

Species	PAIR	SEQ1	SEQ2	KA	KS	BESTHIT	BESTHIT2	DESCRIPTION
Arabidopsis	1	c2992.A13g15710	c1070.A11g52600	0.0793	0.8135	At3g15710	At1g52600	"signal peptidase, putative"
Arabidopsis	2	c1073.A12g33370	c294.A11g04480	0.0007	0.7416	At3g04400	At3g04400	60S ribosomal protein L23 (RPL23C)
Arabidopsis	3	c3127.A13g11250	c1699.A13g09200	0.0142	0.4762	At3g11250	At3g09200	60S acidic ribosomal protein P0 (RPPOC)
Arabidopsis	4	c3365.A12g30870	c3198.A12g30860	0.0805	1.2614	At2g30870	At2g30860	"glutathione S-transferase, putative supported by cDNA GI:443698 GB:D117673"
Arabidopsis	5	8701630.A14g27070	c1093.A15g54810	0.0267	0.7499	A14g27070	A15g54810	"tryptophan synthase, beta subunit 2 (TSB2)"
Arabidopsis	6	c53.A15g25980	c104.A15g26000	0.1504	0.2725	A15g25980	A15g26000	glycosyl hydrolase family 1 protein contains Pfam PF00232 : Glycosyl hydrolase family 1 domain
Arabidopsis	7	c2954.A11g08360	c531.A15g22440	0.1381	1.5448	At2g27530	A15g22440	60S ribosomal protein L10A (RPL10aB)
Arabidopsis	8	c550.A11g57120	c4555.A11g09840	0.0005	0.4724	At1g57120	At1g57120	"elongation factor 1B-gamma, putative"
Arabidopsis	9	c667.A11g75460	c5327.A11g19740	0.0453	0.666	At1g75460	At1g19740	ATP-dependent protease La (LON)
Arabidopsis	10	c1341.A15g24780	c2031.A15g24770	0.0204	0.4709	A15g24780	A15g24770	vegetative storage protein 1 (VSP1)
Arabidopsis	13	c3252.A13g23730	c637.A4g14130	0.0503	0.9458	At3g23730	A4g14130	"xyloglucan:xyloglucosyl transferase, putative"
Arabidopsis	17	c3889.A15g39580	c4035.A15g64120	0.1409	0.6321	A15g39580	A15g64120	"peroxidase, putative"
Arabidopsis	18	c3394.A13g49010	c349.A13g49120	0.0517	1.1559	At3g49010	At3g49120	60S ribosomal protein L13 (RPL13B)
Arabidopsis	19	c2081.A4g20890	c3620.A15g23860	0.0159	1.9813	A4g20890	A15g23860	tubulin beta-9 chain (TUB9)
Arabidopsis	20	c3471.A4g01850	c2277.A13g17390	0.066	1.2087	A4g01850	At3g17390	S-adenosylmethionine synthetase 2 (SAM2)
Arabidopsis	21	c1119.A4g29410	c681.A12g19730	0.0591	0.9454	A4g29410	At2g19730	60S ribosomal protein L28 (RPL28C)
Arabidopsis	22	c2109.A11g30510	8734556.A4g05390	0.0542	0.8081	At1g30510	A4g05390	ferredoxin-NAD(P)+
Arabidopsis	23	c2012.A11g49480	c448.A13g18990	0.0288	0.6342	At1g49480	At3g18990	transcriptional factor B3 family protein contains Pfam profile PF02362: B3 DNA binding domain
Arabidopsis	24	c5244.A4g14040	c2124.A4g14030	0.0631	0.4989	A4g14040	A4g14030	"selenium-binding protein, putative contains Pfam profile PF05694: 56kDa selenium binding protein (SBP56)"
Arabidopsis	25	c922.A11g04270	c4027.A15g09510	0.0211	0.5372	At1g04270	A15g09510	40S ribosomal protein S15 (RPS15A)
Arabidopsis	27	c5276.A11g09210	c2233.A11g56340	0.0662	0.7245	At1g09210	At11g56340	calreticulin 2 (CRT2)
Arabidopsis	28	c4052.A11g66270	c4486.A13g09260	0.0697	0.4283	At1g66270	At3g09260	beta-glucosidase (PSR3.2)
Arabidopsis	29	c4069.A4g13660	c1279.A11g32100	0.1251	0.9989	A4g13660	At11g32100	"pinoreductase, putative"
Arabidopsis	31	c1131.A13g14420	c655.A13g14415	0.0554	0.3031	At3g14420	At3g14415	cellulose synthase family protein
Arabidopsis	32	c4402.A15g16910	c4165.A13g30350	0.031	0.9438	At5g16910	At3g30350	"succinyl-CoA ligase [GDP-forming] alpha-chain, mitochondrial, putative"
Arabidopsis	33	c2420.A15g08300	c2855.A15g23250	0.0493	0.7654	A15g08300	A15g23250	plasma membrane intrinsic protein 1B (PIP1B)
Arabidopsis	34	c3315.A12g45960	c384.A4g23400	0.0445	1.9336	At2g45960	A4g23400	MATE efflux family protein
Arabidopsis	35	c2030.A11g11670	c3033.A11g61890	0.0391	0.9991	At1g11670	At11g61890	40S ribosomal protein S20 (RPS20C)
Arabidopsis	36	c446.A15g62300	c583.A13g45030	0.0043	0.4043	A15g62300	A13g45030	udcacyanin II strong similarity to udcacyanin II
Arabidopsis	37	c3178.A12g44790	c3938.A15g52650	0.0003	0.0008	At2g44790	A15g52650	GI:3399769 from [Arabidopsis thaliana]
Arabidopsis	38	c1959.A15g50680	8728928.A4g24940	0.1171	0.8253	A15g50680	A4g24940	SUMO activating enzyme 1b (SAE1b)
Arabidopsis	39	c5377.A11g03130	c1045.A4g02770	0.0298	0.5427	At1g03130	A4g02770	"photosystem I reaction center subunit II, chloroplast, putative"
Arabidopsis	40	c3261.A4g34670	c2868.A13g04840	0.0337	1.0724	A4g34670	At3g04840	40S ribosomal protein S3A (RPS3aB)
Arabidopsis	41	c5149.A4g37370	c1722.A4g37360	0.0795	0.5701	A4g37370	A4g37360	"cytochrome P450, putative"
Arabidopsis	42	c4928.A11g27130	8726012.A11g27140	0.1219	0.1913	At11g27130	At11g27140	"glutathione S-transferase, putative"
Arabidopsis	43	c1410.A11g47128	c3271.A15g43060	0.0925	0.8312	At11g47128	A15g43060	cysteine proteinase (RD21A)
Arabidopsis	44	8700837.A11g74380	c2890.A11g18690	0.0118	0.5491	At11g74380	At11g18690	galactosyl transferase GMA12/MNN10 family protein very
Arabidopsis	46	c5200.A13g53420	c3753.A15g60660	0.0456	1.5472	At3g53420	A15g60660	plasma membrane intrinsic protein 2A (PIP2A)
Arabidopsis	47	c2545.A15g03300	c4219.A13g09820	0.0402	0.5654	A15g03300	At3g09820	adenosine kinase 2 (ADK2)
Arabidopsis	48	c5618.A15g09870	c2499.A15g64740	0.0256	0.7627	A15g09870	A15g64740	"cellulose synthase, catalytic subunit, putative"
Arabidopsis	49	c3655.A11g52050	c3756.A11g52070	0.168	0.7178	At11g52050	At11g52070	jacalin lectin family protein
Arabidopsis	50	c2385.A12g31610	c2935.A15g35530	0.0375	0.5975	At2g31610	A15g35530	40S ribosomal protein S3 (RPS3A)
Arabidopsis	51	c1630.A4g13170	c137.A13g07110	0.0711	1.7216	A4g13170	At3g07110	60S ribosomal protein L13a (RPL13aC)
Arabidopsis	52	c3701.A11g78660	c109.A11g78680	0.1254	0.3169	At11g78660	At11g78680	"gamma-glutamyl hydrolase, putative"
Arabidopsis	53	c1583.A15g58830	8731097.A15g58840	0.1084	0.5089	A15g58830	A15g58840	subtilase family protein contains similarity to prepro-cucumisain GI:807898 from [Cucumis melo]
Arabidopsis	54	c892.A11g53310	c4325.A13g14940	0.0603	0.5164	At11g53310	At3g14940	"thiopheneoligomycin carboxylase, putative"
Arabidopsis	55	c68.A12g34430	c3025.A12g34420	0.0002	0.1813	At2g34430	At2g34420	chlorophyll A-B binding protein
Arabidopsis	56	c4197.A11g05570	8696051.A12g31960	0.094	0.8948	At11g05570	At2g31960	callose synthase 1 (CAL1)
Arabidopsis	58	8724932.A11g74650	8687425.A13g47600	0.0402	1.0205	At11g74650	At3g47600	myb family transcription factor (cY13)
Arabidopsis	59	c2441.A15g09810	c2248.A13g12110	0.0378	0.9534	A15g09810	At3g12110	actin 7 (ACT7)
Arabidopsis	60	c5296.A12g41840	8734558.A13g57490	0.0072	0.5742	At2g41840	At3g57490	40S ribosomal protein S2 (RPS2C)
Arabidopsis	61	c2010.A11g33590	c156.A11g33610	0.1373	0.485	At11g33590	At11g33610	disease resistance protein-related
Arabidopsis	62	c868.A12g16850	c3094.A4g35100	0.0371	0.6284	At2g16850	A4g35100	"plasma membrane intrinsic protein, putative very strong similarity to plasma membrane intrinsic protein (SMIP)"
Arabidopsis	63	c137.A13g07110	c2712.A13g24830	0.049	1.2315	At3g07110	At3g24830	60S ribosomal protein L13a (RPL13aA)
Arabidopsis	64	c3485.A11g27030	c3492.A11g27020	0.1792	0.3797	At11g27030	At11g27020	expressed protein
Arabidopsis	65	c4588.A15g02490	c5430.A15g02500	0.0252	0.9758	A15g02490	A15g02500	heat shock cognate 70 kDa protein 2 (HSC70-2)
Arabidopsis	66	c3952.A11g66280	c4486.A13g09260	0.0835	0.4476	At11g66280		glycosyl hydrolase family 1 protein contains Pfam PF00232 : Glycosyl hydrolase family 1 domain
Arabidopsis	68	8683481.A15g40450	c3049.A11g56075	0	0.0021	A15g40450	At11g56075	expressed protein
Arabidopsis	69	8726880.A11g28600	8682141.A12g27360	0.1737	0.3821	At11g28600	At2g27360	"lipase, putative"
Arabidopsis	70	c1412.A11g16700	8730777.A11g79010	0.0241	0.207	At11g16700	At11g79010	"NADH-ubiquinone oxidoreductase 23 kDa subunit, mitochondrial, putative very strong similarity to SPI042599 NADH-ubiquinone oxidoreductase 23 kDa subunit, mitochondrial precursor (EC 1.6.5.3)"
Arabidopsis	72	c5501.A11g18460	8682841.A11g73920	0.1084	1.0539	At11g18460	At11g73920	lipase family protein
Arabidopsis	74	c369.A15g38410	c695.A15g38420	0.0172	0.0791	A15g38410	A15g38420	ribulose biphosphate carboxylase small chain 3B
Arabidopsis	76	c2147.A12g05220	c4793.A15g04800	0.0065	0.1303	At2g05220	A15g04800	40S ribosomal protein S17 (RPS17B)
Arabidopsis	77	c576.A15g13490	c2667.A13g08580	0.0287	0.783	A15g13490	At3g08580	"ADP, ATP carrier protein 2, mitochondrial"
Arabidopsis	79	8728838.A12g19860	8721509.A4g29130	0.0634	0.6059	At2g19860	A4g29130	hexokinase 2 (HXK2)
Arabidopsis	81	c3157.A4g12480	c3288.A4g12490	0.0801	0.395	A4g12480	A4g12490	protease inhibitor/seed storage/lipid transfer protein (LTP)
Arabidopsis	82	c3409.A15g14120	c5601.A13g01930	0.0883	1.0498	At5g14120	At3g01930	nodulin family protein
Arabidopsis	83	c1251.A15g18900	c1667.A13g06300	0.0756	0.6419	A15g18900	At3g06300	"oxidoreductase, 2OG-Fe(II)"
Arabidopsis	84	c890.A11g12240	c2950.A11g62660	0.07	0.5527	At11g12240	At11g62660	beta-fructosidase (BFRUCT14)
Arabidopsis	85	c793.A15g13430	c1900.A15g13440	0.0997	0.2259	A15g13430	A15g13440	"ubiquinol-cytochrome C reductase iron-sulfur subunit, mitochondrial, putative"
Arabidopsis	86	c4055.A15g37600	c1922.A11g66200	0.0454	0.57	A15g37600	At11g66200	"glutamine synthetase, putative"
Arabidopsis	87	8732095.A12g17340	c3971.A4g35360	0.0692	0.468	At2g17340	A4g35360	"pantothenate kinase-related contains Pfam domain, PF01937: Protein of unknown function"
Arabidopsis	88	c3025.A12g34420	c2738.A11g29920	0.0058	0.5934	At2g34420	At11g29920	chlorophyll A-B binding protein
Arabidopsis	89	8681554.A11g32960	8681808.A11g32940	0.0963	0.3112	At11g32960	At11g32940	subtilase family protein contains similarity to subtilase
Arabidopsis	91	8715768.A12g27010	c3193.A15g47990	0.1979	0.4307	At2g27010	A15g47990	cytochrome P450 family protein
Arabidopsis	92	c344.A15g62690	c2081.A4g20890	0.0149	1.5193	A15g62700		tubulin beta-2/beta-3 chain (TUB3)
Arabidopsis	93	8695945.A12g21130	c3638.A4g38740	0.0339	0.9839	At2g21130	A4g38740	peptidyl-prolyl cis-trans isomerase
Arabidopsis	94	c114.A4g03520	c2159.A11g3675	0.162	0.7306	A4g03520	At11g3675	"thioredoxin M-type 2, chloroplast (TRX-M2)"
Arabidopsis	95	c3538.A13g50060	c3432.A15g67300	0.0497	1.462	A15g50060	A15g67300	myb family transcription factor contains Pfam profile: PF00249 myb-like DNA-binding domain
Arabidopsis	96	c3106.A13g02230	c3180.A15g15650	0.0202	0.7735	At3g02230	A15g15650	reversibly glycosylated polypeptide-1 (RGP1)
Arabidopsis	97	c3166.A11g30230	c3238.A12g18110	0.0319	0.3346	At11g30230	At2g18110	elongation factor 1-beta
Arabidopsis	99	8700599.A4g36195	8684100.A4g36190	0.0806	0.4467	A4g36195	A4g36190	serine carboxypeptidase S28 family protein contains Pfam PF05577: Serine carboxypeptidase S28
Arabidopsis	100	c3904.A4g35630	8728250.A12g17630	0.0189	0.8909	A4g35630	At2g17630	"phosphoserine aminotransferase, chloroplast (PSAT)"
Arabidopsis	101	c3486.A11g34030	c202.A4g09800	0.0027	0.6616	A4g09800	A4g09800	40S ribosomal protein S18 (RPS18C)
Arabidopsis	102	c5320.A12g17930	c2864.A4g36080	0.1621	0.6991	At2g17930	A4g36080	FAT domain-containing protein
Arabidopsis	103	8738516.A4g39490	c1097.A12g23180	0.0799	0.4655	A4g39490	At2g23180	
Arabidopsis	104	c3619.A11g23290	c5036.A11g70600	0.003	0.5054	At11g23290	At11g70600	60S ribosomal protein L27A (RPL27aB)

Arabidopsis	105	c488.A1g14320	c1617.A1g66580	0.0528	1.8786	A1g26910	A1g66580	60S ribosomal protein L10 (RPL10B)
Arabidopsis	106	c21.A1g17880	c3276.A1g73230	0.0528	0.481	A1g17880	A1g73230	nascent polypeptide-associated complex (NAC)
Arabidopsis	107	c2408.A1g231350	c5174.A1g06130	0.0914	0.637	A1g231350	A1g06130	"hydroxyacylglutathione hydrolase, putative"
Arabidopsis	108	c3981.A1g237190	c809.A1g560670	0.0198	1.0028	A1g237190	A1g560670	60S ribosomal protein L12 (RPL12A)
Arabidopsis	109	c2960.A1g21830	c3506.A1g21850	0.094	0.7652	A1g21840	A1g21850	methionine sulfoxide reductase domain-containing protein
Arabidopsis	110	c55.A1g415000	c165.A1g322230	0.07	1.007	A1g415000	A1g322230	60S ribosomal protein L27 (RPL27C)
Arabidopsis	111	c809.A1g560670	c1008.A1g53430	0.016	0.9306	A1g560670	A1g53430	60S ribosomal protein L12 (RPL12C)
Arabidopsis	112	8734558.A1g57490	c2811.A1g58380	0.0043	0.9192	A1g57490	A1g59359	40S ribosomal protein S2 (RPS2D)
Arabidopsis	113	c720.A1g221580	c639.A1g39200	0.0151	0.3956	A1g221580	A1g39200	40S ribosomal protein S25 (RPS25B)
Arabidopsis	114	c5262.A1g27240	c1345.A1g540810	0.0189	0.7446	A1g27240	A1g540810	"cytochrome c1, putative cytochrome c1, heme protein, mitochondrial precursor (Clone PC13III)"
Arabidopsis	115	c371.A1g222240	c5108.A1g439800	0.0232	0.8917	A1g222240	A1g39800	inositol-3-phosphate synthase isozyme 2
Arabidopsis	117	c1865.A1g237180	c5200.A1g353420	0.0472	0.6873	A1g237180	A1g237180	plasma membrane intrinsic protein 2C (PIP2C)
Arabidopsis	118	c3647.A1g316410	c3092.A1g316400	0.0083	0.0466	A1g316410	A1g316400	jacalin lectin family protein
Arabidopsis	119	c3458.A1g316440	c3398.A1g316420	0.1267	0.5791	A1g316440	A1g316420	jacalin lectin family protein contains Pfam profile: PF01419 jacalin-like lectin domain
Arabidopsis	121	c1440.A1g432970	8686885.A1g432960	0.1617	0.3404	A1g432970	A1g432960	expressed protein
Arabidopsis	123	c4138.A1g62020	c1780.A1g21390	0.0989	0.4122	A1g62020	A1g21390	"coatamer protein complex, subunit alpha, putative contains Pfam PF00400: WD domain, G-beta repeat"
Arabidopsis	125	c642.A1g243020	c4779.A1g359050	0.0743	0.8991	A1g243020	A1g359050	amine oxidase family protein
Arabidopsis	126	c2738.A1g29920	c68.A1g234430	0.0059	0.6978	A1g29930	A1g29930	"chlorophyll A-B binding protein 2, chloroplast"
Arabidopsis	127	c2886.A1g514740	c127.A1g301500	0.0492	0.3923	A1g514740	A1g301500	carbonic anhydrase 2
Arabidopsis	128	c209.A1g439730	c3640.A1g22170	0.0983	0.9337	A1g439730	A1g22170	"lipid-associated family protein contains PLAT/LH2 (Polycystin-1, Lipoxigenase, Alpha-Toxin/Lipoxygenase homology)"
Arabidopsis	129	c1427.A1g237620	c2248.A1g312110	0.0307	0.9338	A1g53750	A1g53750	actin 3 (ACT3)
Arabidopsis	130	c3956.A1g313470	c4571.A1g55490	0.0206	0.781	A1g313470	A1g55490	"chaperonin, putative similar SWISS-PROT:P21240-RuBisCO subunit binding-protein beta subunit, chloroplast precursor (60 kDa chaperonin beta subunit, CPN-60 beta)"
Arabidopsis	132	c249.A1g308940	c787.A1g501530	0.0299	0.8855	A1g308940	A1g501530	chlorophyll A-B binding protein (LHCb4.2)
Arabidopsis	133	c1845.A1g328715	c2566.A1g328710	0.0033	0.2737	A1g328715	A1g328715	"H+-transporting two-sector ATPase, putative"
Arabidopsis	135	c5369.A1g541700	c719.A1g553300	0.0213	1.2618	A1g541700	A1g553300	ubiquitin-conjugating enzyme 8 (UBC8)
Arabidopsis	136	c1518.A1g437520	8702373.A1g437530	0.0304	0.1283	A1g437520	A1g437530	peroxidase 50 (PER50)
Arabidopsis	137	c1259.A1g401480	c2114.A1g101050	0.0337	0.6322	A1g401480	A1g101050	"inorganic pyrophosphatase, putative [soluble]"
Arabidopsis	139	8680290.A1g326300	c2530.A1g326290	0.0825	0.7434	A1g326300	A1g326290	cytochrome P450 family protein contains Pfam profile: PF00067 cytochrome P450
Arabidopsis	140	c1214.A1g227860	c3862.A1g08200	0.0205	0.9371	A1g227860	A1g08200	expressed protein
Arabidopsis	141	c5374.A1g21100	c3189.A1g76790	0.0715	1.0154	A1g21100	A1g76790	"O-methyltransferase, putative"
Arabidopsis	142	c2971.A1g21340	c5304.A1g51805	0.0874	0.7367	A1g21340	A1g51805	"leucine-rich repeat protein kinase, putative"
Arabidopsis	144	c3537.A1g28580	8682141.A1g27360	0.2036	0.3667	A1g28580	A1g28580	"GDSL-motif lipase, putative"
Arabidopsis	145	c2793.A1g122840	8681466.A1g410040	0.0408	1.0215	A1g122840	A1g410040	"cytochrome c, putative"
Arabidopsis	147	c1076.A1g508670	c4233.A1g508680	0.0002	0.2139	A1g508670	A1g508690	"ATP synthase beta chain 1, mitochondrial"
Arabidopsis	148	c1278.A1g319130	c2853.A1g49600	0.0973	0.5107	A1g319130	A1g49600	"RNA-binding protein, putative"
Arabidopsis	149	c3838.A1g314790	c2734.A1g53500	0.0389	0.9578	A1g314790	A1g53500	NAD-dependent epimerase/dehydratase family protein
Arabidopsis	150	c3854.A1g414100	8681671.A1g323760	0.0802	1.5123	A1g414100	A1g323760	expressed protein
Arabidopsis	151	c4591.A1g523020	c3727.A1g523010	0.0858	0.3616	A1g523020	A1g523010	2-isopropylmalate synthase 2 (IMS2)
Arabidopsis	152	c4923.A1g52580	c871.A1g311510	0.0374	0.7756	A1g52580	A1g311510	40S ribosomal protein S14 (RPS14C)
Arabidopsis	153	c2290.A1g30530	c3258.A1g517050	0.112	0.3777	A1g30530	A1g517050	UDP-glucuronosyl/UDP-glucosyl transferase family protein contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase
Arabidopsis	154	c1306.A1g205840	c92.A1g535590	0.0454	0.7545	A1g205840	A1g535590	20S proteasome alpha subunit A2 (PAA2)
Arabidopsis	155	c580.A1g218020	c1384.A1g436130	0.0162	0.5839	A1g218020	A1g436130	60S ribosomal protein L8 (RPL8A)
Arabidopsis	156	c3070.A1g508730	8702438.A1g506720	0.0836	0.4039	A1g506730	A1g506720	"peroxidase, putative"
Arabidopsis	157	c1283.A1g510450	c1252.A1g55430	0.0315	0.8605	A1g510450	A1g55430	14-3-3 protein GF14 lambda (GRF6)
Arabidopsis	158	c4233.A1g508680	c3147.A1g508690	0.0002	0.207	A1g508690	A1g508690	"ATP synthase beta chain 2, mitochondrial"
Arabidopsis	160	c5048.A1g219110	8683676.A1g30110	0.1103	1.0266	A1g219110	A1g30110	ATPase E1-E2 type family protein
Arabidopsis	161	c2811.A1g58380	c5296.A1g241840	0.0035	0.8337	A1g58380	A1g241840	40S ribosomal protein S2 (RPS2B)
Arabidopsis	162	c1400.A1g223610	c3713.A1g223560	0.1734	0.3774	A1g223610	A1g223560	"esterase, putative"
Arabidopsis	163	c1216.A1g20010	c3796.A1g175780	0.0283	0.9034	A1g20010	A1g175780	tubulin beta-5 chain (TUB5)
Arabidopsis	164	c1342.A1g04340	c167.A1g543460	0.1099	0.6005	A1g04340	A1g543460	lesion inducing protein-related
Arabidopsis	165	c254.A1g318410	c4067.A1g49140	0.0129	0.6967	A1g318410	A1g49140	NADH-ubiquinone oxidoreductase-related
Arabidopsis	166	8692815.A1g19890	c584.A1g510980	0.0336	1.2354	A1g19890	A1g510980	"histone H3, putative"
Arabidopsis	167	c3599.A1g326520	c3341.A1g236830	0.0677	0.7822	A1g326520	A1g236830	"tonoplast intrinsic protein, putative"
Arabidopsis	168	c109.A1g79680	c536.A1g78670	0.2436	0.5341	A1g79680	A1g78670	gamma-glutamyl hydrolase (GGH1)
Arabidopsis	169	c1311.A1g29930	c68.A1g234430	0.0063	0.5835	A1g29930	A1g234430	"chlorophyll A-B binding protein 2, chloroplast"
Arabidopsis	170	c5503.A1g320130	c2532.A1g320100	0.1337	0.5288	A1g320130	A1g320100	cytochrome P450 family protein contains Pfam profile: PF00067 cytochrome P450
Arabidopsis	172	c3126.A1g316450	c3458.A1g316440	0.1212	0.5504	A1g316450	A1g316450	jacalin lectin family protein
Arabidopsis	173	c452.A1g80560	c3580.A1g514200	0.039	0.5516	A1g80560	A1g514200	"3-isopropylmalate dehydrogenase, chloroplast, putative strong similarity to 3-ISOPROPYLMALATE DEHYDROGENASE PRECURSOR GB-P29102 SPP29102 from [Brassica napus]"
Arabidopsis	174	c5743.A1g70850	8725944.A1g70890	0.1262	0.3939	A1g70850	A1g70890	Bet v I allergen family protein
Arabidopsis	175	c1856.A1g326650	c712.A1g12900	0.0243	0.7487	A1g12900	A1g12900	"glyceraldehyde 3-phosphate dehydrogenase, chloroplast, putative"
Arabidopsis	176	c1922.A1g66200	c4327.A1g317820	0.0954	0.9337	A1g66200	A1g317820	"glutamine synthetase, putative"
Arabidopsis	177	c1008.A1g353430	c3981.A1g237190	0.0081	0.8177	A1g353430	A1g237190	60S ribosomal protein L12 (RPL12B)
Arabidopsis	179	c3617.A1g525460	c3160.A1g511420	0.053	1.1277	A1g525460	A1g511420	"expressed protein contains Pfam profile PF04862: Protein of unknown function, DUF642"
Arabidopsis	181	c384.A1g423400	c3402.A1g361430	0.0363	1.4565	A1g423400	A1g361430	major intrinsic family protein
Arabidopsis	182	c202.A1g409800	c2371.A1g122780	0.0056	1.0899	A1g409800	A1g09800	40S ribosomal protein S18 (RPS18C)
Arabidopsis	183	c5178.A1g43450	8729077.A1g43440	0.1077	0.5488	A1g43450	A1g43440	"2-oxoglutarate-dependent dioxygenase, putative"
Arabidopsis	184	c3060.A1g305590	c3710.A1g527850	0.126	0.821	A1g305590	A1g527850	60S ribosomal protein L18 (RPL18B)
Arabidopsis	185	c4372.A1g24200	c3142.A1g430910	0.0624	0.7612	A1g24200	A1g430910	cytosol aminopeptidase
Arabidopsis	186	c2065.A1g52870	c3613.A1g247610	0.0171	0.9496	A1g52870	A1g247610	60S ribosomal protein L7A (RPL7aB)
Arabidopsis	188	c5132.A1g09795	c3310.A1g58080	0.097	0.5735	A1g09795	A1g58080	ATP phosphoribosyl transferase 2 (ATP-PR2)
Arabidopsis	189	c2969.A1g418710	c441.A1g230980	0.0264	1.5538	A1g418710	A1g230980	shaggy-related protein kinase eta
Arabidopsis	190	c3400.A1g542020	c3291.A1g528540	0.0031	0.1333	A1g542020	A1g528540	luminal binding protein 2 (BIP-2)
Arabidopsis	194	c258.A1g132220	c206.A1g236170	0.0007	0.7055	A1g132220	A1g236170	expressed protein
Arabidopsis	196	c4769.A1g38920	c4627.A1g434720	0.0028	1.0328	A1g38920	A1g38920	vacuolar ATP synthase 16 kDa proteolipid subunit 3
Arabidopsis	197	c3398.A1g316420	c3126.A1g316450	0.1086	0.3258	A1g316420	A1g316450	jacalin lectin family protein
Arabidopsis	198	c2000.A1g311400	8734632.A1g506000	0.0729	0.7977	A1g311400	A1g506000	eukaryotic translation initiation factor 3G
Arabidopsis	200	c1733.A1g303780	c4570.A1g517920	0.0348	0.5855	A1g303780	A1g517920	"5-methyltetrahydropteroyl/triglutamate--homocysteine methyltransferase, putative"
Arabidopsis	201	8682758.A1g221410	c3061.A1g439080	0.0488	0.6158	A1g221410	A1g439080	"vacuolar proton ATPase, putative"
Arabidopsis	202	c5138.A1g78830	c5089.A1g78820	0.0336	0.3586	A1g78830	A1g78820	curculin-like (mannose-binding)
Arabidopsis	203	8715897.A1g219760	c3410.A1g429350	0.0876	0.8083	A1g219760	A1g429350	profilin 1 (PRO1)
Arabidopsis	204	8715260.A1g72730	c1759.A1g313920	0.0263	1.1149	A1g72730	A1g313920	"eukaryotic translation initiation factor 4A, putative"
Arabidopsis	205	c695.A1g538420	c2878.A1g67090	0.043	0.3544	A1g538420	A1g67090	ribulose biphosphate carboxylase small chain 2B
Arabidopsis	206	c3713.A1g23560	c2174.A1g23550	0.21	0.3168	A1g23560	A1g23550	"hydrolase, alpha/beta fold family protein"
Arabidopsis	207	c2514.A1g62290	c758.A1g111910	0.0591	0.9504	A1g62290	A1g111910	"aspartyl protease family protein contains Pfam profiles: PF00026 eukaryotic aspartyl protease, PF03489 surfactant protein B, PF05184 saposin-like type B, region 1"
Arabidopsis	208	c4617.A1g57785	c1648.A1g242310	0.0333	0.7939	A1g57785	A1g242310	expressed protein
Arabidopsis	209	c2937.A1g221430	c2881.A1g439090	0.0749	1.0391	A1g221430	A1g439090	"cysteine proteinase A494, putative"
Arabidopsis	210	c4977.A1g320060	8724608.A1g50490	0.0461	0.5554	A1g320060	A1g50490	ubiquitin-conjugating enzyme 19 (UBC19)

