999924	5	-	5	0.3125	AVLVDKQNP K YSKEPESFAQ	
331	8	Q9SYK9	UDP-glycosyltransferase (74E2)	<i>Arabidopsis thaliana</i>	AT1G05680	10 Signal transduction	10.04 Mediators	e-102	61	0.0076681	1.16096	0.33556	3.45981	evm_27.model.AmTr.v1.0_scaffold00066.2.09	-7.81E+00	4	56.40000153	2	-	2	0.1111	VTELAGEGSK RPGDAEIVYAS TK	
645	7	Q9SYT0	Annexin 1	<i>Arabidopsis thaliana</i>	AT1G35720	10 Signal transduction	10.99 Others	e-100	78	0.000128	1.30225	4.22239	0.30842	evm_27.model.AmTr.v1.0_scaffold00060.1.14	-4.23E+01	33	35.5	10	-	10	0.5263	VTELAGEGSK RPGDAEIVYAS TK	
782	9	Q9SZH2	Peroxidase	<i>Arabidopsis thaliana</i>	AT4G25980	11 Disease/defence	11.06 Detoxification	e-109	75	0.0006529	0.74675	3.14802	0.23721	evm_27.model.AmTr.v1.0_scaffold00071.6.1	-1.02E+01	11	34.5	2	-	2	0.2143	CGADRSINFR DSIVVNSGPN YQVPTGR	
294	8	Q9T074	Phosphoenolpyruvate carboxylase	<i>Arabidopsis thaliana</i>	AT4G37870	02 Energy	02.10 TCA pathway	7.00E-55	68	0.0070497	3.75653	4.0454	0.92859	evm_27.model.AmTr.v1.0_scaffold00033.3	-3.44E+01	26	22.89999962	8	-	8	0.8000	SHVTSIFEPAR TSHVTSIFEPAR	
294	8	Q9T074	Phosphoenolpyruvate carboxylase	<i>Arabidopsis thaliana</i>	AT4G37870	02 Energy	02.10 TCA pathway	0.00E+00	91	0.0070497	3.75653	4.0454	0.92859	evm_27.model.AmTr.v1.0_scaffold00033.2	-7.99E+01	37	50.70000076	18	-	14	0.9500	YAAMLAEK TGWSGGSYG SGNR	
564	8	Q9T0A7	UDP-glucose 4-epimerase	<i>Arabidopsis thaliana</i>	AT4G23920	01 Metabolism	01.05 Sugars and polysaccharides	e-156	85	0.011869	1.54894	2.36483	0.65499	evm_27.model.AmTr.v1.0_scaffold00024.7.8	-7.94E+01	49	37.90000153	17	-	14	1.2353	VTELAGEGSK RPGDAEIVYAS TK	
1013	6	Q9T0A7	UDP-glucose 4-epimerase	<i>Arabidopsis thaliana</i>	AT4G23920	01 Metabolism	01.05 Sugars and polysaccharides	e-156	85	2.22E-05	1.46601	3.04975	0.4807	evm_27.model.AmTr.v1.0_scaffold00024.7.8	-3.48E+01	32	37.90000153	10	-	9	0.5882	VTELAGEGSK RPGDAEIVYAS TK	
510	9	Q9T0K7	3-hydroxyisobutyl-CoA hydrolase-like protein	<i>Arabidopsis thaliana</i>	AT4G13360	01 Metabolism	01.01 Amino Acid	e-148	67	0.0003295	2.01724	2.58062	0.78169	evm_27.model.AmTr.v1.0_scaffold00142.4.0	-7.73E+01	42	48.70000076	20	-	17	8.33E-001	AVLVDKQNP K YSKEPESFAQ	
224	2	Q9XI01	Protein disulfide isomerase	<i>Arabidopsis thaliana</i>	AT1G21750	06 Protein destination and storage	06.01 Folding and stability	e-172	79	0.0007787	6.66879	4.48676	1.48633	evm_27.model.AmTr.v1.0_scaffold00186.1.4	-1.28E+02	44	57.40000153	25	-	24	0.8621	VDEANVKN GGASVQVEYK GGASVQVEYK SEPIPEVNNFP VK	
252	3	Q9XI01	Protein disulfide isomerase	<i>Arabidopsis thaliana</i>	AT1G21750	06 Protein destination and storage	06.01 Folding and stability	e-172	79	0.0016951	4.19739	3.87379	1.08354	evm_27.model.AmTr.v1.0_scaffold00186.1.4	-9.74E+00	8	57.40000153	3	-	3	0.1034	JDSTANDIPSD R	
818	7	Q9XI05	20S proteasome beta subunit C1	<i>Arabidopsis thaliana</i>	AT1G21720	06 Protein destination and storage	06.13 Proteolysis	e-103	89	0.0072403	1.69716	3.47994	0.4877	evm_27.model.AmTr.v1.0_scaffold00002.1.42	-7.01E+00	12	22.7	2	-	2	0.2222	VWVTPDDITE R SDEEHFEPFR LPTDESLHTQI R	
926	6	Q9XI91	Eukaryotic translation initiation factor	<i>Arabidopsis thaliana</i>	AT1G13950	05 Protein synthesis	05.04 Translation factors	2.00E-77	92	0.0110232	2.96598	2.57879	1.15015	evm_27.model.AmTr.v1.0_scaffold00065.1.57	-1.94E+01	39	17.39999962	5	4	5	0.7143	AVLVDKQNP K YSKEPESFAQ	
926	6	Q9XI91	Eukaryotic translation initiation factor	<i>Arabidopsis thaliana</i>	AT1G13950	05 Protein synthesis	05.04 Translation factors	8.00E-75	91	0.0110232	2.96598	2.57879	1.15015	evm_27.model.AmTr.v1.0_scaffold00058.5.4	-1.05E+01	19	17.20000076	2	1	2	0.2857	LPTDESLCSQI K	
600	6	Q9ZP06	Malate dehydrogenase	<i>Arabidopsis thaliana</i>	AT1G53240	02 Energy	02.10 TCA pathway	e-143	90	0.0178552	5.14912	4.89334	1.05227	evm_27.model.AmTr.v1.0_scaffold00021.8.7	-2.02E+02	71	36.99999847	41	38	35	7.5000	DVSHINTR RTQDGGTEVV FAK	
1013	6	Q9ZP06	Malate dehydrogenase	<i>Arabidopsis thaliana</i>	AT1G53240	02 Energy	02.10 TCA pathway	e-143	90	2.22E-05	1.46601	3.04975	0.4807	evm_27.model.AmTr.v1.0_scaffold00021.8.7	-2.35E+01	15	36.99999847	4	-	4	0.6667	VPVEGVNVPV VGGH SNALSDFEIQIA	
828	6	Q9ZRW8	Glutathione S-transferase	<i>Arabidopsis thaliana</i>	AT1G78380	11 Disease/defence	11.06 Detoxification	4.00E-74	76	0.014279	0.94689	1.68458	0.56209	evm_27.model.AmTr.v1.0_scaffold00092.8.1	-4.49E+01	52	24.5	20	-	14	2.3333	VEYREENLAN KIPVLHDKG KIPVLHDKG	
793	12	Q9ZRW8	Glutathione S-transferase	<i>Arabidopsis thaliana</i>	AT1G78380	11 Disease/defence	11.06 Detoxification	4.00E-74	76	0.0010663	2.43627	6.5698	0.37083	evm_27.model.AmTr.v1.0_scaffold00092.8.1	-4.41E+00	10	24.5	2	-	2	0.2222	NPPLLPEDAYE R	
818	7	Q9ZRW8	Glutathione S-transferase	<i>Arabidopsis thaliana</i>	AT1G78380	11 Disease/defence	11.06 Detoxification	4.00E-74	76	0.0072403	1.69716	3.47994	0.4877	evm_27.model.AmTr.v1.0_scaffold00092.8.1	-8.98E+00	12	24.5	3	-	3	0.4444	KIPVLHDKG FWADFADKK ILFEVGLFK	
583	10	Q9ZU52	Fructose-bisphosphate aldolase (chloroplastic)	<i>Arabidopsis thaliana</i>	AT2G01140	02 Energy	02.01 Glycolysis	0.00E+00	89	0.0182765	1.26554	2.01037	0.62503	evm_27.model.AmTr.v1.0_scaffold00001.1.61	-1.08E+01	6	42.40000153	2	-	2	0.1429	LSSIGLDNTEP NR GSAIDESNAT RVDCMIDEK	
627	6	Q9ZU52	Fructose-bisphosphate aldolase (chloroplastic)	<i>Arabidopsis thaliana</i>	AT2G01140	02 Energy	02.01 Glycolysis	0.00E+00	89	0.0003956	3.60946	5.35739	0.67374	evm_27.model.AmTr.v1.0_scaffold00001.1.61	-5.87E+01	35	42.40000153	14	-	11	1.1429	ANSLAQLGR JLLDGHSDIR	