Arabidopsis	211	c3439 At5g43010	c3586 At1g45000	0.0144	0.9054	At5g43010	At1g45000	26S proteasome AAA-ATPase subunit (RPT4a)
Arabidopsis	213	c5255 At2g44160	c476 At3g59970	0.1656	1.1984	At2g44160	At3g59970	methylenetetrahydrofolate reductase 2 (MTHFR2)
Arabidopsis	214	c3077 At5g07090	c2951 At2g17360	0.0822	0.7563	At5g07090	At2g17360	40S ribosomal protein S4 (RPS4B)
Arabidopsis	215	c3341 At2g36830	c3876 At2g19340	0.0002	0.0002	At2g36830	At4g29870	major intrinsic family protein
Arabidopsis	216	c402 At1g01620	c384 At4g23400	0.021	0.9532	At1g01620		plasma membrane intrinsic protein 1C (PIP1C)
Arabidopsis	218	c2174 At2g23550	c1400 At2g23610	0.1372	0.27	At2g23550		"hydrolase, alpha/beta fold family protein"
Arabidopsis	219	c3332 At5g26280	c3122 At5g26260	0.0837	0.2297	At5g26280	At5g26260	meprin and TRAF homology domain-containing protein
Arabidopsis	220	8729434 At3g02730	c281 At5g16400	0.043	0.7884	At3g02730	At5g16400	"thioredoxin, putative"
Arabidopsis	221	c3245 At3g16430	c3126 At3g16450	0.0954	0.3373	At3g16430		jacalin lectin family protein
Arabidopsis	222	c4955 At3g05840	c2787 At5g26751	0.0908	0.9379	At5g26751	At5g26751	shaggy-related protein kinase alpha
Arabidopsis	223	c2935 At5g35530	c2272 At3g53870	0.027	0.9911	At5g35530	At3g53870	40S ribosomal protein S3 (RPS3C)
Arabidopsis	224	c5058 At1g17620	c741 At4g17390	0.0003	0.0007	At1g17620	At4g17390	expressed protein
Arabidopsis	226	c749 At4g27130	c1624 At5g54760	0.0148	0.4654	At4g27130	At5g54760	"eukaryotic translation initiation factor SU11, putative"
Arabidopsis	227	c866 At3g03940	c1473 At5g18190	0.0469	0.6938	At3g03940	At5g18190	"protein kinase family protein contains Pfam domains PF00689: Protein kinase domain"
Arabidopsis	228	c936 At1g78670	c3701 At1g78660	0.1248	0.4478	At1g78670		"gamma-glutamyl hydrolase, putative"
Arabidopsis	230	c2933 At3g23300	c3911 At4g14360	0.0739	1.0468	At3g23300	At4g14360	dehydration-responsive protein-related
Arabidopsis	231	c1734 At5g06290	c3161 At3g11630	0.0238	0.5951	At5g06290	At3g11630	"2-cys peroxiredoxin, chloroplast, putative very strong similarity to SP1Q96291 2-cys peroxiredoxin BAS1, chloroplast precursor (Arabidopsis thaliana)"
Arabidopsis	233	c792 At5g19250	c5431 At5g19240	0.265	0.5391	At5g19250	At5g19240	expressed protein
Arabidopsis	234	c3147 At5g08690	c1076 At5g08670	0.0003	0.3216	At5g08690		"ATP synthase beta chain 2, mitochondrial"
Arabidopsis	235	c282 At3g60770	c149 At4g00100	0.0029	1.5664	At3g60770	At4g00100	40S ribosomal protein S13 (RPS13A)
Arabidopsis	236	c1720 At5g20020	c4012 At5g20010	0.0332	0.2038	At5g20020	At5g20010	Ras-related GTP-binding nuclear protein (RAN-2)
Arabidopsis	237	c2272 At3g53870	c2385 At2g31610	0.0348	0.3498	At3g53870		40S ribosomal protein S3 (RPS3B)
Arabidopsis	238	c5479 At1g54010	c3295 At1g54000	0.0666	0.2024	At1g54010	At1g54000	"myosinase-associated protein, putative"
Arabidopsis	242	8693992 At5g18280	c2202 At3g04080	0.1056	0.5784	At5g18280	At3g04080	apvrase (APY2)
Arabidopsis	243	c2878 At1g67090	c369 At5g38410	0.0422	0.3727	At1g67090		ribulose biphosphate carboxylase small chain 1A
Arabidopsis	244	c3305 At3g59920	c1901 At2g44100	0.0512	0.6402	At3g59920	At2g44100	Rab GDP dissociation inhibitor (GDI2)
Arabidopsis	245	8700637 At5g26734	c4489 At3g05940	0.1703	0.5414	At5g26734	At3g05940	elongation factor 1-alpha
Arabidopsis	246	c3296 At1g07920	c4228 At1g07930	0.0001	0.0986	At5g60390		ubiquitin-specific protease 12 (UBP12)
Arabidopsis	247	8704730 At1g80820	c649 At1g15950	0.1555	1.6921	At1g80820	At1g15950	"cinnamoyl-CoA reductase, putative"
Arabidopsis	249	c2845 At5g58420	c2951 At2g17360	0.0875	0.8515	At5g58420		40S ribosomal protein S4 (RPS4D)
Arabidopsis	250	c3073 At2g30050	8704832 At3g01340	0.0408	0.6667	At2g30050	At3g01340	transducin family protein
Arabidopsis	251	c66 At4g33010	c4544 At2g26080	0.029	0.6252	At4g33010	At2g26080	"glycine dehydrogenase [decarboxylating], putative"
Arabidopsis	254	c138 At1g65010	c2036 At1g04820	0.0003	0.5552	At1g65010	At4g14960	tubulin alpha-2/alpha-4 chain (TUA2)
Arabidopsis	255	c1635 At1g12010	c1472 At1g62380	0.0405	0.7038	At1g12010	At1g62380	"1-aminocyclopropane-1-carboxylate oxidase, putative"
Arabidopsis	256	c47 At3g53020	c3290 At2g36620	0.0152	1.2068	At3g53020	At2g36620	60S ribosomal protein L24 (RPL24B)
Arabidopsis	257	c6199 At5g06600	c6132 At3g11910	0.1309	0.7892	At5g06600	At3g11910	ubiquitin-specific protease 12 (UBP12)
Arabidopsis	258	c1543 At1g19660	c1482 At1g17580	0.0897	0.7705	At1g19660	At1g17580	wound-responsive family protein
Arabidopsis	259	c3225 At3g18780	c2441 At5g09810	0.044	1.2032	At3g18780		actin 2 (ACT2)
Arabidopsis	260	c187 At1g04510	c457 At2g33340	0.1333	1.0172	At1g04510		transducin family protein
Arabidopsis	261	c400 At3g53500	8695860 At2g37340	0.2772	0.9989	At3g53500	At2g37340	zinc knuckle (CCHC-type)
Arabidopsis	262	c5490 At2g40510	c146 At3g56340	0.0072	1.12	At2g40510	At3g56340	40S ribosomal protein S26 (RPS26A)
Arabidopsis	264	c2371 At1g22780	c3496 At1g34030	0.0056	1.133	At4g09800		40S ribosomal protein S18 (RPS18C)
Arabidopsis	265	c1956 At3g04710	c1964 At2g23910	0.0673	0.7318	At4g30470		cinnamoyl-CoA reductase-related
Arabidopsis	266	c5594 At2g39800	c533 At3g55610	0.0323	0.741	At2g39800	At3g55610	delta 1-pyrroline-5-carboxylate synthetase A
Arabidopsis	269	c2367 At1g76260	c2863 At1g20540	0.0788	0.514	At1g76260	At1g20540	transducin family protein
Arabidopsis	271	c986 At1g26630	c3999 At1g69410	0.0417	0.7197	At1g26630	At1g69410	"eukaryotic translation initiation factor 5A, putative"
Arabidopsis	272	c211 At1g78300	c3587 At1g35160	0.0313	0.921	At1g78300	At1g35160	14-3-3 protein GF14 omega (GRF-z)
Arabidopsis	273	c2112 At1g69369	8734558 At3g57490	0.0042	0.9115	At1g69369		40S ribosomal protein S2 (RPS2B)
Arabidopsis	274	c2702 At2g37270	c177 At3g11940	0.0279	0.6445	At2g37270	At3g11940	40S ribosomal protein S5 (RPS5A)
Arabidopsis	275	c2234 At5g55190	c4012 At5g20010	0.0311	1.09	At5g55190		Ras-related GTP-binding protein (RAN3)
Arabidopsis	276	8680442 At4g11240	c1159 At1g64040	0.0552	1.6777	At4g11240	At1g64040	serine/threonine protein phosphatase PP1 isozyme 6 (PP1BG)
Arabidopsis	277	c5975 At1g21130	c4767 At1g21120	0.0364	0.3268	At1g21130	At1g21120	"O ⁶ -methyltransferase, putative"
soybean	1	Contig1	Contig649	0.0034	0.8224	At5g59850	At5g59850	40S ribosomal protein S15A (RPS15aF)
soybean	2	Contig6	Contig1241	0.1084	1.2776	At5g60390	At5g60390	elongation factor 1-alpha
soybean	3	Contig10	Contig591	0.0232	1.0026	At4g36130	At4g36130	60S ribosomal protein L8 (RPL8C)
soybean	4	Contig13	Contig17	0.1076	0.7015	At5g07090	At5g07090	40S ribosomal protein S4 (RPS4B)
soybean	5	Contig16	Contig642	0.0393	0.3987	At4g01850		S-adenosylmethionine synthetase 1 (SAM1)
soybean	6	Contig19	Contig76	0.0119	0.4885	At2g36830	At2g36830	major intrinsic family protein
soybean	8	Contig36	Contig412	0.0613	0.8214	At4g17390	At4g16720	60S ribosomal protein L15 (RPL15B)
soybean	11	Contig50	Contig1368	0.0075	0.4549	At4g23400	At4g00430	major intrinsic family protein
soybean	13	Contig58	Contig195	0.0513	0.3819	At3g47340	At3g47340	asparagine synthetase 1 [glutamine-hydrolyzing]
soybean	14	Contig65	Contig364	0.0082	0.1065	At3g16740	At1g36240	60S ribosomal protein L30 (RPL30C)
soybean	15	Contig69	Contig1308	0.055	0.066	At4g31700	At4g31700	40S ribosomal protein S6 (RPS6A)
soybean	16	Contig72	Contig1317	0.1203	0.7005	At3g47340	At3g47340	asparagine synthetase 1 [glutamine-hydrolyzing]
soybean	17	Contig73	4395976	0.121	0.9626	At3g09630	At5g02870	60S ribosomal protein L4/L1 (RPL4A)
soybean	18	Contig75	Contig1310	0.0115	0.809	At2g32060	At2g32060	40S ribosomal protein S12 (RPS12C)
soybean	19	Contig82	Contig104	0.0927	1.3419	At5g14670	At2g47170	"ADP-ribosylation factor, putative"
soybean	20	Contig85	Contig800	0.0853	0.4842	At5g12110	At5g12110	elongation factor 1B alpha-subunit 1 (eEF1Balpha1)
soybean	21	Contig93	Contig264	0.0196	0.9207	At3g05560	At3g05560	60S ribosomal protein L22-2 (RPL22B)
soybean	22	Contig108	Contig131	0.0983	1.7946	At1g74270		60S ribosomal protein L35a (RPL35aC)
soybean	23	Contig118	Contig189	0.0131	0.0843			
soybean	24	Contig126	7591354	0.0509	0.0385			
soybean	25	Contig134	8283757	0.0157	0.6292	At1g69620	At1g26880	60S ribosomal protein L34 (RPL34B)
soybean	26	Contig148	Contig904	0.0932	0.771	At3g49910	At5g67510	60S ribosomal protein L26 (RPL26A)
soybean	31	Contig170	Contig1339	0.0133	0.4563	At5g20620	At4g02890	polyubiquitin (UBQ4)
soybean	32	Contig175	Contig1309	0.0847	0.5853	At5g28050	At5g28050	cytidine/deoxycytidylate deaminase family protein
soybean	34	Contig178	Contig325	0.0217	1.6015	At1g50010	At1g50010	tubulin alpha-2/alpha-4 chain (TUA2)
soybean	37	Contig186	Contig1170	0.0006	0.6388	At1g69410	At1g69410	"eukaryotic translation initiation factor 5A, putative"
soybean	39	Contig217	7638377	0.0881	0.5097	At2g26080	At4g33010	"glycine dehydrogenase [decarboxylating], putative"
soybean	40	Contig279	Contig468	0.0081	0.95	At1g67430	At1g27400	60S ribosomal protein L17 (RPL17B)
soybean	42	Contig318	Contig1025	0.0049	0.618	At2g47110	At2g47110	ubiquitin extension protein 6 (UBQ6)
soybean	44	Contig320	7691460	0.2217	1.0561	At3g05590	At3g05590	60S ribosomal protein L18 (RPL18B)
soybean	45	Contig331	Contig726	0.1921	0.4902	At3g62410	At3g62410	CP12 domain-containing protein contains Pfam domain PF02672: CP12 domain
soybean	46	Contig338	Contig1122	0.2306	0.4412	At5g59720	At1g07400	18.1 kDa class I heat shock protein (HSP18.1-C1)
soybean	47	Contig351	Contig790	0.0727	1.4758	At1g79750	At2g19900	"malate oxidoreductase, putative"
soybean	48	Contig403	Contig1253	0.0018	1.785	At4g05050	At5g20620	polyubiquitin (UBQ11)
soybean	49	Contig410	Contig1218	0.0093	1.6167	At4g14320	At4g14320	60S ribosomal protein L36a/L44 (RPL36aB)
soybean	50	Contig422	Contig1283	0.0403	0.1843	At1g55020	At1g55020	lipoxigenase (LOX1)
soybean	52	Contig440	6455110	0.0799	1.5781	At5g60670	At5g60670	60S ribosomal protein L12 (RPL12C)
soybean	53	Contig450	17022227	0.1351	0.5319	At4g04880	At4g04880	adenosine/AMP deaminase family protein
soybean	54	Contig472	15815176	0.0269	0.4613	At5g17310		"UTP-glucose-1-phosphate uridylyltransferase, putative"
soybean	55	Contig474	Contig515	0.005	0.3135	At2g34430	At2g34430	chlorophyll A-B binding protein
soybean	56	Contig484	16277122	0.0177	0.6512	At5g17330	At5g17330	glutamate decarboxylase 1 (GAD 1)
soybean	58	Contig498	7029171	0.0164	0.0002			
soybean	59	Contig511	7691033	0.0387	0.0449	At5g54190	At5g54190	"protochlorophyllide reductase A, chloroplast"
soybean	61	Contig536	7028227	0.1002	0.5006	At1g35720	At5g12380	annexin 1 (ANN1)
soybean	62	Contig569	Contig893	0.0526	0.7237	At1g27970	At1g27970	nuclear transport factor 2 (NTF2)
soybean	63	Contig583	Contig881	0.0162	0.0139			
soybean	64	Contig584	16278757	0.0032	0.585	At5g02960	At5g02960	40S ribosomal protein S23 (RPS23B)
soybean	67	Contig596	14259897	0.0473	0.8186	At4g35090	At4g35090	catalase 2
soybean	72	Contig630	Contig1136	0.0696	0.4323	At1g06680	At1g06680	photosystem II oxygen-evolving complex 23 (OEC23)