639	5	Q9ZU52	Fructose-bisphosphate aldolase (chloroplastic)	<i>Arabidopsis thaliana</i>	AT2G01140	02 Energy	02.01 Glycolysis	0.00E+00	89	0.003018	2.45421	4.50863	0.54434	evm_27.model.AmTr.v1.0_scaffold00001.1.61	-7.32E+00	10	42.40000153	2	-	2	0.1429	LSSIGLDNTEP NR YAAIQDNGIK YSAAGESEEA KK	
1018	9	Q9ZU52	Fructose-bisphosphate aldolase (chloroplastic)	<i>Arabidopsis thaliana</i>	AT2G01140	02 Energy	02.01 Glycolysis	0.00E+00	89	7.51E-05	2.87435	3.95283	0.72716	evm_27.model.AmTr.v1.0_scaffold00001.1.61	-3.52E+01	29	42.40000153	9	-	9	0.6429	ANSLAQLGR	

1019	4	Q9ZU52	Fructose-bisphosphate aldolase (chloroplastic)	<i>Arabidopsis thaliana</i>	AT2G01140	02 Energy	02.01 Glycolysis	0,00E+00	89	0,0016868	2,39482	3,51011	0,68226	evm_27.model.AmTr.v1.0_scaffold00001.1	-2,45E+01	20	42,40000153	6	-	6	0,4286	ALQNTVLK FVDCMIDEK GILAIJESNAT	
631	1	Q9ZUB3	Spermidine synthase	<i>Arabidopsis thaliana</i>	AT1G23820	20 Secondary metabolism	20.5 Amines	e-145	87	0,0039311	3,69168	3,28531	1,12369	evm_27.model.AmTr.v1.0_scaffold00061.1	-4,23E+01	41	36,5	12	-	9	1,2500	FGDMEADGKN FGDMEADGKN HPVNIILDDCD	
638	4	Q9ZUB3	Spermidine synthase	<i>Arabidopsis thaliana</i>	AT1G23820	20 Secondary metabolism	20.5 Amines	e-145	87	0,0027807	7,4861	4,88871	1,53131	evm_27.model.AmTr.v1.0_scaffold00061.1	-1,67E+01	14	36,5	4	-	4	0,3333	FGDMEADGKN HPVNIILDDCD GK	
944	8	Q9ZVA5	D-mannose binding lectin protein	<i>Arabidopsis thaliana</i>	AT1G78860	11 Disease/defence	11.09 Others	7,90E-02	54	0,0003015	0,69549	7,23177	0,09617	evm_27.model.AmTr.v1.0_scaffold00012.3	-9,77E+00	12	17,5	-	-	2	0,5000	PIWASQTYNR GEDYVFLVR	
342	65	3	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	7,00E-70	51	0,0079229	0,26673	0,11466	2,34363	evm_27.model.AmTr.v1.0_scaffold00067.7	-1,17E+01	6	54,5	3	-	3	0,1429	ISNQQAQDIK GEGQIQIGTN GOK
424	9	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	7,00E-70	51	0,0156606	1,00376	0,52462	1,91332	evm_27.model.AmTr.v1.0_scaffold00067.7	-9,64E+01	35	54,5	20	17	17	1,0000	GEGYEGEEQ RGEQGEKE GRQFGEYEE	
424	9	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	2,00E-64	51	0,0156606	1,00376	0,52462	1,91332	evm_27.model.AmTr.v1.0_scaffold00067.1	-5,74E+01	33	49,09999847	12	9	12	0,6316	VLPEEEREE EERER VLPEEEREE	
467	11	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	7,00E-70	51	0,0173342	0,83843	2,86452	0,29269	evm_27.model.AmTr.v1.0_scaffold00067.7	-4,94E+00	4	54,5	2	-	2	0,0952	ISNQQAQDIK OFFIAGGQPR	
647	106	3	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	7,00E-70	51	0,0049465	0,22485	0,1798	1,25058	evm_27.model.AmTr.v1.0_scaffold00067.7	-1,59E+02	32	54,5	55	-	35	2,9524	LSDAQQR SFFSGESGI OHR