soybean	73	Contig672	13789365	0.4381	0.873			
soybean	74	Contig697	Contig827	0.024	0.1262	At1g07890	At3g09640	"L-ascorbate peroxidase 1, cytosolic (APX1)"
soybean	75	Contig714	15813270	0.0346	0.5442	At5g46860	At5g46860	syntaxin 22 (SYP22)
soybean	78	Contig820	13252345	0.0785	0.6898	At4g34050	At4g34050	"caffeoyl-CoA 3-O-methyltransferase, putative nearly"
soybean	79	Contig835	Contig1222	0.0493	0.8664	At1g78300	At4g09000	14-3-3 protein GF14 omega (GRF2)
soybean	80	Contig849	Contig1172	0.017	0.7696	At3g04840	At4g34670	40S ribosomal protein S3A (RPS3aA)
soybean	81	Contig852	7692922	0.0323	0.7085	At5g60790	At5g60790	ABC transporter family protein
soybean	82	Contig860	6567346	0.0956	0.2943	At5g20630	At5g20630	germin-like protein (GER3)
soybean	83	Contig863	4395717	0.0386	0.9334	At1g11650	At5g54900	RNA-binding protein 45 (RBP45)
soybean	84	Contig867	8403325	0.1654	1.1672	At1g74920	At1g74920	"betaine-aldehyde dehydrogenase, putative"
soybean	86	Contig891	6096252	0.074	0.4937	At4g14420	At4g14420	lesion inducing protein-related
soybean	87	Contig894	10842963	0.1213	0.4016	At5g10450	At5g65430	14-3-3 protein GF14 lambda (GRF6)
soybean	88	Contig895	Contig1020	0.1077	0.1521	At5g25610	At5g25610	dehydration-responsive protein (RD22)
soybean	89	Contig901	6455224	0.0647	0.3357	At5g11160	At5g11160	"adenine phosphoribosyltransferase, putative strong similarity to SPIQ42563 Adenine phosphoribosyltransferase 2 (EC 2.4.2.7)"
soybean	91		Contig916					
soybean	92	Contig927	7028323	0.0927	0.6824	At3g45310	At5g60360	"cysteine proteinase, putative"
soybean	94	Contig953	Contig1125	0.0107	0.167	At4g09800	At4g09800	40S ribosomal protein S18 (RPS18C)
soybean	96	Contig996	8283676	0.0928	0.557	At5g02230	At5g02230	haloacid dehalogenase-like hydrolase family protein contains InterPro accession IPR005834: Haloacid dehalogenase-like hydrolase
soybean	97	Contig1014	Contig1163	0.0343	0.5035	At3g18130	At1g48630	guanine nucleotide-binding family protein
soybean	99	Contig1027	Contig1095	0.0577	0.0852	At4g34590	At2g27860	bZIP transcription factor family protein
soybean	100	Contig1040	5126754	0.0263	0.8961	At5g62300	At3g47370	40S ribosomal protein S20 (RPS20C)
soybean	101	Contig1042	Contig1246	0.0002	0.1797	At5g17920	At5g17920	5-methyltetrahydropteroyltryglutamate--homocysteine methyltransferase
soybean	102	Contig1123	Contig1187	0.0093	1.9592	At5g41700	At1g64230	ubiquitin-conjugating enzyme 8 (UBC8)
soybean	103	Contig1134	Contig1261	0.1168	0.2476	At4g25150	At4g25150	"acid phosphatase, putative"
soybean	105	Contig1151	10845533	0.0278	0.7055	At4g02470	At4g02470	
soybean	107	Contig1204	8282592	0.0245	1.0243	At3g44110	At3g44110	"DNAJ heat shock protein, putative (J3)"
soybean	109	Contig1226	Contig1287	0.0391	0.7203	At5g02500	At5g02500	heat shock cognate 70 kDa protein 1 (HSC70-1)
soybean	113	Contig1326	7796588	0.0554	1.6878	At2g36530	At2g36530	enolase
soybean	114	Contig1338	Contig1114	0.1182	1.6967	At3g09800	At1g60970	clathrin adaptor complex small chain family protein contains Pfam profile: PF01217 clathrin adaptor complex small chain
soybean	115	Contig1341	6964555	0.1446	0.1523	At2g38540	At2g38540	nonspecific lipid transfer protein 1 (LTP1)
soybean	116	Contig1342	6502239	0.1083	0.3686	At5g54500	At5g54500	"quinone reductase, putative"
soybean	117	Contig1343	4313897	0.0722	0.2989	At2g24520	At4g30190	"ATPase, plasma membrane-type, putative"
soybean	118	Contig1346	10233842	0	0.0018	At5g10170	At4g39800	"inositol-3-phosphate synthase, putative"
soybean	119	Contig1349	4291120	0.0636	0.4084	At2g35120	At2g35120	"glycine cleavage system H protein, mitochondrial, putative"
soybean	120	4405586	7589833	0.0559	0.5641	At2g38400	At2g38400	"alanine--glyoxylate aminotransferase, putative"
soybean	121	4291569	7796620	0.0271	1.2784	At5g09810	At5g09810	actin 7 (ACT7)
soybean	122	6964527	8284525	0.1361	0.6679	At1g55860	At1g55860	ubiquitin-protein ligase 1 (UPL1)
soybean	123	7029342	13789771	0.0223	0.1521	At2g03390	At2g03390	uvrB/uvrC motif-containing protein contains Pfam profile PF02151: UvrB/uvrC motif
soybean	124	7028750	6964031	0.0422	0.2225			
soybean	125	7028474	16278969	0.0606	0.5281	At5g66190	At5g66190	ferredoxin--NADP(++)
soybean	126	7589734	6454134	3.2779	2			
soybean	127	7589058	10845775	0.1174	1.0121			
soybean	129	6455313	7478905	0.483	0.3991	At4g39840	At4g39840	expressed protein
soybean	130	7924661	7691802	0.1548	0.1128			
soybean	131	7796605	16348094	0.0644	1.4485	At5g48230	At5g48230	"acetyl-CoA C-acyltransferase, putative"
soybean	132	7796585	13790060	0.0869	0.5086	At3g54020	At3g54020	phosphatidic acid phosphatase-related
soybean	133	7692572	8283047	0.1193	0.522	At1g80410	At1g80410	acetyltransferase-related
soybean	134	7692420	7691358	0.1311	0.5832	At5g02790	At5g02790	"hn2-1 protein, putative"
soybean	135	7691841	6567201	0.0182	1.6831	At5g60860	At5g60860	"Ras-related GTP-binding protein, putative"
soybean	137	7691687	7690853	0.0493	0.5429	At5g66570	At3g50820	"oxygen-evolving enhancer protein 1-1, chloroplast"
soybean	138	6481950	13789912	0.0761	0.7095	At3g15730	At3g15730	phospholipase D alpha 1
soybean	139	8283209	11411993	0.1024	0.3836	At2g45820	At2g45820	"DNA-binding protein, putative"
soybean	140	7588348	10847437	0.2107	0.1277			
soybean	141	16279657	7588366	0.1286	0.3621	At1g02890	At4g02470	"AAA-type ATPase family protein contains Pfam domain, PF00004: ATPase, AAA family"
soybean	142	13789740	13252748	0.0245	0.1624	At2g25750	At3g03940	
tomato	2	Contig29	Contig239	0.1767	0.9757	At3g25800	At3g25800	serine/threonine protein phosphatase 2A (PP2A)
tomato	3	Contig30	Contig829	0.023	0.2633	At5g61970	At5g61970	signal recognition particle-related
tomato	4	Contig34	Contig1681	0.1738	1.8602	At4g09800	At4g09800	40S ribosomal protein S18 (RPS18C)
tomato	5	Contig47	16236927	0.0121	0.3574	At3g13920	At3g13920	eukaryotic translation initiation factor 4A-1
tomato	6	Contig59	Contig694	0.0548	1.1782	At1g64980	At1g64980	expressed protein
tomato	7	Contig60	Contig1663	0.0737	1.6084	At4g35090	At4g35090	catalase 2
tomato	8	Contig61	16247996	0.0171	1.7394	At1g75780	At5g23860	tubulin beta-1 chain (TUB1)
tomato	9	Contig78	Contig1133	0.0637	0.1039	At5g20240	At5g20240	floral homeotic protein PISTILLATA (PI)
tomato	10	Contig82	Contig636	0.021	1.2527	At1g51060	At5g54640	"histone H2A, putative"
tomato	11	Contig83	16241150	0.0457	0.9388	At1g27400	At1g67430	60S ribosomal protein L17 (RPL17A)
tomato	12	Contig84	16226905	0.035	0.6568	At1g57860	At1g57860	60S ribosomal protein L21
tomato	14	Contig93	16244977	0.1609	0.3543	At1g52190	At1g52190	proton-dependent oligopeptide transport (POT)
tomato	15	Contig102	Contig1332	0.0116	0.5903	At1g29930	At1g29930	"chlorophyll A-B binding protein 2, chloroplast"
tomato	16	Contig105	16230158	0.0006	0			
tomato	17		Contig108	0	0.012	At3g13470	At5g56500	"chaperonin, putative similar SWISS-PROT:P21240-RuBisCO subunit binding-protein beta subunit, chloroplast precursor (60 kDa chaperonin beta subunit, CPN-60 beta)"
tomato	18	Contig117	Contig1408	0.0231	1.3228	At5g61170	At5g61170	40S ribosomal protein S19 (RPS19C)
tomato	20	Contig130	Contig1086	4.3063	1.0771			
tomato	21	Contig143	Contig515	0.0351	1.3961	At1g33140	At1g33140	60S ribosomal protein L9 (RPL90A/C)
tomato	22	Contig157	Contig483	0.0293	0.6595	At1g72370	At3g04770	40S ribosomal protein SA (RPSaA)
tomato	23	Contig165	Contig1145	0.0166	0.4943	At2g36880	At2g36880	"S-adenosylmethionine synthetase, putative"
tomato	24	Contig166	Contig1711	0.0219	0.904	At5g23860	At5g23860	tubulin beta-8 chain (TUB8)
tomato	25	Contig168	Contig479	0.0106	0.6374	At5g10360	At5g10360	40S ribosomal protein S6 (RPS6B)
tomato	26	Contig179	16226042	0.0392	0.9405	At3g09630	At3g09630	60S ribosomal protein L4/L1 (RPL4A)
tomato	27	Contig190	Contig516	0.0039	0			
tomato	28	Contig211	Contig574	0.0476	0.5399	At4g38970	At4g38970	"fructose-bisphosphate aldolase, putative strong similarity to plastidic fructose-bisphosphate aldolase (EC 4.1.2.13)"
tomato	29	Contig212	Contig1140	0.0495	0.0682	At3g14690	At3g14620	"cytochrome P450, putative"
tomato	30	Contig218	16246572	0.1811	1.0494	At3g06430	At3g06430	pentatricopeptide (PPR)
tomato	32	Contig221	Contig943	0.0019	0.6259	At5g60390	At5g60390	elongation factor 1-alpha
tomato	33	Contig224	Contig1222	0.0578	0.5201	At5g50620	At3g50620	"oxygen-evolving enhancer protein, chloroplast, putative"
tomato	34		Contig231	0.0731	0.7465	At2g28000	At2g28000	"RuBisCO subunit binding-protein alpha subunit, chloroplast"
tomato	35	Contig237	16245806	0.0929	0.4688	At5g47770	At4g17190	"farnesyl pyrophosphate synthetase 1, mitochondrial (FPS1)"
tomato	37	Contig246	Contig624	0.1248	0.8275	At1g16880	At1g16880	uridylyltransferase-related
tomato	38	Contig249	Contig1063	0.0927	1.431	At2g34250	At2g34250	"protein transport protein sec61, putative"
tomato	39	Contig284	Contig867	0	0.0015	At1g24510	At1g67760	"T-complex protein 1 epsilon subunit, putative"
tomato	40	Contig298	Contig792	0.0506	0.623	At1g23820	At1g70310	spermidine synthase 1 (SPDSYN1)
tomato	42	Contig343	Contig1811	0.1982	0.9021	At5g41600	At5g41600	reticulon family protein (RTNLRB4)
tomato	43	Contig344	16224853	0.0032	0.0117	At5g27740	At5g27740	expressed protein

tomato	44	Contig353	Contig1196	0	0.0017	At5g01720	At5g54190	F-box family protein (FBL3)
tomato	45	Contig358	16244756	0.5192	1.31	At3g42050	At3g42050	vacuolar ATP synthase subunit H family protein
tomato	46	Contig386	16242901	0.0408	0.9028	At4g27440	At4g27440	"protochlorophyllide reductase B, chloroplast"
tomato	47	Contig388	Contig960	0	0.0018	At3g05840	At5g26751	shaggy-related protein kinase gamma
tomato	48	Contig389	Contig1098	0.0763	0.1509	At4g10500	At2g44800	"oxidoreductase, 2OG-Fe(II)"
tomato	50	Contig394	Contig1678	0.066	0.987	At5g59010	At5g41260	protein kinase-related
tomato	52	Contig418	16246599	0.0004	0.0007	At3g44750	At3g44750	"histone deacetylase, putative (HD2A)"
tomato	53	Contig423	16246473	0.0471	0.9494	At5g10170	At5g10170	"inositol-3-phosphate synthase, putative"
tomato	54	Contig473	Contig1058	0.005	0.1819	At1g29930	At1g29930	"chlorophyll A-B binding protein 2, chloroplast"
tomato	55	Contig487	Contig1443	0.0212	1.8406	At1g56410	At5g02500	"heat shock cognate 70 kDa protein, putative"
tomato	56	Contig488	16243416	0.0471	1.0471	At2g36460	At2g36460	"fructose-bisphosphate aldolase, putative"
tomato	57	Contig489	16246558	0.0951	0.6462	At1g11890	At1g11890	"vesicle transport protein SEC22, putative identified as SEC22 by Raikheil, NV, et al. in Plant Physiol. 124: 1558-69 (2000)"
tomato	58	Contig495	16245501	0.1206	0.7063	At5g02770	At5g02770	expressed protein
tomato	59	Contig510	Contig903	0.0257	0.69	At5g54270	At5g54270	chlorophyll A-B binding protein
tomato	63	Contig546	Contig890	0	0.0016	At5g38410	At5g38410	ribulose bispophosphate carboxylase small chain 3B
tomato	65	Contig553	Contig1290	0.0544	0.5751	At5g46750	At4g17890	human Rev interacting-like family protein
tomato	67	Contig562	Contig1296	0.0264	0.9188	At3g13200	At3g13200	Cwf15
tomato	68	Contig575	Contig1257	0.0842	0.6335	At5g38410	At5g38410	ribulose bispophosphate carboxylase small chain 3B
tomato	70	Contig607	16236840	0.1103	0.7227	At3g22200	At3g22200	4-aminobutyrate aminotransferase
tomato	71	Contig615	16244691	0.0297	1.6046	At1g76300	At1g76300	14-3-3 protein GF14 omega (SRF2)
tomato	73	Contig630	16247327	0.0383	0.5873	At2g19730	At2g19730	60S ribosomal protein L28 (RPL28A)
tomato	74	Contig634	Contig687	0.0118	1.1774	At2g34480	At3g14600	60S ribosomal protein L18A (RPL18aB)
tomato	76	Contig645	16242313	0.0276	0.8554	At2g20450	At2g20450	60S ribosomal protein L14 (RPL14A)
tomato	78	Contig669	Contig1232	0.5736	0.3671			
tomato	79	Contig674	Contig1007	0.089	0.9383			
tomato	80	Contig675	16233902	0.0418	0.583	At5g29771	At5g29771	
tomato	81	Contig690	Contig1112	0.0293	0.864	At4g11820	At4g11820	hydroxymethylglutaryl-CoA synthase
tomato	82	Contig723	Contig994	0.0128	0.5398	At3g11940	At2g37270	40S ribosomal protein S5 (RPS5B)
tomato	85	Contig737	Contig938	0.0284	0.9015	At1g66580	At1g26910	60S ribosomal protein L10 (RPL10C)
tomato	88	Contig828	Contig882	0.0789	0.5735	At1g74270	At1g74270	60S ribosomal protein L35a (RPL35aC)
tomato	89	Contig834	Contig1105	0.0152	0.7233	At4g06390	At5g06390	"L-ascorbate peroxidase, stromal (aAPX)"
tomato	90	Contig835	Contig1775	0.0422	0.7605	At2g39770	At2g39770	GDP-mannose_ pyrophosphorylase (GMP1)
tomato	91	Contig853	16246134	0.0001	0.0004	At3g49010	At3g49010	60S ribosomal protein L13 (RPL13B)
tomato	93	Contig871	16235927	4.3129	1.875	At1g76520	At1g20925	"auxin efflux carrier family protein contains auxin efflux carrier domain, Pfam:PF03547"
tomato	94	Contig881	Contig1119	0.029	0.7266			expressed protein
tomato	96	Contig926	16239121	0.0793	0.6878	At1g08200	At1g08200	60S ribosomal protein L23A (RPL23aA)
tomato	97	Contig947	16236722	0.0375	0.9078	At2g39460	At2g39460	60S ribosomal protein L23A (RPL23aA)
tomato	98	Contig966	Contig1278	0.1006	0.5484	At5g09510	At1g04270	40S ribosomal protein S15 (RPS15D)
tomato	99	Contig979	16228711	0.0027	1.1157	At4g23430	At4g23430	short-chain dehydrogenase/reductase (SDR)
tomato	100	Contig1019	Contig1301	0.0724	0.8831	At1g13950	At1g13950	eukaryotic translation initiation factor 5A-1
tomato	102	Contig1054	16245743	0.075	0.4212	At3g44110	At3g44110	"DNAJ heat shock protein, putative (J3)"
tomato	104	Contig1070	16246354	0.0005	0	At5g67090	At5g67090	subtilase family protein contains similarity to subtilisin-like protease ag12 Gi:757522 from [Ainus glutinosa]
tomato	105	Contig1071	16235274	0.0505	0.0228			
tomato	106	Contig1124	16248573	0.0829	1.0167			
tomato	107	Contig1144	16237377	0.0178	1.0585	At4g36130	At4g36130	ABC transporter family protein
tomato	108	Contig1184	Contig1336	0.0388	1.1421	At4g13940	At4g13940	60S ribosomal protein L8 (RPL8C)
tomato	109	Contig1209	Contig1771	0.1922	0.6073	At4g13940	At4g13940	adenosylhomocysteine
tomato	111	Contig1226	16241093	0.0086	1.2712	At1g73600	At1g73600	"phosphoethanolamine N-methyltransferase 2, putative (NMT2)"
tomato	112	Contig1238	Contig1381	0	0.0008	At3g62290	At3g62290	ADP-ribosylation factor
tomato	115	Contig1280	Contig1779	0.0426	1.7915	At5g19760	At5g19760	dicarboxylate/tricarboxylate carrier (DTC)
tomato	117	Contig1300	16247450	0.0034	0	At5g28540	At5g28540	luminal binding protein 1 (BiP-1)
tomato	119	Contig1320	16245717	0.1121	0.8459			expressed protein
tomato	120	Contig1329	Contig1519	0.0516	0.0547	At5g65810	At3g49720	expressed protein
tomato	121	Contig1331	Contig1843	0.084	1.4928	At3g17860	At3g17860	expressed protein
tomato	122	Contig1379	16223549	0.0903	0.6527	At1g05010	At1g05010	1-aminocyclopropane-1-carboxylate oxidase
tomato	123	Contig1384	16248811	0.0302	0.8302	At3g01280	At3g01280	"porin, putative"
tomato	124	Contig1396	16250222	0.0719	0.8293	At1g52150	At1g52150	homeobox-leucine zipper family protein
tomato	127	Contig1477	16247903	0.0962	0.8922	At1g60970	At1g60970	clathrin adaptor complex small chain family protein contains Pfam profile: PF01217 clathrin adaptor complex small chain
tomato	128	Contig1495	Contig1550	0.0912	0.8958	At4g23630	At4g23630	reticulon family protein (RTN1B1)
tomato	129	Contig1499	16250447	1.1753	0.9102	At4g23630	At4g23630	reticulon family protein (RTN1B1)
tomato	130	Contig1510	16235211	0.0455	0.349	At1g72330	At1g72330	"alanine aminotransferase, putative"
tomato	131	Contig1522	16233956	0.0004	0.0008	At5g62890	At5g62890	"permease, putative"
tomato	133	Contig1543	16244837	0.0914	0.9246	At1g51610	At1g51610	cation efflux family protein
tomato	134	Contig1545	16245338	0.0296	0.6278	At2g44120	At3g13580	60S ribosomal protein L7 (RPL7C)
tomato	135	Contig1613	16249412	0.1305	1.9125	At1g48850	At1g48850	"chorismate synthase, putative"
tomato	136	Contig1631	16235080	0.0332	0.9732	At3g12160	At5g05270	Ras-related GTP-binding family protein
tomato	137	Contig1649	16248160	0.0505	0.6711	At3g44110	At3g44110	"DNAJ heat shock protein, putative (J3)"
tomato	138	Contig1652	Contig1875	0.0617	0.6846	At3g42640	At3g42640	"ATPase, plasma membrane-type, putative"
tomato	139	Contig1673	16248958	0.0416	0.5881	At1g69040	At1g69040	ACT domain containing protein (ACR4)
tomato	140	Contig1679	16236710	0.0188	0.663	At2g39840	At2g39840	serine/threonine protein phosphatase PP1 isozyme 4 (TOPP4)
tomato	141	Contig1713	16249483	3.8694	1.6833	At5g49460	At5g49460	"ATP-citrate synthase, putative"
tomato	143	Contig1764	16245907	0.0465	0.8664			
tomato	144	Contig1765	16247078	0.0012	1.2173	At2g26980	At1g30270	CBL-interacting protein kinase 3 (CIPK3)
tomato	145	Contig1780	16241419	0.0362	0.5185	At5g10980	At5g10980	histone H3
tomato	146	Contig1782	16223608	0.1344	0.9941	At1g65840	At1g65840	amine oxidase family protein
tomato	147	Contig1791	16234442	0.0289	0.5749	At5g54510	At5g54510	"auxin-responsive GH3 protein, putative (DFL-1)"
tomato	149	16232642	16246524	0.0792	0.5784	At5g23860	At5g23860	tubulin beta-8 chain (TUB8)
tomato	150	16232007	16248938	0.086	1.5299	At3g21865	At3g21865	expressed protein
tomato	151	16231493	16246123	0.0876	0.7119	At5g47880	At5g47880	eukaryotic peptide chain release factor subunit 1-1 (ERF1-1)
tomato	152	16231396	16247382	0.0038	0			phosphoinositide-specific phospholipase C (PLC2)
tomato	153	16231298	16238933	0.0156	0.4841	At3g08510	At3g08510	
tomato	154	16230891	16246584	0.0782	0.7047	At3g54560	At3g54560	histone H2A F/Z
tomato	155	16229892	16246763	0.0805	0.5218	At5g45180	At5g45180	flavin-containing monooxygenase family protein
tomato	156	16229284	16246465	0.0557	1.1782	At3g63520	At3g63520	9-cis-epoxycarotenoid dioxygenase
tomato	157	16228875	16250043	0.0844	0.7617	At1g18540	At1g18540	60S ribosomal protein L6 (RPL6A)
tomato	158	16228797	16247156	0.0831	1.4966	At1g32700	At4g17900	zinc-binding family protein
tomato	161	16228434	16240017	0.0925	0.8762	At3g46000	At3g46010	"actin-depolymerizing factor, putative (ADF2)"
tomato	162	16228237	16248109	0.0619	0.6688	At5g48760	At5g48760	60S ribosomal protein L13A (RPL13aD)
tomato	163	16228156	16248558	0.0457	0.5684	At1g50430	At1g50430	7-dehydrocholesterol reductase
tomato	164	16227744	16250268	0.1749	0.4562	At5g07920	At5g07920	diacylglycerol kinase 1 (DGK1)
tomato	165	16227587	16238395	0.0504	0.4873	At1g05820	At1g05820	protease-associated (PA)
tomato	167	16225369	16248701	0.0908	0.5025	At3g15640	At3g15640	"cytochrome c oxidase family protein contains Pfam domain, PF01215: Cytochrome c oxidase subunit Vb"
tomato	168	16223114	16240848	0.0001	0.0006	At2g28000	At2g28000	"RuBisCO subunit binding-protein alpha subunit, chloroplast"
tomato	169	16244084	16237827	0.0143	0.9428			
tomato	170	16242054	16247214	0.0955	1.4023	At4g16720	At4g17390	60S ribosomal protein L15 (RPL15A)
tomato	171	16241026	16249496	0.1379	0.6195	At3g13810	At3g13810	zinc finger (C2H2 type)
						At1g06780	At1g06780	glycosyl transferase family 8 protein contains Pfam profile: PF01501 glycosyl transferase family 8