407	14	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	7,00E-70	51	0,0092583	1,69181	1,84846	0,91526	evm_27.model.AmTr.v1.0_scaffold00067.7	-1,57E+02	50	54,5	53	41	35	2,8095	GRQEGYEE EQRGEQK GROFGEYEE	
407	14	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	2,00E-64	51	0,0092583	1,69181	1,84846	0,91526	evm_27.model.AmTr.v1.0_scaffold00067.1	-8,67E+01	51	49,09999847	27	15	20	1,5263	LRDQHQVQ R IRONDITLR	
663	2	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	7,00E-70	51	0,004841	1,94845	2,43558	0,79999	evm_27.model.AmTr.v1.0_scaffold00067.7	-9,27E+00	5	54,5	2	-	2	0,0952	GEGQIQIGTN GOK TVTDVTSYDN	
675	8	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	7,00E-70	51	6,01E-05	4,28718	3,84318	1,11553	evm_27.model.AmTr.v1.0_scaffold00067.7	-1,91E+01	9	54,5	5	-	4	0,2381	ISNQQAQDIK GEGYEGEEQ R	
689	9	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	7,00E-70	51	3,23E-06	0,06804	4,88286	1,65232	evm_27.model.AmTr.v1.0_scaffold00067.7	-2,31E+01	14	54,5	6	3	6	0,2857	GEGYEGEEQ R ANVIGVGER	
689	9	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	2,00E-64	51	3,23E-06	0,06804	4,88286	1,65232	evm_27.model.AmTr.v1.0_scaffold00067.1	-1,80E+01	12	49,09999847	4	1	4	0,2105	FLAESFGIPDE LAQR	
789	7	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	7,00E-70	51	0,017244	1,64782	1,94	0,84939	evm_27.model.AmTr.v1.0_scaffold00067.7	-2,88E+01	19	54,5	8	4	7	0,4286	TVTDVTSYDN QLDTK OFFIAGGQPR	
789	7	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	2,00E-64	51	0,017244	1,64782	1,94	0,84939	evm_27.model.AmTr.v1.0_scaffold00067.1	-1,62E+01	11	49,09999847	5	1	4	0,2632	FLAESFGIPDE LAQR	
793	12	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	7,00E-70	51	0,0010663	2,43627	6,5698	0,37083	evm_27.model.AmTr.v1.0_scaffold00067.7	-2,77E+01	16	54,5	7	4	6	0,3810	GRQEGYEE EQR EEDMIFPSSS	
793	12	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	2,00E-64	51	0,0010663	2,43627	6,5698	0,37083	evm_27.model.AmTr.v1.0_scaffold00067.1	-1,89E+01	12	49,09999847	5	2	4	0,2632	SR FLAESFGIPDE	
810	12	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	7,00E-70	51	0,0021851	1,58254	4,0931	0,38664	evm_27.model.AmTr.v1.0_scaffold00067.7	-9,46E+01	36	54,5	20	15	17	0,9524	GRQEGYEE EQRGEQK GROFGEYEE	
810	12	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	2,00E-64	51	0,0021851	1,58254	4,0931	0,38664	evm_27.model.AmTr.v1.0_scaffold00067.1	-4,24E+01	23	49,09999847	9	4	7	0,5263	TSDLPIHTPLV GYTSAIK TSDIPIHTPLV	
832	3	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	7,00E-70	51	0,0172602	3,86032	2,10717	1,84148	evm_27.model.AmTr.v1.0_scaffold00067.7	-1,03E+01	8	54,5	3	-	3	0,1429	GEGQIQIGTN GOK TVTDVTSYDN	