tomato	172	16239666	16245167	0.1211	0.322	At3g55120	At3g55120	chalcone-flavanone isomerase
tomato	173	16239117	16250188	0.0271	0.8246	At3g25150	At3g25150	nuclear transport factor 2 (NTF2)
tomato	174	16247650	16250277	0.0678	1.0933	At1g47380	At1g47380	protein phosphatase 2C-related
tomato	175	16247635	16248029	0.1228	1.1587	At1g12050	At1g12050	*fumarylacetoacetase, putative"
tomato	177	16246720	16246037	0	0.0024	At3g52310		
tomato	178	16246570	16250488	0.0307	0.0232			
tomato	179	16246355	16245590	0.0253	0.5018	At1g30820	At3g12670	"CTP synthase, putative"
tomato	180	16246339	16245987	0.1288	0.5887	At5g61210	At5g61210	SNAP25 homologous protein SNAP33 (SNAP33)
tomato	182	16245751	16249798	0	0.0007	At3g13390		
tomato	183	16249919	16249096	0.0962	0.8526	At5g25350	At2g25490	F-box family protein contains Pfam PF00646: F-box domain and Pfam PF00560: Leucine Rich Repeat (6 copies)
Eschscholzia	1	Contig13	Contig916	0.0049	0.4169	At5g09810	At5g09810	actin 7 (ACT7)
Eschscholzia	2	Contig17	Contig108	0.0508	0.6609	At5g37600	At5g37600	"glutamine synthetase, putative"
Eschscholzia	3	Contig22	eca01-46ms2-c09-24367	0.009	0.7291	At3g05590	At3g05590	60S ribosomal protein L18 (RPL18B)
Eschscholzia	4	Contig31	Contig468	0.0111	0.3706	At3g08900	At3g02230	reversibly glycosylated polypeptide-3 (RGP3) nearly
Eschscholzia	5	Contig33	Contig1060	0.1347	0.1574			
Eschscholzia	6	Contig38	eca01-4cs2-a04-19331	0.0591	0.7944	At1g73230	At1g73230	nascent polypeptide-associated complex (NAC) domain-containing protein
Eschscholzia	7	Contig40	Contig69	0.0527	0.8065	At4g00100	At4g00100	40S ribosomal protein S13 (RPS13A)
Eschscholzia	8	Contig41	Contig316	0.0962	1.8321	At5g14670	At5g14670	"ADP-ribosylation factor, putative"
Eschscholzia	9	Contig42	Contig816	0.0672	0.885	At5g55190	At5g55190	Ras-related GTP-binding protein (RAN3)
Eschscholzia	10	Contig47	Contig497	0.0722	0.64	At3g53620	At3g53620	"inorganic pyrophosphatase, putative [soluble]"
Eschscholzia	11	Contig54	Contig288	0.0537	0.5069	At5g03300	At5g03300	adenosine kinase 2 (ADK2) contains Pfam profile: PF00294 pfkB family carbohydrate kinase
Eschscholzia	12	Contig56	Contig1090	0.0045	0.5453	At5g58290	At5g58290	26S proteasome AAA-ATPase subunit (RPT3)
Eschscholzia	13	Contig1052	Contig1052	0.0271	0.5588	At2g01250	At2g01250	60S ribosomal protein L7 (RPL7B)
Eschscholzia	14	Contig94	Contig1037	0.0042	0.8287	At5g09810	At5g09810	actin 7 (ACT7)
Eschscholzia	15	Contig97	Contig103	0.0004	0.4409	At4g02080	At4g02080	GTP-binding protein (SAR1A)
Eschscholzia	16	Contig104	eca01-5cs1-d02-35929	0.0442	0.8116	At5g01710	At5g01710	expressed protein
Eschscholzia	17	Contig115	Contig1141	0.0442	0.3281	At5g17920	At5g17920	5-methyltetrahydropteroyltryglutamate-homocysteine methyltransferase
Eschscholzia	19	Contig126	Contig905	0.0575	0.4852	At1g20950	At1g76550	pyrophosphate-fructose-6-phosphate 1-phosphotransferase-related
Eschscholzia	20	Contig136	Contig1323	0.0756	1.0087	At3g01280	At3g01280	"porin, putative"
Eschscholzia	22	Contig149	Contig897	0.026	0.1379	At3g08580	At3g08580	"ADP, ATP carrier protein 1, mitochondrial"
Eschscholzia	23	Contig153	Contig433	0.0279	0.8088	At5g59910		histone H2B nearly
Eschscholzia	24	Contig157	Contig161	0.0931	0.7091	At1g21750	At1g77510	"protein disulfide isomerase, putative"
Eschscholzia	25	Contig160	Contig489	0.0453	0.7926	At3g50750	At1g78700	brassinosteroid signalling positive regulator-related contains similarity to BZR1 protein [Arabidopsis thaliana] gi20270971 gb AAM18490
Eschscholzia	26	Contig165	Contig734	0.0005	0.5072	At5g20620	At5g20620	polyubiquitin (UBQ4)
Eschscholzia	27	Contig169	eca01-6ms1-c06-15776	0.0123	0.7634	At5g09550	At2g44100	"Rab GDP dissociation inhibitor, putative strong similarity to GDP dissociation inhibitor protein OsGDI1 [Oryza sativa] GI:2384758"
Eschscholzia	28	Contig171	eca01-3cs3-f06-33297	0.0759	0.5498	At4g37930	At4g37930	glycine hydroxymethyltransferase
Eschscholzia	29	Contig176	Contig176	0.0353	0.6936	At5g10170	At5g10170	"nucleic-3-phosphate synthase, putative"
Eschscholzia	30	Contig182	Contig1078	0.001	1.0495	At5g20620	At5g20620	polyubiquitin (UBQ4)
Eschscholzia	31	Contig193	Contig629	0.0868	0.9007	At3g03440	At3g03440	armadillo/beta-catenin repeat family protein contains Pfam profile: PF00514 armadillo/beta-catenin-like repeat
Eschscholzia	32	Contig195	Contig705	0.0478	0.363	At4g17890	At2g35210	human Rev interacting-like family protein
Eschscholzia	33	Contig206	Contig481	0.0004	0.396	At5g39740	At5g39740	"60S ribosomal protein L5 (RPL5B) ribosomal protein L5, rice"
Eschscholzia	34	Contig232	eca01-40ms1-a05-31401	0.1032	0.3766	At4g23630	At2g46170	reticulon family protein (RTNLB1) weak similarity to Nogo-C protein [Rattus norvegicus] GI:6822251
Eschscholzia	35	Contig234	Contig441	0.0883	0.7025	At1g09840	At1g57720	"elongation factor 1B-gamma, putative"
Eschscholzia	36	Contig235	Contig640	0.0334	0.4083	At5g20290	At5g20290	"40S ribosomal protein S8 (RPS8A) ribosomal protein S8 - Zea mays, PIR:T04088"
Eschscholzia	37	Contig237	Contig495	0.0717	0.6534	At2g26250	At2g26250	beta-ketoadyl-CoA synthase family (FIDDLEHEAD) (FDH)
Eschscholzia	38	Contig238	Contig298	0.0362	0.5492	At3g09630	At5g02870	60S ribosomal protein L4/L1 (RPL4A) strong similarity to 60S ribosomal protein L1 GB:P49691
Eschscholzia	39	Contig240	Contig279	0.0495	0.5136	At5g19760	At5g19760	dicarboxylate/tricarboxylate carrier (DTC)
Eschscholzia	40	Contig247	eca01-36ms2-g09-29292	0.0972	0.8194	At1g67430	At1g67430	60S ribosomal protein L17 (RPL17B)
Eschscholzia	41	Contig253	Contig542	0.0118	0.7446	At1g53240	At1g53240	"malate dehydrogenase [NAD], mitochondrial"
Eschscholzia	42	Contig257	Contig1082	0.051	1.1113	At2g09990	At2g09990	40S ribosomal protein S16 (RPS16A) Same as GB:Q42340
Eschscholzia	43	Contig262	eca01-5cs3-g12-36654	0.003	0.6217	At5g17920	At5g17920	5-methyltetrahydropteroyltryglutamate-homocysteine methyltransferase
Eschscholzia	45	Contig273	Contig1042	0.0272	1.2009	At5g58420	At5g58420	"40S ribosomal protein S4 (RPS4D) ribosomal protein S4, Arabidopsis thaliana, PIR:T48480"
Eschscholzia	46	Contig275	Contig1234	0.0129	0.8975	At2g27530	At2g27530	60S ribosomal protein L10A (RPL10aB)
Eschscholzia	47	Contig283	Contig1390	0.0556	1.2818	At5g62700	At5g62700	tubulin beta-2/beta-3 chain (TUB3) nearly
Eschscholzia	48	Contig284	eca01-40ms1-g08-16125	0.017	0.0608	At5g10980	At5g10980	histone H3
Eschscholzia	49	Contig287	Contig299	0.0003	0.3447	At5g60390	At5g60390	elongation factor 1-alpha
Eschscholzia	50	Contig292	eca01-5cs1-g11-35771	0.099	0.5093	At1g58110	At1g58110	bZIP family transcription factor
Eschscholzia	51	Contig297	Contig674	0.1534	0.6939	At5g15270	At5g48190	"KH domain-containing protein various predicted proteins, Arabidopsis thaliana and Oryza sativa"
Eschscholzia	52	Contig300	Contig596	0.0209	0.9878	At2g30490	At2g30490	trans-cinnamate 4-monooxygenase
Eschscholzia	53	Contig305	eca01-9cs1-h04-38133	0.001	0.9971	At3g22110	At3g22110	20S proteasome alpha subunit C (PAC1) (PRC9)
Eschscholzia	54	Contig311	Contig1150	0.0067	0.8414	At3g13920	At1g54270	eukaryotic translation initiation factor 4A-1
Eschscholzia	55	Contig328	Contig1378	0.0741	0.4691	At1g60390	At1g70370	BURP domain-containing protein
Eschscholzia	56	Contig334	Contig997	0.0178	1.3822	At2g36460	At2g36460	"fructose-bisphosphate aldolase, putative"
Eschscholzia	57	Contig337	Contig463	0.0532	0.6195	At5g58420	At5g07090	"40S ribosomal protein S4 (RPS4D) ribosomal protein S4, Arabidopsis thaliana, PIR:T48480"
Eschscholzia	60	Contig368	Contig377	0.2345	0.304	At4g01260		hypothetical protein
Eschscholzia	61	Contig371	eca01-5cs2-c08-34313	0.0478	0.5665	At3g52990	At3g52990	"pyruvate kinase, putative"
Eschscholzia	62	Contig381	eca01-10cs4-e02-34431	0.078	0.5326	At5g07030	At5g07030	aspartyl protease family protein contains Pfam profile:PF00026 eukaryotic aspartyl protease
Eschscholzia	64	Contig420	Contig1319	0.0455	1.0245	At1g13440	At1g13440	"glyceraldehyde 3-phosphate dehydrogenase, cytosolic, putative"
Eschscholzia	65	Contig430	eca01-9ms2-g11-23338	0.0616	0.5133	At1g24510	At1g24510	"T-complex protein 1 epsilon subunit, putative"
Eschscholzia	66	Contig436	eca01-74ms2-h08-4504	0.0659	0.2526	At3g27740		carbamoyl-phosphate synthase [glutamine-hydrolyzing] (CARA)
Eschscholzia	67	Contig490	eca01-46ms2-b07-22179	0.0642	0.8785	At1g10020	At1g10020	expressed protein
Eschscholzia	68	Contig457	eca01-13ms1-h08-15198	0.0568	0.6296	At3g27090	At3g27090	expressed protein
Eschscholzia	69	Contig465	eca01-9cs2-e06-36172	0.0794	0.9846	At5g40650	At5g40650	"succinate dehydrogenase, iron-sulphur subunit, mitochondrial (SDH2-2) nearly"
Eschscholzia	70	Contig490	Contig722	0.0293	1.0483	At5g56030	At5g56030	heat shock protein 81-2 (HSP81-2) nearly
Eschscholzia	72	Contig506	Contig1316	0.0007	0.7372	At1g72370	At3g04770	40S ribosomal protein SA (RPSaA)
Eschscholzia	73	Contig507	eca01-8cs1-e09-35890	0.0007	0.7356	At1g72370	At1g72370	40S ribosomal protein SA (RPSaA)
Eschscholzia	74	Contig511	eca01-9cs1-f06-38282	0.0477	0.5481	At5g04800	At5g04800	"40S ribosomal protein S17 (RPS17D) 40S ribosomal protein S17, Lycopersicon esculentum, EMBL:AF161704"
Eschscholzia	75	Contig529	Contig724	0.0133	1.0731	At1g78720	At1g78720	"protein transport protein sec61, putative"
Eschscholzia	76	Contig533	Contig584	0.0377	0.5646	At1g48630	At1g48630	guanine nucleotide-binding family protein
Eschscholzia	77	Contig537	eca01-3cs4-f11-19122	0.0071	0.045	At5g20890	At5g20890	"chaperonin, putative"
Eschscholzia	78	Contig538	Contig1363	0.0163	0.7975	At1g19580	At1g19580	bacterial transferase hexapeptide repeat-containing protein contains Pfam profile PF00132: Bacterial

								transferase hexapeptide (four repeats)
Eschscholzia	79	Contig541	eca01-29ms1-b09-17311	0.0187	0.6207	At5g23540	At5g23540	"26S proteasome regulatory subunit, putative"
Eschscholzia	80	Contig549	Contig1255	0.0335	0.6734	At1g09210	At1g09210	calreticulin 2 (CRT2)
Eschscholzia	81	Contig552	Contig1026	0.0417	1.208	At3g25800	At3g25800	serine/threonine protein phosphatase 2A (PP2A) 65 kDa regulatory subunit A
Eschscholzia	82	Contig553	Contig618	0.0551	0.5724	At4g38510	At4g38510	"vacuolar ATP synthase subunit B, putative"
Eschscholzia	83	Contig556	eca01-10ms1-d08-13854	0.0256	0.7935	At5g14040	At5g14040	mitochondrial phosphate transporter
Eschscholzia	84	Contig557	eca01-25ms1-e08-33007	0.0852	0.8927	At1g55840	At1g55840	SEC14 cytosolic factor (SEC14)
Eschscholzia	85	Contig571	eca01-10ms1-g10-8886	0.0404	1.0023	At1g13950	At1g69410	eukaryotic translation initiation factor 5A-1
Eschscholzia	86	Contig577	Contig1012	0.0211	0.0802			
Eschscholzia	87	Contig579	Contig1102	0.0192	1.7915	At1g54270	At3g13920	eukaryotic translation initiation factor 4A-2
Eschscholzia	88	Contig598	eca01-38ms1-e06-57441	0.0449	0.5097	At4g28510	At2g20530	"prohibitin, putative"
Eschscholzia	90	Contig617	eca01-9cs1-b10-37272	0.0164	0.6897	At1g02130	At1g02130	Ras-related protein (ARA-5)
Eschscholzia	91	Contig630	eca01-74ms4-g05-32785	0.0005	0.4858	At5g05010	At5g05010	clathrin adaptor complexes medium subunit-related contains pfam profile: PF00928 adaptor complexes medium subunit family
Eschscholzia	93	Contig645	Contig1310	0.0188	0.5497	At4g34670	At4g34670	40S ribosomal protein S3A (RPS3aB)
Eschscholzia	94	Contig659	Contig1107	0.0236	0.6759	At5g39850	At5g39850	"40S ribosomal protein S9 (RPS9C) 40S ribosomal protein S9 - Chlamydomonas sp., EMBL:AU066528"
Eschscholzia	96	Contig670	eca01-16ms1-e04-13851	0.0082	0.0268			
Eschscholzia	98	Contig694	Contig1156	0.0214	1.274	At2g36880	At2g36880	"S-adenosylmethionine synthetase, putative"
Eschscholzia	100	Contig704	Contig981	0.1291	0.1791	At3g17570		
Eschscholzia	101	Contig708	eca01-67ms1-e12-21577	0.0473	1.587	At5g10840	At3g13772	"endomembrane protein 70, putative TM4 family;"
Eschscholzia	102	Contig715	eca01-3cs3-h01-33997	0.0073	0.9182	At2g47170	At5g14670	ADP-ribosylation factor 1 (ARF1)
Eschscholzia	103	Contig738	eca01-27ms1-f08-2056	0.1484	0.6759	At3g56340	At3g56340	40S ribosomal protein S26 (RPS26C) several 40S ribosomal protein S26
Eschscholzia	105	Contig757	Contig973	0.0856	0.561	At5g15610	At5g15610	"proteasome family protein contains Pfam domain, PF01399: PCI domain"
Eschscholzia	106	Contig758	Contig763	0.1042	1.4707	At3g46460	At3g46460	ubiquitin-conjugating enzyme 13 (UBC13) E2
Eschscholzia	107	Contig764	Contig891	0.0129	0.4454	At4g38970	At4g38970	"fructose-bisphosphate aldolase, putative strong similarity to plastidic fructose-bisphosphate aldolase (EC 4.1.2.13) from Nicotiana paniculata (NPALDP1) [GI:4827251], Oryza sativa, PIR2:T02057 [SPIQ40677]"
Eschscholzia	108	Contig774	Contig1389	0.0047	0.6511	At2g18020	At2g18020	60S ribosomal protein L8 (RPL8A)
Eschscholzia	109	Contig794	eca01-38ms1-f11-74792	0.0008	0.7236	At1g63000	At1g63000	expressed protein
Eschscholzia	112	Contig823	Contig902	0.0287	0.3134	At5g63190	At5g63190	MA3 domain-containing protein
Eschscholzia	113	Contig832	eca01-11cs4-b12-34824	0.0673	0.6323	At1g18540	At1g18540	60S ribosomal protein L6 (RPL6A)
Eschscholzia	114	Contig860	Contig993	0.0209	0.5704	At1g43170	At1g43170	60S ribosomal protein L3 (RPL3A)
Eschscholzia	115	Contig863	Contig1291	0.0855	0.8959	At2g42590	At2g42590	14-3-3 protein GF14 mu (GRF9)
Eschscholzia	116	Contig870	eca01-11cs3-h02-35178	0.06	0.7512	At2g35120	At2g35120	"glycine cleavage system H protein, mitochondrial, putative"
Eschscholzia	117	Contig874	eca01-43ms4-a09-40208	0.0413	1.3269	At5g15490	At5g15490	"UDP-glucose 6-dehydrogenase, putative very strong similarity to SPIQ6658 UDP-glucose 6-dehydrogenase (EC 1.1.1.22) (UDP-Glc dehydrogenase) (UDP-GlcDH) (UDPGDH) (Glycine max)"
Eschscholzia	118	Contig884	eca01-16ms1-b02-30495	0.0091	0.4523	At5g45775	At5g45775	60S ribosomal protein L11 (RPL11D)
Eschscholzia	119	Contig899	eca01-10ms1-b02-3322	0.0375	0.5185	At3g12580	At5g02500	"heat shock protein 70, putative"
Eschscholzia	120	Contig918	Contig972	0.1642	0.498	At3g26210	At2g40890	"cytochrome P450 71B23, putative (CYP71B23) identical to Cytochrome P450 71B23 (SP-Q9LTM0)[Arabidopsis thaliana],contains Pfam profile: PF00067 cytochrome P450"
Eschscholzia	121	Contig932	Contig1047	0.0236	0.3751	At4g29040	At4g29040	26S proteasome AAA-ATPase subunit (RPT2a) almost
Eschscholzia	122	Contig940	eca01-12cs3-a01-35151	0.0059	1.9993	At4g17530	At1g02130	"Ras-related GTP-binding protein, putative very strong similarity to RAB1C [Lotus corniculatus var. japonicus] GI:1370166"
Eschscholzia	123	Contig947	Contig1281	0.0131	0.6063	At5g52840	At5g52840	NADH-ubiquinone oxidoreductase-related contains weak similarity to NADH-ubiquinone oxidoreductase 13 kDa-B subunit (EC 1.6.5.5) (EC 1.6.99.3) (Complex I-13Kd-B) (CI-13Kd-B) (Complex I subunit B13) (Swiss-Prot:Q63362)[Rattus norvegicus]
Eschscholzia	124	Contig964	eca01-6cs1-c12-35461	0.0183	0.9816	At3g13670	At3g13670	"protein kinase family protein contains Pfam domains PF00069: Protein kinase domain"
Eschscholzia	125	Contig971	eca01-3cs1-d03-33862	0.0392	0.5804	At1g69780	At1g69780	homeobox-leucine zipper protein 13 (HB-13)
Eschscholzia	126	Contig998	Contig1138	0.0184	1.1518	At3g57490	At3g57490	"40S ribosomal protein S2 (RPS2D) 40S ribosomal protein S2 - Arabidopsis thaliana, SWISSPROT:RS2_ARATH"
Eschscholzia	128	Contig1032	eca01-43ms3-g11-39806	0.0936	0.6608	At2g28000	At2g28000	"Rubisco small binding-protein alpha subunit, chloroplast"
Eschscholzia	129	Contig1040	eca01-36ms4-c11-28740	0.0406	0.4857	At4g22010	At4g22010	multi-copper oxidase type I family protein
Eschscholzia	130	Contig1051	Contig1325	0.0435	0.7406	At5g36230	At5g36230	eIF4-gamma/eIF5/eIF2-epsilon domain-containing protein
Eschscholzia	131	Contig1062	eca01-8ms2-c01-31389	0.0211	1.9223	At3g53020	At3g53020	"60S ribosomal protein L24 (RPL24B) 60S ribosomal protein L24, Arabidopsis thaliana, EMBL:AC006282"
Eschscholzia	132	Contig1065	eca01-7cs3-e10-34663	0.038	1.3031	At5g47880	At5g47880	eukaryotic peptide chain release factor subunit 1-1 (ERF1-1)
Eschscholzia	134	Contig1097	eca01-35ms2-g08-33433	0.0106	0.4949	At2g45740	At1g01820	peroxisomal biogenesis factor 11 family protein
Eschscholzia	135	Contig1098	eca01-5cs3-c12-35235	0.0781	0.7869	At3g61440	At3g61440	"cysteine synthase, putative"
Eschscholzia	136	Contig1132	eca01-43ms4-g05-39950	0.1214	0.1765			
Eschscholzia	137	Contig1134	eca01-43ms1-g09-40022	0.0333	0.8688	At3g27830	At3g27830	"60S ribosomal protein L12-1, chloroplast (CL12-A)"
Eschscholzia	138	Contig1160	eca01-5cs3-f10-36048	0.0441	0.9779	At4g35100	At4g35100	plasma membrane intrinsic protein (SIMIP) nearly
Eschscholzia	139	Contig1161	eca01-29ms1-e12-29134	0.0314	0.6548	At5g48760	At5g48760	60S ribosomal protein L13A (RPL13aD)
Eschscholzia	140	Contig1172	Contig1190	0.0628	0.5521	At1g26910	At1g06580	60S ribosomal protein L10 (RPL10B) Nearly
Eschscholzia	141	Contig1187	eca01-31ms1-b12-21650	0.073	1.1456	At4g33650	At4g33650	dynammin-like protein 2a (ADL2a)
Eschscholzia	145	Contig1223	eca01-30ms1-h04-19877	0.0855	0.9207	At3g46550	At3g46550	fasciclin-like arabinogalactan family protein
Eschscholzia	146	Contig1230	Contig1240	0.1209	0.9751	At3g16780	At1g02780	60S ribosomal protein L19 (RPL19B)
Eschscholzia	147	Contig1237	eca01-74ms2-g11-1236	0.1294	0.4954	At5g47030	At5g47030	"ATP synthase delta" chain, mitochondrial"
Eschscholzia	148	Contig1264	Contig1410	0.1091	0.5801	At4g00660	At4g00660	"DEAD/DEAH box helicase, putative"
Eschscholzia	149	Contig1275	eca01-33ms1-c08-5962	0.0213	0.7691	At1g21720	At1g21720	20S proteasome beta subunit C1 (PBC1) (PRCT) almost
Eschscholzia	150	Contig1294	eca01-18ms1-f06-4540	0.0529	0.4915	At5g08280	At5g08280	hydroxymethylbilane synthase
Eschscholzia	151	Contig1295	eca01-31ms1-f11-8599	0.0152	0.6236	At5g49460	At5g49460	"ATP-citrate synthase, putative"
Eschscholzia	152	Contig1300	eca01-38ms1-h04-57470	0.0713	0.1108	At1g18070		"EF-1-alpha-related GTP-binding protein, putative"
Eschscholzia	153	Contig1302	eca01-7cs4-c08-36875	0.0482	0.3586	At4g04720	At3g20410	"calcium-dependent protein kinase, putative"
Eschscholzia	154	Contig1318	eca01-35ms1-g06-202	0.0599	0.6854	At3g16240	At3g16240	delta tonoplast integral protein (delta-TIP)
Eschscholzia	155	Contig1339	eca01-33ms1-h08-10839	0.0253	0.8361	At5g52650	At4g25740	40S ribosomal protein S10 (RPS10C) contains similarity to 40S ribosomal protein S10
Eschscholzia	156	Contig1371	eca01-6ms1-f10-11192	0.0001	0.092	At5g59720	At5g59720	18.1 kDa class I heat shock protein (HSP18.1-CI)
Eschscholzia	157	Contig1374	eca01-18ms1-b07-10610	0.0161	0.6506	At5g61170	At5g61170	"40S ribosomal protein S19 (RPS19C) 40S ribosomal protein S19, Oryza sativa, SWISSPROT:RS19_ORYSA"
Eschscholzia	158	Contig1382	eca01-3cs4-a02-33902	0.0966	0.5025	At5g57220	At5g25140	"cytochrome P450, putative"
Eschscholzia	159	Contig1386	eca01-7cs1-h06-34743	0.0581	0.4944	At2g13360	At2g13360	serine-glyoxylate aminotransferase-related
Eschscholzia	160	Contig1393	eca01-7cs3-e11-34057	0.0359	0.7517	At5g28640	At5g28640	NAD-dependent epimerase/dehydratase family protein
Eschscholzia	161	eca01-3cs1-b07-19157	eca01-7cs1-f07-34209	0.0152	0.0234	At4g09320	At4g09320	nucleoside diphosphate kinase 1 (NDK1)
Eschscholzia	162	eca01-3cs2-h06-18527	eca01-7cs3-b11-35344	0.0007	0.7047	At5g08690	At5g08690	"ATP synthase beta chain 2, mitochondrial"
Eschscholzia	163	eca01-4cs1-h08-19194	eca01-30ms1-c12-944	0.0294	0.8816	At3g04920	At3g04920	40S ribosomal protein S24 (RPS24A)

Eschscholzia	164	eca01-32ms1-f06-7327	eca01-38ms3-e05-4094	0.0285	0.6956	A15g54640	A14g27230	histone H2A
Eschscholzia	165	eca01-17ms1-d04-925	eca01-25ms1-d11-33437	0.0914	1.1479	A11g74560	A11g74560	nucleosome assembly protein (NAP) family protein
Eschscholzia	167	eca01-3cs4-g09-18595	eca01-12cs1-e07-36132	0.0108	1.9358	A12g26250	A12g26250	beta-ketoacyl-CoA synthase family (FIDDLEHEAD) (FDH)
Eschscholzia	168	eca01-8cs3-a10-38128	eca01-31ms1-f10-25225	0.0166	0.8366	A13g43190	A13g43190	"sucrose synthase, putative"
Eschscholzia	169	eca01-3cs3-g08-17957	eca01-7cs4-f06-36812	0.0371	1.4467	A15g14670	A15g14670	"ADP-ribosylation factor, putative"
Eschscholzia	171	eca01-10cs3-b01-37595	eca01-7cs4-d03-37342	0.0524	0.0503			
Eschscholzia	173	eca01-37ms3-b10-25841	eca01-6cs2-g04-35346	0.079	0.7054	A14g16143	A14g16143	"importin alpha-2, putative (IMPA-2)"
Eschscholzia	174	eca01-10ms1-c12-18677	eca01-3cs3-c07-33987	0.0537	1.1997	A15g48300	A15g48300	glucose-1-phosphate adenyllyltransferase small subunit 1 (APS1)
Eschscholzia	175	eca01-7cs4-f03-38238	eca01-9cs1-f02-38603	0.1485	0.3491	A15g65620	A15g65620	peptidase M3 family protein
Eschscholzia	178	eca01-9cs2-b09-38381	eca01-22ms1-g08-31115	0.049	0.994	A11g18150	A11g18150	"mitogen-activated protein kinase, putative"
Eschscholzia	179	eca01-13cs4-c04-54002	eca01-43ms1-d07-39810	0.0475	0.1236			
Eschscholzia	180	eca01-10cs1-a01-34480	eca01-13cs3-g05-51240	0.0238	0.0469	A13g50910	A13g50910	expressed protein
Eschscholzia	182	eca01-46ms2-d11-23346	eca01-8cs3-b08-37230	0.0457	0.0801	A15g41950		expressed protein
Eschscholzia	183	eca01-4ms1-b02-23357	eca01-13cs4-a03-46361	0.0439	0.9011	A11g73030	A11g73030	"SNF7 family protein contains Pfam domain, PF03357: SNF7 family"
Eschscholzia	186	eca01-9cs2-b11-37831	eca01-12cs2-h07-35806	0.2396	0.7276	A11g53910		
Eschscholzia	187	eca01-11cs4-e08-35195	eca01-4cs1-f11-17128	0.0532	0.6303	A13g04840	A13g04840	40S ribosomal protein S3A (RPS3aA)
Eschscholzia	188	eca01-33ms1-b04-24027	eca01-10cs1-c11-34846	0.0164	0.8725	A12g20580	A12g20580	26S proteasome regulatory subunit S2 (RPN1) contains an APC-complex (cyclosome) and proteasome component repeat (PS50248)
Eschscholzia	189	eca01-6cs2-f08-35203	eca01-60ms1-e05-31454	0.028	0.1926	A15g61760	A15g61760	"inositol polyphosphate 6-/3-/5-kinase 2b (IPK2b) contains Pfam domain, PF03770: inositol polyphosphate kinase"
Eschscholzia	192	eca01-34ms1-a02-23512	eca01-43ms3-c12-39992	0.0247	0.0454	A11g16860	A11g16860	merozoite surface protein-related contains weak similarity to merozoite surface protein [Plasmodium falciparum] gII12043655[gIb]AAG47601
Eschscholzia	194	eca01-24ms1-a06-20226	eca01-3cs3-e09-33272	0.0545	1.0659	A11g47128	A11g47128	cysteine proteinase (RD21A)
Eschscholzia	195	eca01-13cs3-f07-53667	eca01-16ms1-c08-12705	0.0683	0.763	A15g62890	A15g62890	"permease, putative"
Eschscholzia	196	eca01-36ms2-d09-13082	eca01-19ms1-c07-19995	0.0262	0.5613	A12g19770	A12g19780	profilin 4 (PRF4) (PF14)
Eschscholzia	197	eca01-74ms3-a10-3900	eca01-9cs3-b02-35763	0.1147	1.5121	A15g19290	A15g19290	esterase/lipase/rhoesterase family protein
Eschscholzia	198	eca01-13cs4-d07-53734	eca01-43ms4-f05-40241	0.0326	0.8391	A11g15690	A11g15690	pyrophosphate-energized vacuolar membrane proton pump
Eschscholzia	199	eca01-53ms4-b07-20380	eca01-19ms1-c04-15195	0.0905	1.3355	A14g14240	A14g14240	expressed protein contains Pfam profile PF01595: Domain of unknown function
Eschscholzia	200	eca01-30ms1-h09-4673	eca01-43ms4-e09-40406	0.1095	0.2771	A13g62980	A13g62980	transport inhibitor response 1 (TIR1) (FBL1) E3 ubiquitin ligase SCF complex F-box subunit
Eschscholzia	202	eca01-53ms1-f02-24345	eca01-36ms3-e11-20661	0.072	1.3926	A11g25260	A11g25260	acidic ribosomal protein P0-related contains similarity to 60S acidic ribosomal protein G1:5815233 from [Homo sapiens]
Eschscholzia	203	eca01-46ms2-b02-24375	eca01-15ms1-e06-28972	0.1113	0.3039			
Eschscholzia	204	eca01-3cs1-c08-16567	eca01-4ms1-g01-24770	0.1081	0.27			
Eschscholzia	205	eca01-14ms1-f09-227	eca01-6cs1-d05-35869	0.0786	0.6393	A11g76550	A11g20950	"pyrophosphate-fructose-6-phosphate 1-phosphotransferase alpha subunit, putative"
Eschscholzia	206	eca01-9cs1-f01-36233	eca01-34ms1-e06-22165	0.0808	0.5711	A12g46530	A11g59750	transcriptional factor B3 family protein
Eschscholzia	208	eca01-60ms2-g11-31882	eca01-37ms3-c12-13654	0.1195	0.7074	A11g19110	A11g19110	inter-alpha-trypsin inhibitor heavy chain-related
Eschscholzia	209	eca01-43ms4-e04-39778	eca01-67ms3-e02-33525	0	0.0421	A11g08830	A11g08830	superoxide dismutase [Cu-Zn] (SODCC)
Eschscholzia	210	eca01-16ms1-b04-17628	eca01-8ms2-e12-15092	0.0548	0.9404	A14g39400	A14g39400	brassinosteroid insensitive 1 (BR1)
Eschscholzia	211	eca01-3cs3-b03-17793	eca01-11cs3-d02-34101	0.1215	0.6996	A13g61140	A13g61140	COP9 signalosome complex subunit 1
Acorus	1	261132	262194	0.0022	0.4568	A11g21720	A11g21720	20S proteasome beta subunit C1 (PBC1) (PRCT) almost
Acorus	4	261154	261913	0.0132	1.5425	A15g14640	A13g05840	protein kinase family protein
Acorus	5	261159	261684	0.0363	0.4154	A13g43190	A15g20830	"sucrose synthase, putative"
Acorus	6	261160	261709	0.0912	0.4991	A11g61580	A11g61580	60S ribosomal protein L3 (RPL3B)
Acorus	7	261163	261249	0.0833	0.559	A11g78520	A11g78520	glycosyl hydrolase family protein 17
Acorus	10	261184	261919	0.0176	1.6	A13g08690	A11g64230	ubiquitin-conjugating enzyme 11 (UBC11) E2
Acorus	11	261190	261373	0.0529	0.5932	A14g35100	A14g35100	plasma membrane intrinsic protein (SIMIP) nearly
Acorus	12	261194	261730	0.0373	0.4007	A11g64230	A11g64230	"ubiquitin-conjugating enzyme, putative identical or nearly so to Ubiquitin-conjugating enzymes SPIP35132, SPIP35131, SPIP35133 from [Arabidopsis thaliana]"
Acorus	13	261198	264016	0.1074	0.1422	A11g55360	A15g56530	expressed protein contains Pfam profile PF03080: Arabidopsis proteins of unknown function
Acorus	14	261207	261485	0.0243	0.5681	A13g02080	A13g02080	40S ribosomal protein S19 (RPS19A)
Acorus	15	261209	261644	0.0137	0.1625	A15g60390	A15g60390	elongation factor 1-alpha
Acorus	16	261217	263992	0.0116	0.3158	A13g46460	A13g55380	ubiquitin-conjugating enzyme 13 (UBC13) E2
Acorus	17	261218	261627	0.0101	1.6054	A15g20290	A15g20290	"40S ribosomal protein S8 (RPS8A) ribosomal protein S8 - Zea mays, PIR:T04088"
Acorus	18	261219	262192	0.0749	0.3216	A15g14030	A15g14030	translocon-associated protein beta (TRAPB) family protein
Acorus	19	261235	261293	0.2115	0.3795	A15g65360	A15g65360	histone H3
Acorus	20	261237	261454	0.0143	1.4923	A14g02080	A14g02080	GTP-binding protein (SAR1A)
Acorus	21	261242	264591	0.0137	0.0001	A14g14320	A14g14320	60S ribosomal protein L36a/L44 (RPL36aB)
Acorus	22	261243	261297	0.0067	0.6976	A11g70600	A11g70600	60S ribosomal protein L27A (RPL27aC)
Acorus	25	261260	262086	0.0659	0.5466	A12g37220	A12g37220	"29 kDa ribonucleoprotein, chloroplast, putative"
Acorus	26	261263	261754	0.0025	0.3877	A15g09810	A15g09810	actin 7 (ACT7)
Acorus	27	261264	261445	0.0458	0.7829	A13g05590	A13g05590	60S ribosomal protein L18 (RPL18B)
Acorus	29	261276	261571	0.0191	0.405	A13g62870	A13g62870	"60S ribosomal protein L7A (RPL7aB) 60S RIBOSOMAL PROTEIN L7A - Oryza sativa, SWISSPROT:RL7A_ORYSA"
Acorus	30	261278	261599	0.0014	1.3571	A13g04400	A13g04400	60S ribosomal protein L23 (RPL23C)
Acorus	31	261282	261294	0.4508	1.9236	A15g39850	A15g39850	"40S ribosomal protein S9 (RPS9C) 40S ribosomal protein S9 - Chlamydomonas sp. EMBL-AU066528"
Acorus	33	261292	262566	0.0715	0.6203	A12g20760	A12g20760	expressed protein
Acorus	35	261304	263739	0.0275	0.6978	A15g41070	A15g41070	double-stranded RNA-binding domain (DsRBD)-containing protein contains Pfam profile PF00035: Double-stranded RNA binding motif
Acorus	36	261307	261495	0.0176	0.5424	A15g19780	A15g19780	tubulin alpha-3/alpha-5 chain (TUA5) nearly
Acorus	38	261315	263098	0.0587	0.4719	A13g18760	A13g18760	ribosomal protein S6 family protein contains TIGRFAM profile TIGR00166: ribosomal protein S6
Acorus	39	261324	264883	0.1224	0.4921	A13g51950	A15g12440	zinc finger (CCH-type) family protein
Acorus	40	261330	261808	0.0227	0.4587	A15g02960	A15g02960	"40S ribosomal protein S23 (RPS23B) ribosomal protein S23, Fragaria x ananassa, PIR:S56673"
Acorus	41	261333	261477	0.0213	0.4297	A13g04120	A11g13440	"glyceraldehyde-3-phosphate dehydrogenase, cytosolic (GAPC)"
Acorus	44	261346	261550	0.0115	0.7232	A12g37270	A12g37270	40S ribosomal protein S5 (RPS5A)
Acorus	45	261351	263798	0.1463	0.5673	A14g32720	A14g32720	"RNA recognition motif (RRM)-containing protein RNA-binding protein LAH1, Saccharomyces cerevisiae, PIR2:B48600"
Acorus	47	261354	262099	0.0429	0.9227	A15g14040	A15g14040	mitochondrial phosphate transporter
Acorus	50	261364	265163	0.2203	0.7091	A11g51200	A11g51200	"zinc finger (AN1-like) family protein contains Pfam domains, PF01428: AN1-like Zinc finger and PF01754: A20-like zinc finger"
Acorus	51	261368	262637	0.0091	0.6861	A12g44120	A12g44120	60S ribosomal protein L7 (RPL7C)
Acorus	52	261371	261578	0.0026	0.4242	A13g60820	A13g60820	20S proteasome beta subunit F1 (PBF1)
Acorus	53	261379	261487	0.1249	0.4708	A15g42190	A15g42190	E3 ubiquitin ligase SCF complex subunit SKP1/ASK1 (A12)
Acorus	54	261380	262075	0.0145	0.6685	A15g23740	A15g23740	40S ribosomal protein S11 (RPS11C)
Acorus	55	261387	261798	0.0649	0.503	A11g72370	A11g72370	40S ribosomal protein SA (RPSaA)

Acorus	56	261388	262657	0.149	1.7951	At2g28900		mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 family protein contains Pfam PF02466: Mitochondrial import inner membrane translocase subunit Tim17
Acorus	57	261393	261739	0.0136	0.0001	At1g48030		
Acorus	58	261396	261524	0.0513	0.3622	At1g78900	At1g78900	vacuolar ATP synthase catalytic subunit A
Acorus	59	261397	262010	0.077	0.4726	At3g16640		translationally controlled tumor family protein
Acorus	61	261420	264345	0.015	0.727	At5g28840	At5g28840	NAD-dependent epimerase/dehydratase family protein
Acorus	62	261426	265591	0.0451	0.4142	At5g57290	At5g57290	60S acidic ribosomal protein P3 (RPP3B)
Acorus	63	261429	263392	0.0646	0.1887	At1g18260	At1g18260	suppressor of lin-12-like protein-related
Acorus	64	261434	265017	0.0504	0.4269	At1g48410	At1g48410	argonaute protein (AGO1)
Acorus	65	261439	262044	0.1013	0.6471	At4g09320	At4g09320	nucleoside diphosphate kinase 1 (NDK1)
Acorus	66	261441	265035	0.136	0.5872	At4g17190	At4g17190	farnesyl pyrophosphate synthetase 2 (FPS2)
Acorus	67	261446	261619	0.0019	1.2111	At4g05050	At5g20620	polyubiquitin (UBQ11)
Acorus	68	261449	263292	0.1447	0.7402	At5g45775	At1g09160	protein phosphatase 2C-related
Acorus	70	261457	261570	0.0026	0.2738	At1g50010	At1g50010	tubulin alpha-2/alpha-4 chain (TUA2)
Acorus	71	261459	262960	0.0065	1.228	At1g53750	At1g53750	26S proteasome AAA-ATPase subunit (RPT1a)
Acorus	73	261467	261789	0.1126	0.6227	At3g16780	At3g16780	60S ribosomal protein L19 (RPL19B)
Acorus	74	261473	262526	0.0263	0.5354	At5g67380	At3g50000	casein kinase II alpha chain 1
Acorus	76	261520	264241	0.1628	0.1028			
Acorus	78	261532	261806	0.1004	0.368	At5g43330	At5g43330	"malate dehydrogenase, cytosolic, putative strong similarity to cytosolic malate dehydrogenase (EC 1.1.1.37) SP O24047 (Mesembryanthemum crystallinum), SP O48905 (Medicago sativa), (Prunus persica) GI:15962949"
Acorus	79	261533	262016	0.1511	0.5136	At5g57970	At5g57970	methyladenine glycosylase family protein
Acorus	81	261538	265599	0.0005	0.5056	At5g19990	At5g20000	26S proteasome AAA-ATPase subunit (RPT6a)
Acorus	83	261542	262335	0.0236	0.4847	At1g68060	At1g14840	expressed protein
Acorus	84	261561	265611	0.0764	1.7372	At5g37600	At3g17820	"glutamine synthetase, putative"
Acorus	85	261562	261956	0.1447	0.7402	At5g45775	At5g45775	60S ribosomal protein L11 (RPL11D)
Acorus	86	261566	262206	0.1399	0.4481	At3g60240	At3g60240	MIF4G domain-containing protein
Acorus	87	261568	265786	0.1747	0.5316	At3g17020	At3g17020	universal stress protein (USP) family protein
Acorus	89	261574	264979	0.1302	0.26	At1g11260	At1g11260	glucose transporter (STP1) nearly
Acorus	91	261581	265529	0.0226	0.3906	At1g09210	At1g09210	calreticulin 2 (CRT2)
Acorus	92	261586	265781	0.0385	0.508	At1g04980	At1g04980	thioredoxin family protein
Acorus	94	261609	264535	0.0342	0.3811	At3g25520	At3g25520	60S ribosomal protein L5
Acorus	96	261618	261702	0.023	0.3023	At4g23400	At4g00430	major intrinsic family protein
Acorus	97	261623	265546	0.0536	0.1698	At5g23860	At5g23860	tubulin beta-8 chain (TUBB8)
Acorus	98	261636	264231	0.0251	0.3985	At2g36530	At2g36530	enolase
Acorus	99	261641	262015	0.0147	0.4721	At4g39860	At3g04920	expressed protein
Acorus	101	261654	261777	0.0298	0.6484	At3g12390	At2g33040	"nascent polypeptide associated complex alpha chain protein, putative"
Acorus	102	261655	263443	0.0303	0.4373	At1g24510	At1g24510	"T-complex protein 1 epsilon subunit, putative"
Acorus	103	261657	265652	0.1054	0.4125	At5g43960	At5g43960	nuclear transport factor 2 (NTF2) family protein
Acorus	105	261660	261785	0.0073	0.5082	At2g40590	At2g40590	40S ribosomal protein S26 (RPS26B)
Acorus	106	261663	262179	0.0151	0.3743	At4g25630	At4g25630	fibrillarin 2 (FIB2)
Acorus	107	261669	264962	0.1076	0.3361	At4g29410	At4g29410	"60S ribosomal protein L28 (RPL28C) unknown protein chromosome II BAC F6F22 - Arabidopsis thaliana.PID:g3687251"
Acorus	108	261676	261755	0.016	0.6838	At5g55190	At5g20020	Ras-related GTP-binding protein (RAN3)
Acorus	110	261685	261713	0.033	0.2368	At1g77120	At1g77120	alcohol dehydrogenase (ADH1)
Acorus	111	261701	262083	0.0469	0.4224	At5g13490	At5g13490	"ADP, ATP carrier protein 2, mitochondrial"
Acorus	112	261704	264028	0.0007	0.6591	At5g52650	At4g25740	40S ribosomal protein S10 (RPS10C) contains similarity to 40S ribosomal protein S10
Acorus	113	261710	262008	0.1572	0.9243	At2g26330	At2g26330	"leucine-rich repeat protein kinase, putative (EREC1A)"
Acorus	114	261711	261771	0.0109	0.3928	At3g47810	At3g47810	calcineurin-like phosphoesterase family protein contains Pfam profile: PF00149 calcineurin-like phosphoesterase
Acorus	115	261715	261895	0.0443	0.5242	At5g58420	At5g58420	"40S ribosomal protein S4 (RPS4D) ribosomal protein S4, Arabidopsis thaliana. PIR:148480"
Acorus	116	261724	262001	0.0324	1.0524	At3g09630	At3g09630	60S ribosomal protein L4/L1 (RPL4A) strong similarity to 60S ribosomal protein L1 GB:P49691
Acorus	117	261731	265055	0.0037	0.3957	At1g75840	At1g75840	Rac-like GTP-binding protein (ARAC5)
Acorus	120	261746	264548	0.0155	0.0002	At3g44590		"60S acidic ribosomal protein P2 (RPP2D) acidic ribosomal protein P2, maize. PIR:S64173"
Acorus	121	261753	265519	0.0162	0.6063	At2g37600	At5g02450	60S ribosomal protein L36 (RPL36A)
Acorus	122	261758	264416	0.0473	0.1957	At1g19330	At1g19330	expressed protein
Acorus	123	261772	263995	0.0004	0.419	At4g09800	At4g09800	40S ribosomal protein S18 (RPS18C)
Acorus	124	261773	262149	0.0669	0.6144	At3g52580	At3g52580	"40S ribosomal protein S14 (RPS14C) ribosomal protein S14 - Zea mays.PIR2:A30097"
Acorus	125	261811	265387	0	0.0025	At5g15800	At5g15800	developmental protein SEPALLATA1
Acorus	126	261812	265708	0.0637	0.4559	At4g24190	At4g24190	shepherd protein (SHD)
Acorus	127	261832	262031	0.0284	0.9981	At1g07790	At5g59910	"histone H2B, putative strong similarity to histone H2B Arabidopsis thaliana GI:2407802, Gossypium hirsutum SP O22582, Lycopersicon esculentum GI:3021489, Capsicum annuum SP O49118"
Acorus	128	261837	261996	0.018	0.4636	At3g44110	At3g44110	"DNAJ heat shock protein, putative (J3)"
Acorus	130	261840	265410	0	0.011	At3g49010	At3g49010	60S ribosomal protein L13 (RPL13B)
Acorus	131	261848	262325	0.0266	0.4786	At3g19760	At3g19760	"eukaryotic translation initiation factor 4A, putative"
Acorus	132	261871	265791	0.1555	1.3855	At2g37170	At3g53420	plasma membrane intrinsic protein 2B (PIP2B)
Acorus	133	261874	263462	0.0084	0.0001	At5g59310		lipid transfer protein 4 (LTP4)
Acorus	135	261892	261986	0.1314	0.7231	At4g17390	At4g16720	60S ribosomal protein L15 (RPL15B)
Acorus	136	261899	265371	0.0587	0.4429	At3g01750	At3g01750	"ankyrin repeat family protein contains ankyrin repeats, Pfam:PF00023"
Acorus	137	261908	265478	0.2251	1.4545	At5g62300	At5g62300	"40S ribosomal protein S20 (RPS20C) ribosomal protein S20, Arabidopsis thaliana, PIR:T12992"
Acorus	139	261938	262324	0.0074	0.4568	At1g15690		pyrophosphate-energized vacuolar membrane proton pump
Acorus	140	261941	265065	0.0512	0.3894	At4g29510	At4g29510	"protein arginine N-methyltransferase, putative"
Acorus	141	261944	262896	0.028	0.357	At2g21170	At2g21170	"triosephosphate isomerase, chloroplast, putative"
Acorus	144	261966	263255	0.0145	0.3161	At1g60900	At4g36690	"U2 snRNP auxiliary factor large subunit, putative"
Acorus	146	261979	262090	0.0709	0.721	At1g06030	At2g31390	pkB-type carbohydrate kinase family protein contains Pfam profile: PF00294 pkB family carbohydrate kinase
Acorus	147	261988	263973	0.0017	1.6649	At4g38920	At4g38920	vacuolar ATP synthase 16 kDa proteolipid subunit 3
Acorus	149	262033	264333	0.3598	0.3077	At2g21130	At3g56070	peptidyl-prolyl cis-trans isomerase
Acorus	150	262046	262711	0	0.0012	At5g38890	At5g38890	exoribonuclease-related
Acorus	151	262048	264606	0.1119	1.6558	At5g56030	At5g52640	heat shock protein 81-2 (HSP81-2) nearly
Acorus	153	262069	263526	0.0896	0.4042	At4g16830	At4g16830	nuclear RNA-binding protein (RGGA)
Acorus	154	262079	263095	0.0125	0.8176	At5g02500	At5g02500	heat shock cognate 70 kDa protein 1 (HSC70-1) (HSP70-1)
Acorus	155	262089	262940	0.0466	0.4645	At1g49760	At1g49760	"polyadenylate-binding protein, putative"
Acorus	156	262098	264129	0.1822	0.1639	At4g29040	At4g29040	26S proteasome AAA-ATPase subunit (RPT2a) almost
Acorus	157	262101	262104	0.0398	0.4032	At5g03300	At5g03300	adenosine kinase 2 (ADK2) contains Pfam profile: PF00294 pkB family carbohydrate kinase
Acorus	160	262145	262168	0.048	0.3419	At5g26751	At5g26751	shaggy-related protein kinase alpha
Acorus	161	262153	264965	0.147	0.6351	At2g47710	At2g47710	universal stress protein (USP) family protein

Acorus	165	262195	264595	0.1622	0.8474	At1g26690	At1g69460	emp24(gp25L)p24 family protein
Acorus	170	262267	261211	0.0533	0.6715	At2g47110	At2g47110	ubiquitin extension protein 6 (UBQ6)
Acorus	171	262306	264125	0.0465	0.2205	At1g74560	At1g74560	nucleosome assembly protein (NAP) family protein
Acorus	172	262329	262922	0.0633	0.5021	At2g25180	At4g31920	two-component responsive regulator family protein
Acorus	173	262361	264399	0.0036	0.0126	At5g63640	At5g63640	VHS domain-containing protein
Acorus	174	262391	264736	0.1042	1.174	At5g11980		expressed protein
Acorus	175	262425	264708	0.0647	0.5354	At3g49720		
Acorus	176	262444	264230	0.1849	0.9359	At1g17110	At1g17110	ubiquitin-specific protease 15 (UBP15) almost
Acorus	177	262460	263815	0.0843	1.0243	At1g60590	At1g60590	"polygalacturonase, putative"
Acorus	179	262511	264342	0.0713	0.4821	At3g10300	At3g10300	calcium-binding EF hand family protein
Acorus	180	262595	265322	0.0513	0.2372	At2g01910	At2g01910	microtubule associated protein (MAP65/ASE1) family protein
Acorus	182	262723	263040	0.0046	0.4632	At2g31610	At5g35530	40S ribosomal protein S3 (RPS3A)
Acorus	190	262924	265113	0.0006	0	At3g10950	At3g10950	60S ribosomal protein L37a (RPL37aB)
Acorus	192	262992	263531	0.0655	0.4349	At5g22300	At5g22300	nitrilase 4 (NIT4)
Acorus	193	263012	265705	0.0121	0.0001	At5g23450	At5g23450	"diacylglycerol kinase family protein contains INTERPRO domain, IPR001206, DAG-kinase catalytic domain"
Acorus	196	263190	263862	0.0982	0.5429	At3g22270	At1g79090	expressed protein
Acorus	198	263208	263384	0.2792	0.4881	At3g14640	At3g14640	"cytochrome P450, putative"
Acorus	206	263530	265294	0.062	0.7791	At5g08260	At5g08260	serine carboxypeptidase S10 family protein
Acorus	209	263801	265132	0	0.0008	At1g76490	At1g76490	3-hydroxy-3-methylglutaryl-CoA reductase 1
Acorus	210	263825	265344	0.0768	0.3848	At5g36290	At5g36290	expressed protein contains Pfam profile PF01169: Uncharacterized protein family UPF0016
Acorus	211	263837	264268	0	0.002	At5g17070		
Acorus	214	263990	265164	0.055	0.4567	At4g34500	At4g34500	"protein kinase family protein contains protein kinase domain, Pfam:PF00069"
Acorus	217	264108	264207	0.0892	0.4741			
Acorus	218	264126	264551	0.0602	0.5144	At1g06200	At2g31140	expressed protein
Acorus	219	264247	265013	0.0391	0.7636	At3g02130	At3g02130	"leucine-rich repeat transmembrane protein kinase, putative contains Pfam profile: Eukaryotic protein kinase domain"
Acorus	220	264347	264772	0.1148	0.3744	At5g09650	At5g09650	inorganic pyrophosphatase family protein
Acorus	223	264541	264546	0.064	0.656	At2g19680	At4g26210	mitochondrial ATP synthase g subunit family protein contains Pfam profile: PF04718 mitochondrial ATP synthase g subunit
Acorus	224	264698	265078	0.0304	0.4694	At4g02570	At4g02570	culin family protein
Acorus	226	265290	265464	0.0402	0.3658	At1g53730	At3g14350	"leucine-rich repeat transmembrane protein kinase, putative"
Liriodendron	1	247332	248011	0.0843	0.2596			
Liriodendron	4	247346	247995	0.0142	0.7509	At1g67430	At1g67430	60S ribosomal protein L17 (RPL17B)
Liriodendron	6	247372	250564	0.035	0.3141	At2g33040	At2g33040	"ATP synthase gamma chain, mitochondrial (ATPC)"
Liriodendron	7	247377	247931	0.0235	0.5956	At5g11670	At1g79750	"malate oxidoreductase, putative"
Liriodendron	8	247380	248322	0.0253	1.6241	At5g13490	At4g28390	"ADP, ATP carrier protein 2, mitochondrial"
Liriodendron	9	247381	250460	0.0642	1.1611	At5g56710	At5g56710	60S ribosomal protein L31 (RPL31C)
Liriodendron	10	247397	247563	0.0982	1.4543	At5g23740	At5g23740	40S ribosomal protein S11 (RPS11C)
Liriodendron	11	247404	247636	0.077	0.0933	At3g46280	At1g11610	"cytochrome P450, putative nearly"
Liriodendron	12	247409	247637	0.0103	0.7649	At5g45775	At5g45775	60S ribosomal protein L11 (RPL11D)
Liriodendron	13	247412	247477	0.006	0.5475	At4g09800	At4g09800	40S ribosomal protein S18 (RPS18C)
Liriodendron	14	247416	249438	0.1185	0.2557	At3g23600	At3g23600	dienelactone hydrolase family protein
Liriodendron	16	247420	247736	0.0335	0.3429	At5g59720	At5g59720	18.1 kDa class I heat shock protein (HSP18.1-CI)
Liriodendron	18	247423	252468	0.0701	0.2915	At4g39230	At4g39230	"isoflavone reductase, putative"
Liriodendron	19	247442	247551	0.0139	1.8115	At3g04400	At3g04400	60S ribosomal protein L23 (RPL23C)
Liriodendron	21	247448	247531	0.0156	0.3995	At5g43330	At5g43330	"malate dehydrogenase, cytosolic, putative strong similarity to cytosolic malate dehydrogenase (EC 1.1.1.37) SPI024047 (Mesembryanthemum crystallinum), SPI048505 (Medicago sativa), [Prunus persica] GI:15962948"
Liriodendron	22	247452	251944	0.0324	0.2107	At3g24600	At3g24600	hypothetical protein
Liriodendron	23	247456	252764	0.0799	0.8657	At3g62840	At3g62840	"small nuclear ribonucleoprotein D2, putative"
Liriodendron	24	247464	248022	0.0015	1.5432	At5g60390	At5g60390	elongation factor 1-alpha
Liriodendron	25	247469	247517	0.061	0.3512	At1g76490	At1g76490	3-hydroxy-3-methylglutaryl-CoA reductase 1
Liriodendron	26	247473	248082	0.0009	0.9401	At4g14960	At1g50010	tubulin alpha-6 chain (TUA6) nearly
Liriodendron	27	247485	247709	0.0554	0.5747	At5g57330		aldose 1-epimerase family protein contains Pfam profile PF01263 Aldose 1-epimerase
Liriodendron	28	247501	248089	0.0445	0.7934	At1g09430	At1g09430	"ATP-citrate synthase (ATP-citrate (pro-S-) -lyase/citrate cleavage enzyme), putative"
Liriodendron	30	247530	249481	0.1498	1.9175	At1g64230	At1g64230	"ubiquitin-conjugating enzyme, putative identical or nearly so to Ubiquitin-conjugating enzymes SPIP35132, SPIP35131, SPIP35133 from (Arabidopsis thaliana)"
Liriodendron	31	247550	249845	0.1552	0.3662	At4g02340	At4g02340	"epoxide hydrolase, putative"
Liriodendron	33	247565	247782	0.0507	0.4196	At1g08830	At1g08830	superoxide dismutase [Cu-Zn] (SODCC)
Liriodendron	35	247581	250463	0.1143	0.1192			
Liriodendron	36	247587	248205	0.0316	1.4857	At2g02760	At2g02760	ubiquitin-conjugating enzyme 2 (UBC2) E2
Liriodendron	37	247596	253683	0.0129	0.429	At1g30330	At1g30330	auxin-responsive factor (ARF6)
Liriodendron	41	247625	248554	0.0574	0.6707	At5g20720	At5g20720	"20 kDa chaperonin, chloroplast (CPN21) (CHCPN10) (CPN20)"
Liriodendron	43	247636	251257	0.1379	0.0983	At3g13300	At3g13300	transducin family protein
Liriodendron	44	247639	250693	0.102	0.407	At4g16830	At4g16830	nuclear RNA-binding protein (RGGA)
Liriodendron	46	247648	248382	0.0306	1.1114	At2g47110	At2g47110	ubiquitin extension protein 6 (UBQ6)
Liriodendron	47	247657	249350	0.0932	0.604	At1g64230	At4g27960	"ubiquitin-conjugating enzyme, putative identical or nearly so to Ubiquitin-conjugating enzymes SPIP35132, SPIP35131, SPIP35133 from (Arabidopsis thaliana)"
Liriodendron	48	247659	248547	0.2378	1.2383	At1g48410	At1g48410	argonaute protein (AGO1)
Liriodendron	50	247669	250531	0.0076	0.0001			
Liriodendron	51	247689	247811	0.0187	0.6149	At2g20140	At4g29040	"26S protease regulatory complex subunit 4, putative"
Liriodendron	52	247694	249822	0.026	0.6954	At4g02570	At4g02570	culin family protein
Liriodendron	53	247699	248499	0.0169	0.59	At5g14670	At2g47170	"ADP-ribosylation factor, putative"
Liriodendron	54	247702	248060	0.033	0.7757	At5g52580	At3g52580	"40S ribosomal protein S14 (RPS14C) ribosomal protein S14 - Zea mays PIR2.A30097"
Liriodendron	56	247720	247942	0.042	0.8577	At3g13580	At3g13580	60S ribosomal protein L7 (RPL7D)
Liriodendron	57	247728	252761	0.0562	0.7293	At2g34710	At2g34710	homeobox-leucine zipper transcription factor (HB-14)
Liriodendron	59	247735	249722	0.0378	0.8551	At1g78300	At1g78300	14-3-3 protein GF14 omega (GRF2)
Liriodendron	60	247758	249089	0.0852	0.7595	At3g58500	At3g58500	serine/threonine protein phosphatase PP2A-4 catalytic subunit (PP2A4)
Liriodendron	62	247761	250613	0	0.0488			
Liriodendron	65	247789	251672	0	0.0019	At1g57720	At1g57720	"elongation factor 1B-gamma, putative"
Liriodendron	66	247790	253599	0.0026	0.0159	At1g65870	At1g65870	disease resistance-responsive family protein
Liriodendron	68	247800	249051	0.0143	0.5641	At3g44110	At3g44110	"DNAI heat shock protein, putative (JS)"
Liriodendron	69	247807	248210	0.0673	1.4805	At1g77120	At1g77120	alcohol dehydrogenase (ADH)
Liriodendron	70	247808	251291	0.0926	1.2917	At3g56150	At3g56150	eukaryotic translation initiation factor 3 subunit 8
Liriodendron	71	247809	248222	0.071	0.6374	At2g44350	At2g44350	"citrate synthase, mitochondrial, putative strong similarity to SPIP20115 Citrate synthase, mitochondrial precursor (Arabidopsis thaliana)"
Liriodendron	72	247810	249279	0.0396	0.8835	At4g27090	At4g27090	"60S ribosomal protein L14 (RPL14B) ribosomal protein L14 - Human,PIR3.JC5954"
Liriodendron	73	247817	248411	0.0817	0.8774	At3g46010	At3g46010	actin-depolymerizing factor 1 (ADF1)