833	6	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	2,00E-64	51	0,0133914	4,64276	2,00655	2,31381	evm_27.model.AmTr.v1.0_scaffold00067.1	-9,02E+00	5	49,09999847	2	-	2	0,1053	GEGQIQIGTN GOK GMPFVLTNAY	
833	6	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	7,00E-70	51	0,0133914	4,64276	2,00655	2,31381	evm_27.model.AmTr.v1.0_scaffold00067.7	-9,02E+00	5	54,5	2	-	2	0,0952	GEGQIQIGTN GOK GMPFVLTNAY	
895	4	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	7,00E-70	51	0,0015653	1,69054	10,4031	0,1625	evm_27.model.AmTr.v1.0_scaffold00067.7	-3,94E+01	16	54,5	7	5	7	0,3333	DEPQACGVA TR TVTDVTSYDN	
895	4	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	2,00E-64	51	0,0015653	1,69054	10,4031	0,1625	evm_27.model.AmTr.v1.0_scaffold00067.1	-1,78E+01	9	49,09999847	3	1	3	0,1579	FLAESFGIPDE LAQR	
1002	14	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	7,00E-70	51	0,0179685	1,00507	2,65214	0,37896	evm_27.model.AmTr.v1.0_scaffold00067.7	-1,09E+01	9	54,5	3	2	3	0,1905	GEGYEGEEQ R OFFIAGGQPR	
1002	14	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	2,00E-64	51	0,0179685	1,00507	2,65214	0,37896	evm_27.model.AmTr.v1.0_scaffold00067.1	-1,22E+01	6	49,09999847	2	1	2	0,1053	FLAESFGIPDE LAQR	
842	169	4	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	7,00E-70	51	0,0056319	0,80598	0,20929	3,85098	evm_27.model.AmTr.v1.0_scaffold00067.7	-2,92E+01	13	54,5	5	-	4	0,2381	ISNQQAQDIK TVTDVTSYDN QLDTK
843	4	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	7,00E-70	51	0,0054464	1,06921	0,166	6,44124	evm_27.model.AmTr.v1.0_scaffold00067.7	-3,81E+01	17	54,5	10	-	8	0,4762	TIAYITR GEGQIQIGTN GOK	
871	284	3	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	7,00E-70	51	1,59E-05	0,13357	0,05308	2,51653	evm_27.model.AmTr.v1.0_scaffold00067.7	-3,88E+01	32	54,5	11	-	10	0,6667	GRQEGYEE EQR GEGYEGEEQ

888	188	2	Q9ZWA9	12S Globulin (cruciferin 2)	<i>Arabidopsis thaliana</i>	AT1G03890	06 Protein destination and storage	06.20 Storage proteins	7,00E-70	51	0,0066561	0,38386	0,22927	1,67431	evm_27.model.AmTr.v1.0_scaffold00067.7	-1,61E+01	9	54,5	5	-	5	0,2381	QEGEYEEEQ RGEQ GK ISNQAGDIK
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Supplemental table 7: list of the proteins from various samples of *P. gabriellae* seed

Proteins have been analyzed by two-dimensional electrophoresis and spots of interest recognized by western blot analysis using an anti-DING antibody (Perera et al. 2008). Spots content was then identified by mass spectrometry LC/MS-MS. The protein spots were analysed by LC-MS/MS on the "Centre d'Analyse Protéomique de Marseille" (Maya Belghazi - IFR Jean Roche, Faculté de médecine - <http://cm2m.univ-mrs.fr/plates-formes-pfm/protéomique-capm>). Based on the spectrum generated, proteins were identified using the X-Tandem software. "Echantillon" correspond to the origin of the sample studied. "Protein Name" "Organism" correspond to the name of the organism from which the protein was identified. "Matched queries" "Real Mascot Matched queries" "Mascot cov %" correspond to the coverage of experimentally identified peptide on the peptide sequence from the source organism "Mascot score" "Peptide sequences"

Echantillon	Protein Name	Organism	Matched queries	Real Mascot Matched queries	Mascot cov %	Mascot score	Peptide sequences	
Développement	Stade 2 (développement)	Chain A, High-Resolution Structure Of The Ding Protein From <i>Pseudomonas Fluorescens</i> (gi 190613370)	<i>Pseudomonas Fluorescens</i>	6	4	12	216	R.TGPIVVVYR.S R.INTWDDGISGSGR.T R.SESSGTTTELFR.F R.SESSGTTTELFR.F K.LSATELSTYASAK.Q K.LSATELSTYASAK.Q
		GLP-binding protein 1a [<i>Arabidopsis thaliana</i>] (gi 2973999)	<i>Arabidopsis thaliana</i>	2	2	41	94	K.AAFLTNDYTK.F K.LTATELSTYATNK.Q
	Stade 3 (développement)	Chain A, Serendipitous Discovery And X-Ray Structure Of A Human Phosphate Binding Apolipoprotein (gi 126030177)	Unknown organism	1	1	4	98	K.LIQVPSVATSVAIPIFR.K
		Chain A, High-Resolution Structure Of The Ding Protein From <i>Pseudomonas Fluorescens</i> (gi 190613370)	<i>Pseudomonas Fluorescens</i>	1	1	3	70	R.SESSGTTTELFR.F
	Stade 4 (développement)	phosphate ABC transporter, periplasmic phosphate-binding protein [<i>Pseudomonas putida</i> KT2440] (gi 26989375)	<i>Pseudomonas putida</i> KT2440	4	3	11	152	R.ADSSGTTAVFTK.H K.GSGAGVQDFLNK.T R.QTPGAIGYIEYGFAK.L R.QTPGAIGYIEYGFAK.L
		Chain A, High-Resolution Structure Of The Ding Protein From <i>Pseudomonas Fluorescens</i> (gi 190613370)	<i>Pseudomonas Fluorescens</i>	1	1	3	82	R.SESSGTTTELFR.F R.SESSGTTTELFR.F
		Retinol reductase [<i>Pseudomonas fluorescens</i> Pf-5] (gi 70732884)	<i>Pseudomonas fluorescens</i> Pf-5	2	2	7	122	R.ADLDVIMIAPK.A + Oxidation (M) K.NVALSYAAGVGGGR.T
		elongation factor Tu [<i>Pseudomonas fluorescens</i> Pf-5] (gi 70732884)	<i>Pseudomonas fluorescens</i> Pf-5	2	2	4	113	K.TIAMEDGLR.F + Oxidation (M) R.AGENCGVLLR.G + Carbamidomethyl (C)
		peroxiredoxin [<i>Pseudomonas putida</i> W619] (gi 170722358)	<i>Pseudomonas putida</i> W619	2	2	14	100	K.IVEINDGGVGR.D K.EGEATLAPSLDLVGLK.I
		DNA-directed RNA polymerase subunit alpha [<i>Pseudomonas putida</i> KT2440] (gi 26987220)	<i>Pseudomonas putida</i> KT2440	1	1	3	74	R.HIDVQVVSPTTR.A
GLP-binding protein 1a [<i>Arabidopsis thaliana</i>] (gi 29373999)		<i>Arabidopsis thaliana</i>	1	1	23	87	K.LTATELSTYATNK.Q	
Années de récoltes	Koghis (2006)	Chain A, High-Resolution Structure Of The Ding Protein From <i>Pseudomonas Fluorescens</i> (gi 190613370)	<i>Pseudomonas Fluorescens</i>	1	1	3	88	R.SESSGTTTELFR.F