Liriodendron	74	247822	252339	0.0231	1.0145	At4g17530	At4g17530	"Ras-related GTP-binding protein, putative very strong similarity to RAB1C [Lotus corniculatus var. japonicus] GI:1370166"
Liriodendron	75	247826	250212	0.0042	0	At2g33430	At1g32580	"plastid developmental protein DAG, putative"
Liriodendron	76	247831	251636	0.0513	0.6357	At4g27130	At1g54290	"eukaryotic translation initiation factor SUI1, putative"
Liriodendron	77	247835	248020	0.095	0.1997	At3g09390	At3g09390	"metallothionein protein, putative (MT2A)"
Liriodendron	78	247850	248303	0.0166	1.6914	At1g13950	At1g13950	eukaryotic translation initiation factor 5A-1
Liriodendron	81	247883	248352	0.0888	0.5255	At1g02850	At1g02850	glycosyl hydrolase family 1 protein contains Pfam PF00232 : Glycosyl hydrolase family 1 domain
Liriodendron	82	247902	251667	0.0063	1.1409	At4g38920	At4g38920	vacuolar ATP synthase 16 kDa proteolipid subunit 3 expressed protein
Liriodendron	84	247943	250277	0.0133	0.0178	At5g48480		
Liriodendron	85	247974	250611	0.0926	0.0833	At1g51650		"ATP synthase epsilon chain, mitochondrial"
Liriodendron	87	248007	250876	0.0674	0.5847	At5g46860	At5g46860	syntaxin 22 (SYP22) (VAM3)
Liriodendron	88	248019	253553	0.0367	0.6338	At5g09550	At2g44100	"Rab GDP dissociation inhibitor, putative strong similarity to GDP dissociation inhibitor protein OsGDI1 [Oryza sativa] GI:2364758"
Liriodendron	89	248029	248480	0.6678	1.176			
Liriodendron	92	248078	253044	0.296	0.6979	At1g54690	At1g54690	"histone H2A, putative strong similarity to histone H2A GI:3204129 SPI065759 from Cicer arietinum, Picea abies SPIP35063"
Liriodendron	93	248079	248321	0.0009	0.9489	At5g10980	At5g10980	histone H3
Liriodendron	94	248083	250623	0.0274	0.0503	At4g24340	At4g24340	phosphorylase family protein contains Pfam PF01048: Phosphorylase family
Liriodendron	95	248092	248432	0.0028	0.5398	At5g58420	At5g58420	"40S ribosomal protein S4 (RPS4D) ribosomal protein S4, Arabidopsis thaliana, PIR:T48480"
Liriodendron	97	248099	253658	0.0601	0.7702	At4g29410	At4g29410	"60S ribosomal protein L28 (RPL28C) unknown protein chromosome II BAC F6F22 - Arabidopsis thaliana, PID:g3687251"
Liriodendron	98	248101	250215	0.0417	0.5426	At5g46210	At5g46210	"cullin, putative"
Liriodendron	99	248121	252616	0.0451	0.4047	At1g43190	At1g43190	"polypyrrolidine tract-binding protein, putative"
Liriodendron	102	248140	248488	0.0493	0.6552	At2g22240		inositol 3-phosphate synthase isozyme 2
Liriodendron	103	248185	251988	0.1641	1.0202	At4g10450	At1g33140	"60S ribosomal protein L9 (RPL90D) ribosomal protein L9, cytosolic - garden pea, PIR2:S19978"
Liriodendron	104	248233	248498	0.0319	0.6784	At5g59240	At5g20290	"40S ribosomal protein S8 (RPS8B) 40S ribosomal protein S8, Prunus armeniaca, EMBL:AF071889"
Liriodendron	105	248254	248295	0.0222	1.3609	At4g00100	At4g00100	40S ribosomal protein S13 (RPS13A)
Liriodendron	106	248260	250592	0.0008	0.795	At3g12580		"heat shock protein 70, putative"
Liriodendron	109	248291	248482	0.2491	1.5092	At3g53020	At3g53020	"60S ribosomal protein L24 (RPL24B) 60S ribosomal protein L24, Arabidopsis thaliana, EMBL:AC006282"
Liriodendron	110	248306	251908	0.0774	0.5649	At5g10980	At5g10980	histone H3
Liriodendron	111	248337	248489	0.0258	1.4087	At3g13920	At1g54270	eukaryotic translation initiation factor 4A-1
Liriodendron	112	248339	248453	0.0462	0.9463	At3g60190	At3g60190	dynammin-like protein E (DL1E) nearly
Liriodendron	113	248345	253299	0.0769	0.7979	At3g01280	At3g01280	"porin, putative"
Liriodendron	114	248393	252507	0.0357	1.1584	At5g52650	At4g25740	40S ribosomal protein S10 (RPS10C) contains similarity to 40S ribosomal protein S10
Liriodendron	116	248424	253294	0.0415	0.8451	At5g11200	At5g11200	"DEAD/DEAH box helicase, putative"
Liriodendron	120	248520	251053	0.0187	0.5322	At5g02560	At5g02560	"histone H2A, putative"
Liriodendron	128	248600	250356	0.0131	0.6704	At3g47550	At5g62460	"zinc finger (C3HC4-type RING finger) family protein contains Pfam domain, PF00097: Zinc finger, C3HC4 type (RING finger)"
Liriodendron	129	248608	253583	0.0002	0.0008	At1g52600	At1g52600	"signal peptidase, putative"
Liriodendron	132	248656	250726	0.2411	0.4414	At1g34904		
Liriodendron	136	248815	253020	0.0362	0.6298	At2g36890	At2g36890	myb family transcription factor (MYB38) contains Pfam profile: PF00249 myb-like DNA-binding domain
Liriodendron	137	248852	253312	0	0.0017	At3g06810	At3g06810	DNA-binding enhancer protein-related
Liriodendron	139	248897	247426	0.1179	1.4215	At4g34555	At4g39200	"40S ribosomal protein S25, putative"
Liriodendron	140	248904	253559	0.0518	0.8623	At1g66200	At5g16570	"glutamine synthetase, putative"
Liriodendron	144	249205	250686	0.9254	1.4923	At5g65090	At5g65090	endonuclease/exonuclease/phosphatase family protein
Persea	2	209253	209622	0.0149	1.4805	At1g13950	At1g13950	eukaryotic translation initiation factor 5A-1
Persea	4	209259	212820	0.1982	0.3502			
Persea	5	209260	209975	0.1237	1.0687	At4g01470	At4g01470	major intrinsic family protein
Persea	6	209262	210042	0.0257	0.7343	At5g58420	At5g58420	"40S ribosomal protein S4 (RPS4D) ribosomal protein S4, Arabidopsis thaliana, PIR:T48480"
Persea	7	209266	211349	0.1411	0.546	At1g14510	At1g14510	"PHD finger family protein contains Pfam domain, PF00628: PHD-finger"
Persea	8	209271	213162	0.1086	0.7533	At4g26850	At4g26850	expressed protein
Persea	10	209284	209890	0.1462	0.432	At3g16630	At3g16630	kinesin motor family protein
Persea	11	209285	212601	0.1404	0.6018	At3g52880	At3g52880	"monodehydroascorbate reductase, putative monodehydroascorbate reductase (NADH), Lycopersicon esculentum, PIR:T06407"
Persea	12	209313	210293	0.0275	0.4008	At4g11820	At4g11820	hydroxymethylglutaryl-CoA synthase
Persea	13	209322	209814	0.1117	0.9815	At3g13580	At3g13580	60S ribosomal protein L7 (RPL7D)
Persea	14	209324	209861	0.0561	0.4999	At5g67510	At5g67510	60S ribosomal protein L26 (RPL26B)
Persea	16	209333	212824	0.1161	0.8277	At1g61580	At1g43170	60S ribosomal protein L3 (RPL3B)
Persea	17	209336	209829	0.0484	1.211	At2g36460	At2g36460	"fructose-bisphosphate aldolase, putative"
Persea	18	209345	211675	0.064	0.3469	At4g31340	At2g24420	"myosin heavy chain-related contains weak similarity to Myosin heavy chain, nonmuscle type A (Cellular myosin heavy chain, type A) (Nonmuscle myosin heavy chain-A) (NMHHC-A) (Swiss-Prot:P35579) [Homo sapiens]"
Persea	20	209364	209402	0.029	1.2385	At1g13950	At1g13950	eukaryotic translation initiation factor 5A-1
Persea	21	209384	209535	0.0353	0.6998	At5g56030	At5g56030	heat shock protein 81-2 (HSP81-2) nearly
Persea	23	209398	209439	0.0891	0.7643	At3g52990	At3g52990	"pyruvate kinase, putative"
Persea	24	209409	210267	0.1673	0.934	At2g40590	At2g40590	40S ribosomal protein S26 (RPS26B)
Persea	25	209419	213738	0.1168	1.189	At5g20950	At5g20950	"glycosyl hydrolase family 3 protein beta-D-glucan exohydrolase, Nicotiana tabacum, EMBL:AB017502"
Persea	26	209422	211085	0.106	0.2522			
Persea	27	209425	213431	0.0252	1.5426	At3g44110	At3g44110	"DNAJ heat shock protein, putative (J3)"
Persea	28	209436	215121	0.0004	0	At2g37600	At2g37600	60S ribosomal protein L36 (RPL36A)
Persea	29	209438	210472	0.0497	0.3887	At1g79750	At5g25880	"malate oxidoreductase, putative"
Persea	30	209442	210324	0.0559	0.3453	At1g05260	At1g05260	peroxidase 3 (PER3) (P3)
Persea	31	209447	209733	0.07	0.8762	At1g07890	At3g09640	"L-ascorbate peroxidase 1, cytosolic (APX1)"
Persea	32	209451	212525	0.0899	0.3074	At2g43040	At2g43040	calmodulin-binding protein
Persea	33	209455	210545	0.0486	1.0173	At1g26880	At1g26880	60S ribosomal protein L34 (RPL34A)
Persea	34	209462	210509	0.0408	0.5651	At1g54290	At1g54290	"eukaryotic translation initiation factor SUI1, putative"
Persea	36	209467	213955	0.1804	0.4697	At1g03290	At1g03290	"expressed protein ESTs gb H69666, gb H69511, gb T42324 and gb T20569 come from this gene"
Persea	39	209492	209745	0.012	0.7709	At1g48830	At1g48830	40S ribosomal protein S7 (RPS7A)
Persea	42	209500	209996	0.0295	0.5757	At5g51120	At5g51120	"polyadenylate-binding protein, putative"
Persea	43	209507	211999	0.0254	1.1486	At4g16520	At4g16520	autophagy 8f (APG8f)
Persea	44	209509	213295	0.0034	0.0323	At3g49010	At3g49010	60S ribosomal protein L13 (RPL13B)
Persea	45	209513	210368	0.0386	0.8527	At1g13440	At1g13440	"glyceraldehyde 3-phosphate dehydrogenase, cytosolic, putative"
Persea	46	209514	210211	0.006	0.7419	At5g02960	At5g02960	"40S ribosomal protein S23 (RPS23B) ribosomal protein S23, Fragaria x ananassa, PIR:S56673"
Persea	47	209519	214747	0.0575	0.9614	At5g45750	At4g18800	"Ras-related GTP-binding protein, putative"
Persea	48	209520	212453	0.0654	1.483	At4g32410	At5g05170	"cellulose synthase, catalytic subunit, putative"
Persea	49	209532	210119	0.0261	1.5238	At5g45775		60S ribosomal protein L11 (RPL11D)
Persea	51	209544	209956	0.0099	0.211	At5g02560	At5g02560	"histone H2A, putative"

Persea	52	209545	211486	0.0806	0.4618	At1g05850	At1g05850	chitinase-like protein 1 (CTL1)
Persea	53	209551	209687	0.0369	0.5862	At3g46010	At3g46010	actin-depolymerizing factor 1 (ADF1)
Persea	54	209556	213850	0.0151	1.066	At5g20290	At5g20290	"40S ribosomal protein S8 (RPS8A) ribosomal protein S8 - Zea mays. PIR:T04088"
Persea	56	209572	212199	0.118	0.4365	At3g54020	At3g54020	phosphatidic acid phosphatase-related
Persea	57	209574	214244	0.1631	0.3388	At3g13870	At3g13870	root hair defective 3 (RH3)
Persea	58	209575	212001	0	0.0059	At5g42190	At5g42190	E3 ubiquitin ligase SCF complex subunit SKP1/ASK1 (At2)
Persea	59	209589	210197	0.0244	0.7389	At3g53260	At2g37040	phenylalanine ammonia-lyase 2 (PAL2) nearly
Persea	60	209592	214944	0.0124	0.7411	At5g23740	At4g30800	40S ribosomal protein S11 (RPS11C)
Persea	61	209598	210493	0.0174	1.7185	At5g09810	At5g09810	actin 7 (ACT7)
Persea	62	209615	212578	0.037	0.9135	At4g17390	At4g16720	60S ribosomal protein L15 (RPL15B)
Persea	63	209626	210168	0.0196	1.7631	At2g36620	At3g53020	60S ribosomal protein L24 (RPL24A)
Persea	64	209630	214131	0.0304	1.3248	At1g56075	At1g56075	
Persea	66	209644	211048	0.0479	0.6667	At2g09990	At2g09990	40S ribosomal protein S16 (RPS16A) Same as GB-Q42340
Persea	67	209647	213922	0.0028	0	At5g42190	At5g42190	E3 ubiquitin ligase SCF complex subunit SKP1/ASK1 (At2)
Persea	68	209649	209909	0.0245	0.569	At5g10980	At5g10980	histone H3
Persea	69	209651	211107	0.1199	0.5068	At5g60600	At5g60600	"1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate synthase, putative"
Persea	71	209657	209757	0.0111	0.4097	At5g08690	At5g08690	"ATP synthase beta chain 2, mitochondrial"
Persea	72	209659	211718	0.0039	1.3012	At2g37270	At2g37270	40S ribosomal protein S5 (RPS5A)
Persea	74	209664	209747	0.177	0.2212	At1g20390	At2g15410	
Persea	75	209665	210220	0.0868	0.7431	At3g16640	At3g16640	translationally controlled tumor family protein
Persea	76	209668	210284	0.0599	0.7264	At3g46460	At3g46460	ubiquitin-conjugating enzyme 13 (UBC13) E2
Persea	77	209669	209703	0.0335	0.4979	At4g00430	At4g00430	"plasma membrane intrinsic protein, putative"
Persea	78	209670	213303	0.0255	0.2958	At1g56580	At1g56580	"expressed protein contains Pfam profile PF04398: Protein of unknown function, DUF538"
Persea	80	209679	213613	0.0056	0.0251	At5g22440	At1g08360	60S ribosomal protein L10A (RPL10aC)
Persea	82	209686	210424	0.0381	0.439	At1g67430	At1g67430	60S ribosomal protein L17 (RPL17B)
Persea	83	209716	213370	0.0723	0.5224	At1g26480	At2g42590	14-3-3 protein GF14 iota (GRF12)
Persea	84	209720	210156	0.0341	0.834	At5g40580	At5g40580	20S proteasome beta subunit B (PBB2) (PRCFC)
Persea	85	209724	209753	0.0337	1.6064	At1g56330	At4g02080	GTP-binding protein (SAR1B)
Persea	87	209736	213270	0.1529	0.6322	At1g07380	At2g38010	ceramidase family protein contains similarity to mitochondrial ceramidase [Homo sapiens] gi246893 gb AA186240
Persea	89	209748	210196	0.0801	0.8054	At1g74050	At1g18540	60S ribosomal protein L6 (RPL6C)
Persea	90	209752	214130	0.0238	0.6063	At3g13920	At1g54270	eukaryotic translation initiation factor 4A-1
Persea	91	209760	209816	0.0244	0.5898	At2g16850	At2g16850	"plasma membrane intrinsic protein, putative very strong similarity to plasma membrane intrinsic protein (SIMIP) [Arabidopsis thaliana] G12308917"
Persea	92	209772	210541	0.0997	0.7211	At2g40010	At2g40010	60S acidic ribosomal protein P0 (RPP0A)
Persea	93	209774	210741	0.0171	0.3881	At5g10360	At5g10360	40S ribosomal protein S6 (RPS6B)
Persea	94	209779	209849	0.087	0.5343	At5g46290	At5g46290	3-oxoacyl-[acyl-carrier-protein] synthase 1
Persea	95	209780	209881	0.0115	0.5034	At1g64230	At5g53300	"ubiquitin-conjugating enzyme, putative identical or nearly so to Ubiquitin-conjugating enzymes SPIP35132, SPIP35131, SPIP35133 from [Arabidopsis thaliana]"
Persea	96	209785	214527	0.0613	0.358	At1g47740	At1g47740	expressed protein
Persea	97	209796	210288	0.0301	0.5627	At2g36530	At2g36530	enolase
Persea	99	209811	211733	0.0029	0.696	At1g45000	At1g45000	"26S proteasome regulatory complex subunit p42D, putative"
Persea	100	209817	212627	0.0099	1.4117	At3g62290	At5g14670	ADP-ribosylation factor
Persea	102	209842	212265	0.0533	1.5176	At3g12580	At5g02500	"heat shock protein 70, putative"
Persea	103	209851	212077	0.0683	0.84	At3g25230	At3g25230	peptidyl-prolyl cis-trans isomerase
Persea	104	209855	210043	0.0035	1.33	At5g60390	At5g60390	elongation factor 1-alpha
Persea	105	209856	211640	0	0.0012	At5g09900	At5g09900	"26S proteasome regulatory subunit, putative (RPN5) p55 protein-like"
Persea	106	209859	211680	0.0918	0.395	At4g35360	At2g17340	"pantothenate kinase family protein contains Pfam domain, PF01937: Protein of unknown function"
Persea	107	209863	210406	0.0196	1.7271	At1g57860	At1g57860	60S ribosomal protein L21
Persea	108	209872	215202	0.0383	1.2193	At4g12400	At4g12400	"stress-inducible protein, putative"
Persea	109	209875	210347	0.091	0.4274	At1g11910	At1g11910	"aspartyl protease family protein contains Pfam profiles: PF00026 eukaryotic aspartyl protease, PF03489 surfactant protein B, PF05184 saposin-like type B, region 1"
Persea	110	209879	214663	0.0525	1.4563	At5g16960	At3g03080	"NADP-dependent oxidoreductase, putative"
Persea	111	209880	210198	0.0728	0.8078	At1g09310	At1g56580	"expressed protein contains Pfam profile PF04398: Protein of unknown function, DUF538"
Persea	112	209884	210115	0.0349	0.7137	At3g25800	At3g25800	serine/threonine protein phosphatase 2A (PP2A) 65 kDa regulatory subunit A
Persea	113	209898	209933	0.0481	0.2924	At5g53530	At5g53530	"vacuolar protein sorting-associated protein 26, putative"
Persea	114	209900	209929	0.0095	0.7216	At2g34480	At2g34480	60S ribosomal protein L18A (RPL18aB)
Persea	115	209913	210615	0.0312	1.9283	At4g39200	At4g34555	"40S ribosomal protein S25 (RPS25E) ribosomal protein S25, Lycopersicon esculentum, PIR2:S40089"
Persea	116	209917	214141	0.161	0.3236	At5g16840	At4g17720	RNA recognition motif (RRM)-containing protein predicted proteins - Arabidopsis thaliana
Persea	117	209922	214503	0	0.0024	At2g19770	At2g19770	profilin 4 (PRO4) (PFN4)
Persea	118	209924	214904	0	0.0113	At5g65360	At5g65360	histone H3
Persea	119	209927	211071	0.0073	0.3516	At5g28840	At5g28840	NAD-dependent epimerase/dehydratase family protein
Persea	120	209942	213889	0.0773	0.6612	At5g02230	At5g59490	haloacid dehalogenase-like hydrolase family protein contains InterPro accession IPR005834: Haloacid dehalogenase-like hydrolase
Persea	121	209947	210059	0.0945	1.658	At2g02760	At2g02760	ubiquitin-conjugating enzyme 2 (UBC2) E2
Persea	122	209955	210245	0.1136	0.8123	At3g22760	At3g22780	CXC domain containing TSO1-like protein 1 (SOL1)
Persea	123	209957	210207	0.0254	0.9484	At5g55190	At5g55190	Ras-related GTP-binding protein (RAN3)
Persea	124	209968	213082	0.0613	0.9632	At5g05080	At5g05080	"ubiquitin-conjugating enzyme, putative"
Persea	125	209991	214899	0.0758	0.6891	At5g47720	At5g47720	"acetyl-CoA C-acyltransferase, putative"
Persea	126	210020	211043	0.0044	0.0191	At1g09210	At1g09210	calreticulin 2 (CRT2)
Persea	127	210024	214099	0.0266	0.0003	At1g68540	At1g68540	oxidoreductase family protein
Persea	128	210044	211122	0.0013	1.3368	At3g43810	At3g43810	calmodulin-7 (CAM7) almost
Persea	129	210052	210396	0.0325	0.851	At5g39850	At5g39850	"40S ribosomal protein S9 (RPS9C) 40S ribosomal protein S9 - Chlamydomonas sp. EMBL:AU066528"
Persea	130	210072	211754	0.0355	0.405	At1g79550	At1g79550	"phosphoglycerate kinase, putative"
Persea	131	210073	213415	0.0919	0.3793	At1g09130	At1g09130	"ATP-dependent Clp protease proteolytic subunit, putative"
Persea	133	210082	210294	0.005	0.4591	At5g14670	At5g14670	"ADP-ribosylation factor, putative"
Persea	134	210088	214482	0.1722	0.2673	At1g24020	At1g24020	Bet v1 allergen family protein
Persea	135	210096	214863	0.1431	0.8854	At3g52990	At3g52990	"pyruvate kinase, putative"
Persea	136	210103	210432	0.1178	0.4032	At4g30080	At4g30080	transcriptional factor B3 family protein contains Pfam profile: PF02362 B3 DNA binding domain
Persea	137	210105	211938	0.1181	0.4282	At5g60640	At3g54960	thioredoxin family protein
Persea	138	210116	210903	0.0296	0.4583	At5g62700	At2g29550	tubulin beta-2beta-3 chain (TUB3) nearly
Persea	140	210148	213467	0.033	0.4283	At1g73230	At1g73230	nascent polypeptide-associated complex (NAC) domain-containing protein
Persea	141	210152	212658	0.0131	1.3905	At3g13920	At1g72730	eukaryotic translation initiation factor 4A-1