		phosphate ABC transporter, periplasmic phosphate-binding protein [<i>Pseudomonas putida</i> KT2440] (gi 26989375)	<i>Pseudomonas putida</i> KT2440	2	2	6	76	R.ADSSGTTAVFTK.H K.GSGAGVQDFLNK.T R.FFLAGNPQQQK.E
		11S globulin-like protein [<i>Actinidia chinensis</i>] (gi 82469930)	<i>Actinidia chinensis</i>	3	2	2	114	R.FFLAGNPQQQK.E R.FFLAGNPQQQK.E R.LLAEVLQK.R
		PREDICTED: serine hydroxymethyltransferase-like [<i>Xenopus (Silurana) tropicalis</i>] (gi 301631113)	<i>Xenopus (Silurana) tropicalis</i>	2	2	2	72	R.LLAEVLQK.R R.LLAEVLQK.R
	Koghis (2007)	phosphate ABC transporter, periplasmic phosphate-binding protein [<i>Pseudomonas putida</i> KT2440] (gi 26989375)	<i>Pseudomonas putida</i> KT2440	2	2	7	94	K.GSGAGVQDFLNK.T R.QTPGAIGYIEYGFAK.L
		Chain A, High-Resolution Structure Of The Ding Protein From <i>Pseudomonas Fluorescens</i> (gi 190613370)	<i>Pseudomonas Fluorescens</i>	1	1	3	76	R.SESSGTTTELFR.F
		succinyl-CoA synthetase subunit beta [<i>Pseudomonas fluorescens</i> Pf-5] (gi 70729444)	<i>Pseudomonas fluorescens</i> Pf-5	2	2	7	127	K.ATIDPLVGAQPFGGR.D R.LVITYQTDANGQPVTK.I
		elongation factor Tu [<i>Pseudomonas fluorescens</i>] (gi 270341165)	[<i>Pseudomonas fluorescens</i>]	1	1	9	75	R.AGENCGVLLR.G + Carbamidomethyl (C) K.LVETLDSYIPDPVR.V
		peroxiredoxin [<i>Pseudomonas putida</i> W619] (gi 170722358)	<i>Pseudomonas putida</i> W619	2	1	5	71	K.IVELNDGGVGR.D K.IVELNDGGVGR.D
		PREDICTED: serine hydroxymethyltransferase-like [<i>Xenopus (Silurana) tropicalis</i>] (gi 301631113)	<i>Xenopus (Silurana) tropicalis</i>	4	3	4	129	R.LLAEVLQK.R R.LLAEVLQK.R R.LLAEVLQK.R K.LIISGGSSYPR.E
		GLP-binding protein 1a [<i>Arabidopsis thaliana</i>] (gi 29373999)	<i>Arabidopsis thaliana</i>	1	1		86	K.LTATELSTYATNK.Q
	Koghis (2009)	phosphate ABC transporter, periplasmic phosphate-binding protein [<i>Pseudomonas putida</i> KT2440] (gi 26989375)	<i>Pseudomonas putida</i> KT2440	2	2	6	100	R.ADSSGTTAVFTK.H K.LTDTPTVVVVR.A
		phosphate ABC transporter, periplasmic phosphate-binding protein [<i>Pseudomonas putida</i> KT2440] (gi 26989375)	<i>Pseudomonas putida</i> KT2440	2	2	6	90	R.ADSSGTTAVFTK.H K.LTDTPTVVVVR.A
		Chain A, High-Resolution Structure Of The Ding Protein From <i>Pseudomonas Fluorescens</i> (gi 190613370)	<i>Pseudomonas Fluorescens</i>	1	1	3	74	R.SESSGTTTELFR.F
		elongation factor Tu [<i>Pseudomonas fluorescens</i> SBW25] (gi 229592905)	<i>Pseudomonas fluorescens</i> SBW25	4	3	8	182	K.TIAMEDGLR.F + Oxidation (M) K.TIAMEDGLR.F + Oxidation (M) R.AGENCGVLLR.G + Carbamidomethyl (C) K.LVETLDSYIPDPVR.V
		succinyl-CoA synthetase subunit beta [<i>Pseudomonas fluorescens</i> Pf-5] (gi 70729111)	[<i>Pseudomonas fluorescens</i> Pf-5]	3	2	6	107	K.QLFAEYGLPVS.K.G K.QLFAEYGLPVS.K.G K.ATIDPLVGAQPFGGR.E