Persea	142	210159	210398	0.0276	1.4227	At5g60390	At5g60390	elongation factor 1-alpha
Persea	143	210175	212725	0.0936	0.5658	At3g12390		
Persea	144	210181	210445	0.0254	0.7696	At1g64230	At4g27960	"ubiquitin-conjugating enzyme, putative identical or nearly so to Ubiquitin-conjugating enzymes SPIP35132, SPIP35131, SPIP35133 from [Arabidopsis thaliana]"
Persea	145	210194	211974	0.0848	1.8742	At5g20240	At5g20240	floral homeotic protein PISTILLATA (PI) contains Pfam profiles PF01486: K-box region and PF00319: SRF-type transcription factor (DNA-binding and dimerisation domain)
Persea	146	210200	212584	0.0717	1.4658	At5g26751	At3g05840	shaggy-related protein kinase alpha
Persea	148	210233	214278	0.0835	0.3649	At3g53880	At3g53880	aldo/keto reductase family protein
Persea	149	210239	213982	0.0529	0.3981	At4g30210	At4g24520	"NADPH-cytochrome p450 reductase, putative"
Persea	150	210240	214228	0.0909	0.2167	At1g20696	At1g20696	high mobility group protein beta2 (HMGbeta2)
Persea	151	210247	213056	0.0146	0.9345	At4g35020	At1g75840	Rac-like GTP-binding protein (ARAC3)
Persea	152	210262	214230	0.0835	0.9387	At3g53620	At3g53620	"inorganic pyrophosphatase, putative [soluble]"
Persea	153	210295	214226	0.0889	0.4304	At2g36060	At3g52560	ubiquitin-conjugating enzyme family protein
Persea	154	210330	212251	0.0269	0.0197	At3g55005	At3g55005	tonneau 1b (TON1b)
Persea	155	210339	213721	0.2393	0.8608	At5g26990		
Persea	156	210345	211859	0.1486	0.4082	At5g55530	At5g55530	C2 domain-containing protein
Persea	157	210350	210570	0.07	0.3262	At1g24020	At1g24020	Bet v I allergen family protein
Persea	158	210356	213057	0.0374	0.8899	At5g38410	At5g38410	ribulose biphosphate carboxylase small chain 3B
Persea	160	210362	213651	0	0.0106	At3g21865	At3g21865	expressed protein
Persea	161	210392	213153	0.0388	0.7692	At5g42890	At5g42890	sterol carrier protein 2 (SCP-2) family protein
Persea	162	210395	212940	0.0419	0.4456	At5g61170	At5g15520	"40S ribosomal protein S19 (RPS19C) 40S ribosomal protein S19, Oryza sativa, SWISSPROT:RS19_ORYSA"
Persea	164	210426	211577	0.0238	0.0346	At5g43330	At5g43330	"malate dehydrogenase, cytosolic, putative strong similarity to cytosolic malate dehydrogenase (EC 1.1.1.37) SPI024047 [Mesembryanthemum crystallinum], SPI048905 [Medicago sativa], [Prunus persica] GI:15982948"
Persea	165	210449	215355	0.0623	0.6824	At5g09510	At5g09510	"40S ribosomal protein S15 (RPS15D) ribosomal protein S15 - Arabidopsis thaliana, EMBL:Z23161"
Persea	166	210450	210485	0.0874	0.8643	At5g61790	At5g61790	calnexin 1 (CNX1)
Persea	167	210451	214210	0.0779	0.1277	At2g36390	At2g36390	"1,4-alpha-glucan branching enzyme"
Persea	169	210503	210677	0.0303	1.1996	At3g26618	At3g26618	eukaryotic release factor 1 family protein
Persea	170	210515	215181	0.1702	0.2314	At3g51520	At3g51520	diacylglycerol acyltransferase family contains Pfam PF03982: Diacylglycerol acyltransferase
Persea	171	210520	213902	0.0336	0.5725	At4g09320	At4g09320	nucleoside diphosphate kinase 1 (NDK1)
Persea	172	210530	211189	0.0921	0.4273	At2g43350	At2g43350	"glutathione peroxidase, putative"
Persea	173	210538	211143	0.0232	0.4248	At3g62870	At3g62870	"60S ribosomal protein L7A (RPL7aB) 60S RIBOSOMAL PROTEIN L7A - Oryza sativa, SWISSPROT:RL7A_ORYSA"
Persea	175	210612	214915	0.0535	0.4497	At4g38790	At4g38790	ER lumen protein retaining receptor family protein
Persea	178	210733	214531	0.081	0.5394	At4g36250	At4g36250	"aldehyde dehydrogenase family protein contains aldehyde dehydrogenase (NADP) family protein domain, Pfam:PF00171"
Persea	181	210805	214847	0.0278	0.4704	At5g45820	At5g58380	CBL-interacting protein kinase 20 (CIPK20)
Persea	182	210807	215037	0.1165	0.932	At5g48160	At3g07780	"tropomyosin-related contains weak similarity to Tropomyosin, muscle (Allergen Ani s 3), (Swiss-Prot:Q9NAS5) [Anisakis simplex]"
Persea	183	210832	213967	0.1117	0.5845	At1g07410	At3g46830	"Ras-related GTP-binding protein, putative"
Persea	184	210918	211570	0.0025	0.0103			
Persea	185	210925	212285	0.0973	0.4501	At4g23180	At4g23180	"receptor-like protein kinase 4, putative (RLK4) nearly"
Persea	186	210934	214010	0	0.0013			
Persea	187	210947	211654	0.0437	0.7209	At4g10570	At4g10590	ubiquitin carboxyl-terminal hydrolase family protein
Persea	191	211014	213767	0.0418	0.5308	At2g42320	At2g42320	nucleolar protein gar2-related contains weak similarity to Swiss-Prot:P41891 protein gar2 [Schizosaccharomyces pombe]
Persea	193	211024	213900	0.1123	0.7815	At3g50530	At3g50530	"calcium-dependent protein kinase, putative"
Persea	196	211081	211315	0.1094	1.1923	At4g09720	At4g09720	"Ras-related GTP-binding protein, putative"
Persea	198	211191	213710	0.334	0.4048			
Persea	199	211213	213420	0.0502	1.09	At5g08570	At5g08570	"pyruvate kinase, putative"
Persea	200	211239	212735	0.0896	0.3309	At4g26160	At4g26160	thoredoxin family protein
Persea	205	211440	214138	0.1012	0.0922	At2g39390	At2g39390	60S ribosomal protein L35 (RPL35B)
Persea	206	211456	211606	0.1978	0.2549			
Persea	207	211520	213106	0.0328	0.5158	At1g14830	At1g14830	dynammin-like protein C (DL1C) nearly
Persea	209	211580	213186	0.1149	0.6155	At2g39130	At2g39130	"amino acid transporter family protein belongs to INTERPRO:IPR002422 amino acid/polyamine transporter, family II"
Persea	210	211607	211889	0.0079	0.0252	At3g29180	At1g13970	expressed protein
Persea	211	211641	213859	0.074	1.0239	At4g25050	At1g54580	acyl carrier family protein
Persea	214	211763	214796	0.1217	0.8305	At1g79590	At1g79590	syntaxin 52 (SYP52)
Persea	215	211795	213452	0.0043	0	At2g32080	At2g32080	PUR alpha-1 protein
Persea	217	211816	214434	0.4751	0.651			
Persea	220	211846	214113	0.039	1.2984	At4g27090	At4g27090	"60S ribosomal protein L14 (RPL14B) ribosomal protein L14 - Human,PIR3:JC5954"
Persea	224	211943	214821	0.0489	0.0606	At3g17450	At3g17450	hAT dimerisation domain-containing protein contains Pfam profile PF04937: Protein of unknown function (DUF 659)
Persea	225	211949	212044	0	0.0013	At4g31985		
Persea	229	212017	213867	0.066	0.5996	At5g33320	At5g33320	"triose phosphate/phosphate translocator, putative"
Persea	230	212026	212389	0.1845	0.3745	At1g54580	At1g54580	"acyl carrier protein, chloroplast, putative"
Persea	231	212062	214558	0.1679	0.3971	At4g23160	At4g23160	protein kinase family protein contains Pfam domain PF00069: Protein kinase domain
Persea	232	212110	212892	0.069	0.9779	At1g67280	At1g67280	"lactoylglutathione lyase, putative"
Persea	234	212137	214591	0.0005	0	At4g33210	At4g33210	F-box family protein (FBL15) contains similarity to F-box protein FBL2 GI:6063090 from [Homo sapiens]
Persea	235	212196	213358	0.5806	0.746			
Persea	239	212329	214205	0.2543	1.3907	At4g34160	At5g67260	cyclin delta-3 (CYCD3)
Persea	240	212383	213795	0.1911	0.8331			
Persea	241	212457	215065	0.0542	0.6332	At4g02840	At4g02840	"small nuclear ribonucleoprotein D1, putative"
Persea	242	212488	215422	0.0806	0.5375			
Persea	244	212569	214368	0.1543	0.2348	At1g36035		
Persea	245	212630	214798	0.0836	0.6748	At5g60390	At5g60390	elongation factor 1-alpha
Persea	249	212732	213877	0.0246	0.3955	At5g43810	At5g43810	pinhead protein (PINHEAD)
Persea	250	212761	212893	0.0684	0.7952	At5g59370	At3g12110	actin 4 (ACT4)
Persea	252	213036	213923	0.0005	0	At3g58530	At3g58530	F-box family protein-related contains weak similarity to F-box protein FBL2 (GI:6010699) [Rattus norvegicus]
Persea	253	213262	214932	0.0857	0.3219	At5g03040	At5g03040	calmodulin-binding family protein
Persea	254	213276	213981	0.1077	0.296	At1g79650	At1g79650	"DNA repair protein RAD23, putative"
Persea	257	213591	214927	0.1735	0.5689	At4g14930	At4g14930	"acid phosphatase survival protein SurE, putative"
Persea	260	213653	214451	0.0991	0.4714	At1g15690	At1g15690	pyrophosphate-energized vacuolar membrane proton pump
Persea	261	213754	214093	0.077	0.8953	At5g18230	At5g18230	transcription regulator NOT2/NOT3/NOT5 family protein contains Pfam domain PF04153: NOT2
Persea	262	213758	214088	0.0632	0.6915	At3g58500	At3g58500	serine/threonine protein phosphatase PP2A-4

								catalytic subunit (PP2A4)
Persea	264	213901	215244	0.0395	0.1491	At2g44710	At2g44710	RNA recognition motif (RRM)-containing protein
Persea	265	213993	214307	0.169	1.1474	At3g52590	At3g52590	ubiquitin extension protein 1 (UBQ1)
Persea	268	214621	214812	0.1095	0.8601	At1g59650	At1g59650	expressed protein
Saruma	1	306938	311271	0.036	0.8586	At3g46460	At3g46460	ubiquitin-conjugating enzyme 13 (UBC13) E2
Saruma	3	306944	308724	0.0574	0.2757	At1g66530	At5g36260	serine/threonine protein kinase family protein contains Pfam PF00069: Protein kinase domain
Saruma	5	306957	308932	0.0726	0.5404	At5g02100	At5g02100	oxysterol-binding family protein
Saruma	6	306962	310233	0	0.0009	At1g22730	At1g75660	MA3 domain-containing protein contains Pfam profile PF02847: MA3 domain
Saruma	7	306965	308973	0	0.0014	At5g09810	At5g09810	actin 7 (ACT7)
Saruma	8	306970	307323	0.008	0.8385	At5g02810	At1g27310	"60S ribosomal protein L35 (RPL35D) ribosomal protein L35- cytosolic, Arabidopsis thaliana, PIR:T00549"
Saruma	9	306982	310260	0.0341	0.9379	At5g10980	At5g10980	histone H3
Saruma	10	307005	310378	0	0.0008	At1g73720	At1g73720	transducin family protein
Saruma	11	307006	307345	0.0112	1.3153	At5g02500	At5g02500	heat shock cognate 70 kDa protein 1 (HSC70-1) (HSP70-1)
Saruma	12	307012	308361	0.013	1.0168	At1g72730	At1g72730	"eukaryotic translation initiation factor 4A, putative"
Saruma	14	307033	311781	0.263	1.2152	At4g11220	At4g23630	reticulon family protein (RTNLE2)
Saruma	15	307036	311642	0.0332	0.6493	At5g14040	At5g14040	mitochondrial phosphate transporter
Saruma	16	307039	309393	0.1044	0.4213	At4g39230	At1g75280	"isoflavone reductase, putative"
Saruma	17	307041	307299	0.0092	0.6278	At4g38510	At4g38510	"vacuolar ATP synthase subunit B, putative"
Saruma	18	307045	308133	0.0605	1.0286	At3g58610	At3g58610	ketol-acid reductoisomerase
Saruma	19	307048	308347	0.0374	0.1741	At2g01034	At2g01034	expressed protein
Saruma	20	307049	311707	0.0154	0.0264	At2g46550	At2g46550	ribulose biphosphate carboxylase small chain 1A
Saruma	21	307054	308746	0.0107	0.0001	At1g67090	At5g65360	40S ribosomal protein S3A (RPS3aA)
Saruma	22	307055	307832	0.069	1.2106	At3g04840	At3g04840	"proline-rich family protein contains proline-rich extensin domains, INTERPRO:IPR002965"
Saruma	23	307062	309182	0.0202	0.0289	At5g62640	At5g62640	"ADP- ATP carrier protein, mitochondrial, putative"
Saruma	24	307074	308496	0.0223	0.6307	At4g28390	At4g28390	elongation factor 1-alpha
Saruma	25	307078	308322	0.0115	1.1352	At5g60390	At5g60390	"translocon-associated protein alpha (TRAP alpha) family protein contains Pfam profile: PF03896
Saruma	26	307081	310119	0.1498	0.586	At2g21160	At2g21160	translocon-associated protein (TRAP), alpha subunit"
Saruma	28	307088	308428	0.0452	1.0934	At3g25520	At3g25520	60S ribosomal protein L5
Saruma	29	307094	312306	0.0607	0.7278	At3g06720	At3g06720	"importin alpha-1 subunit, putative (IMPA1)"
Saruma	30	307113	310055	0.021	0.043	At3g19130		"RNA-binding protein, putative"
Saruma	32	307118	307941	0.0361	1.5188	At1g54270	At1g54270	eukaryotic translation initiation factor 4A-2
Saruma	33	307119	312811	0.0504	1.3575	At2g36460	At3g52930	"fructose-biphosphate aldolase, putative"
Saruma	34	307125	307452	0.0058	0.9851	At5g35530	At5g35530	40S ribosomal protein S3 (RPS3C)
Saruma	35	307128	307868	0.057	0.1988	At1g76380	At1g76380	"glutathione S-transferase, putative"
Saruma	36	307134	309639	0.0181	1.6186	At3g44110	At3g44110	"DNAJ heat shock protein, putative (J3)"
Saruma	37	307137	312822	0.0402	0.8242	At1g23750	At1g23750	DNA-binding protein-related contains weak similarity to G-quartet DNA binding protein 3 [Tetrahymena thermophila] gi4583503 gb AAD25098
Saruma	39	307141	309428	0.1004	0.3911	At1g80710	At1g80710	transducin family protein
Saruma	41	307156	309804	0.0002	0.0004	At5g19780	At5g19780	tubulin alpha-3/alpha-5 chain (TUA5) nearly
Saruma	42	307182	307262	0.0143	1.7145	At5g59240	At5g59240	"40S ribosomal protein S8 (RPS8B) 40S ribosomal protein S8, Prunus armeniaca, EMBL:AF071889"
Saruma	43	307187	309277	0.0006	0	At1g43170	At1g61580	60S ribosomal protein L3 (RPL3A)
Saruma	46	307201	307398	0.0386	0.6712	At4g26570	At4g26570	calcineurin B-like protein 3 (CBL3)
Saruma	47	307206	309078	0.0004	0	At3g57490	At1g59359	"40S ribosomal protein S2 (RPS2D) 40S ribosomal protein S2 - Arabidopsis thaliana, SWISSPROT:RS2_ARATH"
Saruma	50	307219	311010	0	0.0018	At1g29630		"exonuclease, putative"
Saruma	53	307235	309687	0.0191	0.751	At4g09800	At4g09800	40S ribosomal protein S18 (RPS18C)
Saruma	55	307237	311252	0.077	0.7263	At4g36760	At4g36760	aminopeptidase P
Saruma	56	307238	308991	0.0007	0.6569	At5g02960	At5g02960	"40S ribosomal protein S23 (RPS23B) ribosomal protein S23, Fragaria x ananassa, PIR:S56673"
Saruma	57	307239	308452	0.0025	1.2144	At1g50010	At1g50010	tubulin alpha-2/alpha-4 chain (TUA2)
Saruma	58	307242	310825	0.0001	0.0004	At1g54510	At1g54510	"protein kinase family protein contains protein kinase domain, Pfam:PF00069"
Saruma	59	307249	312400	0.0625	0.6703	At5g27850	At5g27850	"60S ribosomal protein L18 (RPL18C) 60S ribosomal protein L18, Arabidopsis thaliana, SWISSPROT:RL18_ARATH"
Saruma	60	307255	307316	0.0356	0.9222	At3g25800	At3g25800	serine/threonine protein phosphatase 2A (PP2A) 65 kDa regulatory subunit A
Saruma	62	307270	313172	0.0084	0.6193	At5g62670	At5g62670	"ATPase, plasma membrane-type, putative"
Saruma	63	307285	307622	0.002	1.3137	At1g50010	At1g50010	tubulin alpha-2/alpha-4 chain (TUA2)
Saruma	64	307289	308161	0.0402	1.3597	At4g00430	At1g01620	"plasma membrane intrinsic protein, putative"
Saruma	66	307306	307614	0.0691	0.7656	At4g09830	At4g09830	expressed protein
Saruma	67	307313	311330	0.0035	0	At5g65360	At5g65360	histone H3
Saruma	68	307315	312375	0.0006	0.844	At1g70490	At3g62290	"ADP-ribosylation factor, putative nearly"
Saruma	69	307318	313050	0.3713	1.4167	At5g62890	At5g62890	"permease, putative"
Saruma	70	307351	308255	0.0493	0.4712	At1g29150	At1g29150	"26S proteasome regulatory subunit, putative (RPN6)"
Saruma	74	307380	310759	0	0.0014	At5g41890	At5g41890	GDSL-motif lipase/hydrolase family protein
Saruma	75	307389	310129	0.0271	0.7264	At1g13950	At1g13950	eukaryotic translation initiation factor 5A-1
Saruma	77	307394	308898	0.0194	0.7622	At1g74040	At3g53020	2-isopropylmalate synthase 1 (IMS1)
Saruma	78	307445	310870	0.0486	0.6523	At1g09430	At1g09430	"ATP-citrate synthase (ATP-citrate (pro-S)-)- lyase/citrate cleavage enzyme), putative"
Saruma	79	307471	308306	0.0909	0.4467	At3g02540	At3g02540	"ubiquitin family protein contains Pfam profiles PF00240: Ubiquitin family, PF00627: UBA/TS-N domain,"
Saruma	80	307477	313106	0	0.0016	At5g65360	At5g65360	histone H3
Saruma	81	307487	308183	0.0027	1.5402	At5g48760	At5g48760	60S ribosomal protein L13a (RPL13aD)
Saruma	82	307495	308381	0.0907	0.5889	At4g35450	At4g35450	ankyrin repeat family protein
Saruma	83	307497	307697	0.0001	0.1467	At4g36130	At4g36130	"60S ribosomal protein L8 (RPL8C) ribosomal protein L8, cytosolic, tomato, PIR1:R5TOL8"
Saruma	84	307502	307581	0.068	0.6809	At4g36910	At4g36910	CBS domain-containing protein contains Pfam profile PF00571: CBS domain
Saruma	85	307519	308274	0.0083	0.8909	At5g58420	At5g07090	"40S ribosomal protein S4 (RPS4D) ribosomal protein S4, Arabidopsis thaliana, PIR:T48480"
Saruma	86	307523	311201	0.0312	0.8403	At3g50530	At3g50530	"calcium-dependent protein kinase, putative"
Saruma	87	307532	310943	0.0385	0.0277	At5g09900	At5g09900	"26S proteasome regulatory subunit, putative (RPN5) p55 protein-like"
Saruma	88	307536	312869	0.0816	1.0563	At1g74110	At1g74110	cytochrome P450 family protein
Saruma	89	307564	307951	0.0828	1.1	At1g74050	At1g76080	60S ribosomal protein L6 (RPL6C)
Saruma	90	307567	308537	0.0073	1.8718	At1g75780	At1g20010	tubulin beta-1 chain (TUB1) nearly
Saruma	92	307636	309376	0.0781	1.0484	At1g64390	At1g64390	"endo-1,4-beta-glucanase, putative"
Saruma	94	307644	308402	0.0108	0.587	At4g37930	At4g37930	glycine hydroxymethyltransferase
Saruma	95	307655	308400	0.0273	1.1296	At1g75630	At4g38920	vacuolar ATP synthase 16 kDa proteolipid subunit 4
Saruma	96	307665	309545	0	0.0017	At1g32350	At5g64210	"alternative oxidase, putative"
Saruma	97	307679	312477	0.0909	0.3682	At5g25090	At5g25090	plastocyanin-like domain-containing protein
Saruma	98	307691	312381	0.106	0.795	At1g52150	At1g52150	homeobox-leucine zipper family protein
Saruma	99	307695	309415	0.1119	0.4992	At1g60800	At1g60800	leucine-rich repeat family protein
Saruma	100	307696	308395	0.0975	1.2749	At5g13440	At5g13440	"ubiquinol-cytochrome C reductase iron-sulfur subunit, mitochondrial, putative"
Saruma	101	307710	311840	0.0534	1.1601	At4g22570	At4g22570	"adenine phosphoribosyltransferase, putative strong