		PREDICTED: serine hydroxymethyltransferase-like [<i>Xenopus (Silurana) tropicalis</i>] (gi 301631113)	<i>Xenopus (Silurana) tropicalis</i>	4	4	6	162	R.LLAEVLQK.R K.TVEGYGPKR.F R.LLAEVLQK.R K.LIISGGSSYPR.E
		11S globulin-like protein [<i>Actinidia chinensis</i>] (gi 82469930)	<i>Actinidia chinensis</i>	9	2	2	161	R.FFLAGNPQQQK.E R.FFLAGNPQQQK.E
		peroxidase 12 precursor [<i>Zea mays</i>] (gi 195629804)	<i>Zea mays</i>	14	1	3	82	R.VVSCADIVALAAR.E + Carbamidomethyl (C) R.VVSCADIVALAAR.E + Carbamidomethyl (C)

Koghis (2010)	phosphate ABC transporter, periplasmic phosphate-binding protein [Pseudomonas putida KT2440] (gi 26989375)	<i>Pseudomonas putida</i> KT2440	4	3	11	152	R.ADSSGTTAVFTK.H K.GSGAGVQDFLNK.T R.QTPGAIGYIEYGFAK.L R.QTPGAIGYIEYGFAK.L
	Chain A, High Resolution Structure Of The Ding Protein From <i>Pseudomonas fluorescens</i>	<i>Pseudomonas fluorescens</i>	1	1	3	82	R.SESSGTTTELFR.F R.SESSGTTTELFR.F
	ketol-acid reductoisomerase [Pseudomonas fluorescens Pf-5] (gi 70732562)	<i>Pseudomonas fluorescens</i> Pf-5	2	2	7	122	R.ADLDVIMIAPK.A + Oxidation (M) K.NVALSYAAGVGGGR.T
	elongation factor Tu [Pseudomonas fluorescens Pf-5] (gi 70732884)	<i>Pseudomonas fluorescens</i> Pf-5	2	2	4	113	K.TIAMEDGLR.F + Oxidation (M) R.AGENCGVLLR.G + Carbamidomethyl (C)
	peroxiredoxin [Pseudomonas putida W619] (gi 170722358)	<i>Pseudomonas putida</i> W619	2	2	14	100	K.IVEINDGGVGR.D K.EGEATLAPSLDLVGI.- R.HIDVQVWSPTR.A
	DNA-directed RNA polymerase subunit alpha [Pseudomonas putida KT2440] (gi 26987220)	<i>Pseudomonas putida</i> KT2440	1	1	3	74	
GLP-binding protein 1a [Arabidopsis thaliana] (gi 29373999)	<i>Arabidopsis thaliana</i>	1	1	23	87	K.LTATELSTYATNK.Q	
Autre population	phosphate ABC transporter, periplasmic phosphate-binding protein [Pseudomonas putida KT2440] (gi 26989375)	<i>Pseudomonas putida</i> KT2440	3	2	7	92	R.ADSSGTTAVFTK.H R.ADSSGTTAVFTK.H R.QTPGAIGYIEYGFAK.L
	Chain A, High Resolution Structure Of The Ding Protein From <i>Pseudomonas fluorescens</i>	<i>Pseudomonas fluorescens</i>	2	1	3	82	R.SESSGTTTELFR.F R.SESSGTTTELFR.F
	elongation factor Tu [Pseudomonas fluorescens Pf-5] (gi 70732884)	<i>Pseudomonas fluorescens</i> Pf-5	3	2	4	149	K.TIAMEDGLR.F + Oxidation (M) K.TIAMEDGLR.F + Oxidation (M) R.AGENCGVLLR.G + Carbamidomethyl (C)
	ketol-acid reductoisomerase [Pseudomonas fluorescens Pf-5] (gi 70732562)	<i>Pseudomonas fluorescens</i> Pf-5	1	1	4	100	K.NVALSYAAGVGGGR.T
	peroxiredoxin [Pseudomonas putida W619] (gi 170722358)	<i>Pseudomonas putida</i> W619	2	2	14	100	K.IVEINDGGVGR.D
	succinyl-CoA synthetase subunit beta [Pseudomonas fluorescens Pf-5] (gi 70729111)	<i>Pseudomonas fluorescens</i> Pf-5	1	1	3	86	R.LVTYQTANGQPVTK.I