								similarity to Adenine phosphoribosyltransferase [Hordeum vulgare subsp. vulgare] GI:9711921"
Saruma	102	307721	311977	0.0344	0.7392	At3g46010	At3g46010	actin-depolymerizing factor 1 (ADF1)
Saruma	104	307727	308336	0.0041	0.5751	At3g54560	At3g54560	histone H2A.F/Z
Saruma	105	307728	307825	0.013	0.6999	At1g26910	At1g26910	60S ribosomal protein L10 (RPL10B) Nearly
Saruma	106	307744	310259	0	0.0123	At5g65470	At5g65470	expressed protein contains Pfam PF03138. Plant protein family. The function of this family of plant proteins is unknown;
Saruma	107	307755	311472	0.0003	0.0004	At2g47110	At2g47110	ubiquitin extension protein 6 (UBQ6)
Saruma	108	307769	310947	0.0722	0.8852	At3g47370	At3g47370	"40S ribosomal protein S20 (RPS20B) 40S RIBOSOMAL PROTEIN S20 - ARABIDOPSIS THALIANA, PID:g1350956"
Saruma	109	307770	307867	0.0183	1.3583	At5g60390	At5g60390	elongation factor 1-alpha
Saruma	110	307790	312882	0.0356	0.7971	At1g65930	At1g65930	"isocitrate dehydrogenase, putative"
Saruma	112	307818	310706	0.0623	1.3734	At3g51800	At3g51800	metallopeptidase M24 family protein
Saruma	113	307821	308326	0.002	1.1485	At5g20010	At5g20010	Ras-related GTP-binding nuclear protein (RAN-1)
Saruma	114	307823	310183	0	0.0018	At5g08890	At5g23250	"ATP synthase beta chain 2, mitochondrial"
Saruma	116	307861	308258	0.0001	0.0003	At3g56150	At1g70600	eukaryotic translation initiation factor 3 subunit 8
Saruma	117	307874	313066	0.0006	0	At5g51560	At4g22730	"leucine-rich repeat transmembrane protein kinase, putative"
Saruma	118	307890	308337	0.1233	0.7008	At5g43060	At5g43060	"cysteine proteinase, putative"
Saruma	119	307891	310889	0	0.0013	At1g07790	At4g12320	"histone H2B, putative strong similarity to histone H2B Arabidopsis thaliana GI:2407802, Gossypium hirsutum SP O22582, Lycopersicon esculentum GI:3021489, Capsicum annuum SP Q49118"
Saruma	120	307899	308986	0.0353	0.0939	At1g30440		"phototropic-responsive NPH3 family protein contains NPH3 family domain, Pfam:PF03000"
Saruma	121	307902	308236	0	0.0016	At1g48750	At5g54270	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein
Saruma	122	307904	311899	0.0195	0.7369	At3g01090	At3g01090	Snf1-related protein kinase (KIN10) (SKIN10)
Saruma	123	307919	311589	0.0903	0.6898	At4g39860	At4g39860	expressed protein
Saruma	124	307962	311016	0	0.002	At1g14220	At1g14220	ribonuclease T2 family protein contains similarity to S-like ribonuclease PD1 GI:9957752 from [Prunus dulcis]
Saruma	125	307965	308169	0.0855	0.8646	At2g19770	At5g56600	profilin 4 (PRO4) (PFN4)
Saruma	127	307987	308321	0.0358	0.714	At3g63410	At3g63410	"chloroplast inner envelope membrane protein, putative (APG1)"
Saruma	128	307998	308529	0.2168	1.1102	At3g24120	At3g24120	myb family transcription factor contains Pfam profile: PF00249 myb-like DNA-binding domain
Saruma	129	308012	308135	0.094	0.9368	At1g72370	At1g72370	40S ribosomal protein S4 (RPS4A)
Saruma	130	308024	311343	0.1067	0.4694	At3g29100	At3g29100	vesicle transport v-SNARE 13 (VT113)
Saruma	131	308028	312850	0.0108	0.0001	At3g25520	At5g39740	60S ribosomal protein L5
Saruma	134	308124	312323	0.0146	0.2683	At1g57720	At1g57720	"elongation factor 1B-gamma, putative"
Saruma	135	308126	308761	0	0.0019	At3g08590	At3g08590	"2,3-biphosphoglycerate-independent phosphoglycerate mutase, putative"
Saruma	136	308137	311177	0.0093	0.7703	At3g19760	At3g19760	"eukaryotic translation initiation factor 4A, putative"
Saruma	137	308143	312376	0.0002	0.0005	At4g00100	At5g56670	40S ribosomal protein S13 (RPS13A)
Saruma	139	308170	311724	0.0021	0.0052	At3g56860	At3g56860	UBP1 interacting protein 2a (UBA2a)
Saruma	142	308190	311394	0.0313	1.1657	At5g28840	At5g28840	NAD-dependent epimerase/dehydratase family protein
Saruma	144	308208	309741	0.0727	0.6253	At5g66080	At5g66080	protein phosphatase 2C family protein
Saruma	145	308224	308406	0.1119	0.796	At4g30210	At4g30210	"NADPH-cytochrome p450 reductase, putative"
Saruma	146	308227	308328	0.0423	0.8993	At3g49010	At3g49010	60S ribosomal protein L13 (RPL13B)
Saruma	147	308267	309125	0.039	0.7932	At2g27530	At2g27530	60S ribosomal protein L10A (RPL10aB)
Saruma	148	308270	312049	0.0145	0.8292	At1g78570	At3g14790	NAD-dependent epimerase/dehydratase family protein
Saruma	150	308288	312538	0.0002	0.0004	At2g42600	At3g60240	"phosphoenolpyruvate carboxylase, putative"
Saruma	151	308311	312873	0	0.0012	At3g18740	At1g20693	60S ribosomal protein L30 (RPL30C)
Saruma	153	308330	311861	0.0295	1.5001	At1g60970	At4g27230	clathrin adaptor complex small chain family protein contains Pfam profile: PF01217 clathrin adaptor complex small chain
Saruma	154	308353	310903	0.0578	1.2857	At2g39700	At2g28950	"expansin, putative (EXP4)"
Saruma	155	308363	309853	0.1547	0.4632	At2g35530	At2g35530	bZIP transcription factor family protein contains Pfam domain PF00170: bZIP transcription factor
Saruma	156	308377	308409	0.0266	0.7039	At1g13440	At1g13440	"glyceraldehyde 3-phosphate dehydrogenase, cytosolic, putative"
Saruma	157	308379	308731	0.0003	0	At5g59870	At5g59870	"histone H2A, putative"
Saruma	159	308411	312399	0.0302	0.873	At2g33840	At2g33840	tRNA synthetase class I (W and Y) family protein
Saruma	160	308423	309107	0.1104	0.9605	At1g79940	At1g79940	DNAJ heat shock N-terminal domain-containing protein
Saruma	162	308453	310734	0.016	1.1387	At1g27530	At3g04920	expressed protein Similar to gb AF151884 CGI-126 protein from Homo sapiens. EST gb Z18048 comes from this gene
Saruma	163	308455	312102	0.0058	0.5214	At1g07790	At1g07790	"histone H2B, putative strong similarity to histone H2B Arabidopsis thaliana GI:2407802, Gossypium hirsutum SP O22582, Lycopersicon esculentum GI:3021489, Capsicum annuum SP Q49118"
Saruma	164	308460	310178	0	0.0015	At3g58500	At2g42500	serine/threonine protein phosphatase PP2A-4 catalytic subunit (PP2A4)
Saruma	165	308463	312695	0.0033	0.0571	At1g71691	At1g71691	GDSL-motif lipase/hydrolase family protein
Saruma	166	308477	311235	0.0073	0.448	At5g14670	At3g62290	"ADP-ribosylation factor, putative"
Saruma	167	308479	310857	0.0241	0.6399	At3g56340	At3g56340	40S ribosomal protein S26 (RPS26C) several 40S ribosomal protein S26
Saruma	168	308504	312320	0.062	1.0761	At1g69620	At1g69620	60S ribosomal protein L34 (RPL34B)
Saruma	169	308539	309725	0.0482	0.7427	At5g65270	At5g65270	Ras-related GTP-binding family protein
Saruma	170	308543	312558	0.1179	0.547	At2g33120	At2g32670	synaptobrevin-related protein
Saruma	171	308544	310641	0	0.0365	At3g08030	At3g08030	"expressed protein contains Pfam profile PF04862: Protein of unknown function, DUF642"
Saruma	172	308545	309169	0.273	0.6686	At2g21310	At4g09595	
Saruma	178	308626	311782	0.0002	0.0004	At5g16790		
Saruma	181	308684	311301	0.0384	0.602	At2g42960	At2g42960	"protein kinase family protein contains protein kinase domain, Pfam:PF00069"
Saruma	183	308730	310960	0	0.0018			
Saruma	184	308732	312667	0.0943	0.2252	At3g32950		
Saruma	185	308747	312437	0	0.0014	At3g02790	At3g17390	"zinc finger (C2H2 type) family protein contains Pfam profile: PF00096 zinc finger, C2H2 type"
Saruma	187	308760	311041	0.0002	0.0005			
Saruma	192	308804	309003	0.0328	0.7012	At5g08300	At5g23250	"succinyl-CoA ligase (GDP-forming) alpha-chain, mitochondrial, putative"
Saruma	193	308810	310444	0.0341	1.5242	At4g17530	At1g02130	"Ras-related GTP-binding protein, putative very strong similarity to RAB1C [Lotus corniculatus var. japonicus] GI:1370166"
Saruma	198	308879	312604	0.0562	1.0839	At2g17200	At2g17190	ubiquitin family protein weak similarity to PLIC-2 (ubiquitin-like type II) [Homo sapiens] GI:9937505
Saruma	199	308902	311834	0.0004	0.0008			
Saruma	202	308916	310500	0.0952	0.1942	At5g32426	At1g37060	
Saruma	203	308956	312805	0.0732	0.2456	At5g06060	At5g06060	"tropinone reductase, putative"
Saruma	213	309156	312131	0.2285	0.167			
Saruma	214	309170	311094	0	0.0008			
Saruma	215	309172	310496	0.1484	0.4035	At2g01034	At2g01034	

Saruma	216	309204	311446	0.0317	0.7432	A14g27090	A14g27090	"60S ribosomal protein L14 (RPL14B) ribosomal protein L14 - Human,PIR3.JC5954"
Saruma	219	309230	311441	0.0404	0.9264	A14g19110	A14g19110	"protein kinase, putative contains protein kinase domain, Pfam:PF00069"
Saruma	221	309254	309574	0.0002	0.0004	A13g43810	A13g43810	calmodulin-7 (CAM7) almost
Saruma	223	309258	309512	0.0238	0.6148	A14g24830	A14g24830	arginosuccinate synthase family contains Pfam profile: PF00764 arginosuccinate synthase
Saruma	224	309286	310164	0.0005	0.0003	A12g35490		"plastid-lipid associated protein PAP, putative"
Saruma	225	309303	310081	0	0.0013			
Saruma	232	309459	308884	0.0839	1.9104	A11g27680	A11g27680	glucose-1-phosphate adenylyltransferase large subunit 2 (APL2)
Saruma	234	309498	312063	0.1456	0.0716			
Saruma	238	309610	311628	0.0855	0.4494	A13g26744	A13g26744	basix helix-loop-helix (bHLH) family protein contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain
Saruma	244	309763	311224	0.0289	0.0297	A13g13235	A14g24880	ubiquitin family protein contains INTERPRO:IPR000626 ubiquitin domain
Saruma	247	309834	310357	0.0081	0.7763	A11g77940	A13g18740	60S ribosomal protein L30 (RPL30B)
Saruma	252	309970	312472	0.1316	0.4139	A12g47180	A12g47180	"galactinol synthase, putative"
Saruma	259	310125	313214	0.3414	0.2269			
Saruma	261	310130	310381	0.0739	0.481	A14g33950	A14g33950	"protein kinase, putative"
Saruma	267	310275	311712	0.0176	0.4929	A11g16890	A11g78870	"ubiquitin-conjugating enzyme, putative nearly"
Saruma	268	310288	310636	0.127	0.3416	A12g13330		
Saruma	269	310294	311359	0.0456	0.6829	A14g31540	A14g31540	"exocyst subunit EXO70 family protein (EXO70-G1) tomato leucine zipper-containing protein - Lycopersicon esculentum, PIR2.S21495"
Saruma	272	310321	312365	0.0158	0.0079	A12g01060	A12g01060	myb family transcription factor contains Pfam profile: PF00249 myb-like DNA-binding domain
Saruma	275	310380	313083	0.0759	0.4171	A12g44680	A12g44680	"casein kinase II beta chain, putative"
Saruma	278	310521	310740	0.0276	0.0214	A12g12220	A12g12220	
Saruma	281	310587	312421	0.1395	0.2519	A15g48930	A15g48930	transferase family protein
Saruma	282	310607	310919	0.0087	0.0122	A15g48390	A15g48390	tetratricopeptide repeat (TPR)-containing protein contains Pfam profile PF00515: TPR Domain
Saruma	286	310765	311852	0.044	0.5485	A11g24360	A11g24360	"3-oxoacyl-[acyl-carrier protein] reductase, chloroplast"
Saruma	287	310832	312453	0.1001	0.9082	A11g75990	A11g20200	"26S proteasome regulatory subunit S3, putative (RPN3)"
Saruma	288	310894	311731	0.0143	0.0001	A11g47710	A11g47710	"serpin, putative"
Saruma	293	311142	311953	0.032	1.0721	A13g62290	A15g14670	ADP-ribosylation factor
Saruma	297	311273	313102	0.4861	0.4849	A11g64390	A11g64390	"endo-1,4-beta-glucanase, putative"
Saruma	298	311344	312151	0.0855	0.9857	A13g04830		expressed protein
Saruma	306	311759	312954	0.0506	0.3482	A14g09320	A14g09320	nucleoside diphosphate kinase 1 (NDK1)
Saruma	310	311888	312524	0.2116	0.2559			
Saruma	312	311997	312154	0.1816	1.4493	A14g29160		
Saruma	315	312108	312832	0.0182	0.0002	A11g68010	A11g68010	glycerate dehydrogenase
Saruma	324	312896	313155	0.032	1.067	A15g24940	A15g24940	"protein phosphatase 2C, putative"
Nuphar	1	190626	192476	0.0362	1.5199	A12g47240	A12g47240	long-chain-fatty-acid-CoA ligase family protein
Nuphar	3	190619	189791	0.019	0.016	A12g45180	A14g12470	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein
Nuphar	4	190617		0.0089	0.0001	A15g20620	A15g20620	polyubiquitin (UBQ4)
Nuphar	5	190612	190490	0.0333	0.2905	A15g65360	A15g65360	histone H3
Nuphar	7	190609	191934	0.0316	0.4758	A14g00100	A14g00100	40S ribosomal protein S13 (RPS13A)
Nuphar	8	190592	194961	0.1332	0.4389	A13g12860	A13g12860	"nucleolar protein Nop56, putative"
Nuphar	9	190590	192056	0.0463	1.5946	A13g04120		"glyceraldehyde-3-phosphate dehydrogenase, cytosolic (GAPC)"
Nuphar	11	190583	192277	0.0564	0.414	A12g21790	A12g21790	"ribonucleoside-diphosphate reductase small chain, putative"
Nuphar	12	190582	190193	0.0461	0.5718	A11g69620	A11g69620	60S ribosomal protein L34 (RPL34B)
Nuphar	13	190560	190419	0.0181	0.4689	A13g52580	A13g52580	"40S ribosomal protein S14 (RPS14C) ribosomal protein S14 - Zea mays,PIR2.A30097"
Nuphar	16	190543	192837	0.0305	0.2206	A12g37600	A12g37600	60S ribosomal protein L36 (RPL36A)
Nuphar	17	190536	190073	0.0951	0.0594	A15g57920		"squamosa promoter-binding protein, putative"
Nuphar	19	190520	195640	0.0095	0.0001	A15g59870	A15g59870	"histone H2A, putative"
Nuphar	20	190518	189966	0.0337	0.4334	A13g25520	A15g39740	60S ribosomal protein L5
Nuphar	21	190517	190221	0.0403	1.529	A12g47160	A12g47160	anion exchange family protein contains some similarity to SWISS-PROT:P04919 anion transport protein (anion exchange protein 1) [Mouse] [Mus musculus]
Nuphar	23	190505	194712	0.0586	0.593	A12g36620	A12g36620	60S ribosomal protein L24 (RPL24A)
Nuphar	24	190504	193029	0.0147	1.2268	A13g04920	A13g04920	40S ribosomal protein S24 (RPS24A)
Nuphar	25	190502	190370	0.0336	0.5124	A15g55230	A15g55230	microtubule associated protein (MAP65/ASE1) family protein
Nuphar	26	190492	192394	0.0716	0.2199	A14g18970		GDSL-motif lipase/hydrolase family protein
Nuphar	27	190488	189853	0.0892	0.5649	A14g09320	A14g09320	nucleoside diphosphate kinase 1 (NDK1)
Nuphar	29	190479	191164	0.0825	0.5465	A15g15270	A15g15270	"KH domain-containing protein various predicted proteins, Arabidopsis thaliana and Oryza sativa"
Nuphar	30	190477	194078	0.0837	0.2681	A12g36580	A13g52990	"pyruvate kinase, putative"
Nuphar	31	190476	194094	0.0886	0.1911	A15g50670		"squamosa promoter-binding protein, putative"
Nuphar	33	190470	191996	0.0195	0.3384	A13g23730	A14g14130	"xyloglucan:xyloglucosyl transferase, putative"
Nuphar	34	190468	189474	0.0589	0.4372	A11g73230	A11g73230	nascent polypeptide-associated complex (NAC) domain-containing protein
Nuphar	36	190465	189585	0.1946	0.8202	A15g06770	A15g06770	KH domain-containing protein
Nuphar	37	190461	191528	0.0033	1.286	A15g02960	A15g02960	"40S ribosomal protein S23 (RPS23B) ribosomal protein S23, Fragaria x ananassa, PIR:S56673"
Nuphar	38	190449	190366	0.0952	0.2569	A11g42960	A11g42960	expressed protein
Nuphar	39	190444	189530	0.0667	0.5557	A12g40300	A12g40300	"feritin, putative"
Nuphar	40	190438	189675	0.0066	0.2367	A15g02560	A15g02560	"histone H2A, putative"
Nuphar	41	190435	190363	0.0062	1.9989	A15g09810	A15g09810	actin 7 (ACT7)
Nuphar	42	190427	190666	0.1414	0.3756	A14g34160	A14g34160	cyclin delta-3 (CYCD3)
Nuphar	48	190376	193039	0.0628	0.2305	A15g19440	A15g19440	"cinnamyl-alcohol dehydrogenase, putative (CAD)"
Nuphar	49	190375	189666	0.0352	0.4274	A13g14290	A13g14290	20S proteasome alpha subunit E2 (PAE2)
Nuphar	51	190372	189763	0.06	0.2915	A15g49190	A14g02280	sucrose synthase
Nuphar	53	190331	194298	0.0603	0.4677	A11g15030	A11g15030	expressed protein
Nuphar	54	190330	194454	0.1673	1.3628	A13g06580	A13g06580	galactokinase (GAL1)
Nuphar	55	190328	189531	0.1221	0.32	A12g10940	A12g10940	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein
Nuphar	57	190322	191144	0.0788	0.3662	A11g55500	A13g13460	expressed protein contains Pfam profile PF04146: Y1521-B-like family
Nuphar	58	190320	195476	0.0303	0.2936	A11g69420		zinc finger (DHHC type) family protein contains Pfam profile: PF01529: DHHC zinc finger domain
Nuphar	59	190317	191056	0.2723	0.1831			
Nuphar	60	190310	193814	0.0104	1.4644	A15g23860	A15g23860	tubulin beta-8 chain (TUB8) (TUBB8)
Nuphar	63	190276	194577	0.0703	1.3822	A12g32060	A12g32060	40S ribosomal protein S12 (RPS12C)
Nuphar	64	190268	190184	0.0564	0.5297	A12g18600	A12g18600	"RUB1-conjugating enzyme, putative strong similarity to gi:6635457 RUB1 conjugating enzyme [Arabidopsis thaliana]"
Nuphar	65	190254	189707	0.0624	0.1034	A13g15790		
Nuphar	66	190252	189572	0.0273	0.2603	A14g27090	A14g27090	"60S ribosomal protein L14 (RPL14B) ribosomal protein L14 - Human,PIR3.JC5954"
Nuphar	67	190243	189696	0.0175	0.4533	A13g02560	A11g48830	40S ribosomal protein S7 (RPS7B)

Nuphar	69	190229	192441	0.0004	0.3561	At5g60390	At5g60390	elongation factor 1-alpha
Nuphar	70	190225	191112	0.0769	1.1064	At3g02080	At5g15520	40S ribosomal protein S19 (RPS19A)
Nuphar	71	190215	189543	0.0349	0.3242	At4g21960	At4g21960	peroxidase 42 (PER42) (P42) (PRXR1)
Nuphar	72	190194	189925	0.0174	0.4202	At5g05000	At5g05000	translocate of chloroplast 34 (TOC34)
Nuphar	74	190189	193263	0.0424	0.5654	At5g20290	At5g59240	"40S ribosomal protein S8 (RPS8A) ribosomal protein S8 - Zea mays, PIR:T04088"
Nuphar	75	190177	189882	0.0715	0.4965	At1g07890	At1g07890	"L-ascorbate peroxidase 1, cytosolic (APX1)"
Nuphar	80	190143	195175	0.0746	0.4925	At3g48170	At1g74920	"betaine-aldehyde dehydrogenase, putative"
Nuphar	81	190107	191854	0.0434	0.1655	At3g14230	At3g14230	AP2 domain-containing protein RAP2.2 (RAP2.2)
Nuphar	82	190103	192437	0.1235	0.2193	At5g09440	At1g35140	"phosphate-responsive protein, putative"
Nuphar	84	190069	199479	0	0.024	At5g10980	At5g10980	histone H3
Nuphar	85	190049	190813	0.1007	0.4549	At5g27950	At5g27950	"kinesin motor protein-related kinesin heavy chain-like protein, potato, PIR:T07397"
Nuphar	86	190043	193959	0.1664	0.5957	At3g07170	At3g07170	sterile alpha motif (SAM) domain-containing protein contains Pfam profile PF00536: SAM domain (Sterile alpha motif)
Nuphar	87	190031	191032	0	0.0352	At3g44110	At3g44110	"DNAJ heat shock protein, putative (J3)"
Nuphar	88	190024	189534	0.0387	0.2285	At1g20693	At1g20693	high mobility group protein beta1 (HMGbeta1)
Nuphar	89	190018	189800	0.0393	0.3819	At3g46010	At4g00680	actin-depolymerizing factor 1 (ADF1)
Nuphar	90	190012	189579	0.0491	0.4063	At1g20693	At1g20693	high mobility group protein beta1 (HMGbeta1)
Nuphar	91	190000	189941	0.0253	0.236	At5g02560	At5g02560	"histone H2A, putative"
Nuphar	93	189964	191744	0.034	1.3263	At5g09810	At5g09810	actin 7 (ACT7)
Nuphar	98	189943	193089	0.0507	0.288	At5g60390	At5g60390	elongation factor 1-alpha
Nuphar	99	189942	194302	0.004	0	At3g48110	At3g48110	"aminoacyl-t-RNA synthetase, putative"
Nuphar	101	189916	194205	0.0232	0.5061	At2g47170	At5g14670	ADP-ribosylation factor 1 (ARF1)
Nuphar	102	189899	192923	0.0696	0.4868	At5g36230	At5g36230	eIF4-gamma/eIF5/eIF2-epsilon domain-containing protein
Nuphar	103	189895	193557	0.0249	0.308	At5g05780	At5g05780	"26S proteasome non-ATPase regulatory subunit 7, putative"
Nuphar	104	189892	191041	0.0219	0.3649	At1g57720	At1g57720	"elongation factor 1B-gamma, putative"
Nuphar	105	189880	192223	0.0813	0.5987	At3g12780	At3g12780	"phosphoglycerate kinase, putative"
Nuphar	106	189875	195296	0.0422	0.7134	At1g56540	At1g56540	calreticulin 1 (CRT1)
Nuphar	108	189866	189504	0.0285	1.2962	At2g01250	At2g01250	60S ribosomal protein L7 (RPL7B)
Nuphar	109	189861	189484	0.0452	0.4571	At3g01280	At3g01280	"porin, putative"
Nuphar	110	189857	195460	0.0168	0.516	At2g40010	At2g40010	60S acidic ribosomal protein P0 (RPP0A)
Nuphar	111	189845	193408	0	0.0138	At1g73230	At1g73230	nascent polypeptide-associated complex (NAC) domain-containing protein
Nuphar	112	189841	193294	0.0583	0.3658	At3g14750	At3g14750	expressed protein weak similarity to Septation ring formation regulator (Swiss-Prot:O34894) [Bacillus subtilis]
Nuphar	113	189834	195622	0.0618	0.2518	At4g23430	At4g23430	short-chain dehydrogenase/reductase (SDR) family protein contains INTERPRO family IPR002198 Short-chain dehydrogenase/reductase (SDR) superfamily
Nuphar	114	189827	193639	0.0322	0.0003			
Nuphar	117	189792	189629	0.1602	0.8747	At5g19320	At3g63130	RAN GTPase activating protein 2 (RanGAP2)
Nuphar	118	189772	194594	0.1282	0.5286	At2g01910	At2g01910	microtubule associated protein (MAP65/ASE1) family protein
Nuphar	119	189762	194262	0.0677	0.6608	At3g29320	At3g29320	"glucan phosphorylase, putative"
Nuphar	122	189729	192466	0.1019	0.7778	At5g51100	At5g51100	"superoxide dismutase [Fe], putative"
Nuphar	124	189722	193626	0.0119	0.0346	At3g08030	At3g08030	"expressed protein contains Pfam profile PF04862: Protein of unknown function, DUF642"
Nuphar	125	189713	190720	0.1596	0.3263	At2g05250	At5g53150	DNAJ heat shock N-terminal domain-containing protein contains Pfam profile PF00226 DnaJ domain
Nuphar	126	189691	195523	0.033	0.1173	At1g65930	At1g54340	"isocitrate dehydrogenase, putative"
Nuphar	127	189671	192009	0.0095	0.363	At4g02080	At4g02080	GTP-binding protein (SAR1A)
Nuphar	129	189647	193948	0.0124	0.7554	At1g72370	At1g72370	40S ribosomal protein SA (RPSaA)
Nuphar	131	189634	192045	0.0656	0.4241	At5g10290	At5g10290	leucine-rich repeat family protein
Nuphar	132	189615	192231	0.0632	0.1415	At1g76690		12-oxophytodienate reductase (OPR2)
Nuphar	134	189602	191735	0.0004	0.3839	At5g58420	At5g58420	"40S ribosomal protein S4 (RPS4D) ribosomal protein S4, Arabidopsis thaliana, PIR:T48480"
Nuphar	135	189582	195004	0.017	0.6398	At3g62870	At2g47610	"60S ribosomal protein L7A (RPL7aB) 60S RIBOSOMAL PROTEIN L7A - Oryza sativa, SWISSPROT:RL7A, ORYSA"
Nuphar	136	189574	194805	0.0001	0.0638			
Nuphar	137	189560	195081	0.0385	0.1709	At2g41830	At5g26850	"cyclin-related contains Pfam profile PF02984: Cyclin, C-terminal domain"
Nuphar	138	189513	192680	0.0422	0.0627	At2g30410	At2g30410	tubulin folding cofactor A (KIESEL)
Nuphar	143	189459	194660	0.0667	0.04	At1g63770	At1g63770	peptidase M1 family protein
Nuphar	144	189452	195156	0.0421	0.3074	At4g09800	At4g09800	40S ribosomal protein S18 (RPS18C)
Nuphar	145	190878	192829	0.0566	0.7721	At1g62990	At1g62990	"homeodomain transcription factor (KNAT7) contains Pfam profiles: PF03789 ELK domain, PF03790 KNOX1 domain, PF03791 KNOX2 domain"
Nuphar	146	190856	193415	0.0659	0.1983	At4g30890	At4g30890	"ubiquitin-specific protease 24, putative (UBP24)"
Nuphar	148	190838	191018	0.0657	0.1537	At4g22410	At4g22350	ubiquitin carboxyl-terminal hydrolase family protein
Nuphar	149	190812	193618	0	0.001	At3g11630	At5g06290	"2-cys peroxiredoxin, chloroplast (BAS1)"
Nuphar	151	190756	191516	0.0529	0.1072			
Nuphar	152	190746	194811	0.0455	0.3348	At5g01650	At5g01650	macrophage migration inhibitory factor family protein
Nuphar	163	195304	193916	0.1487	0.6563	At5g50400	At1g13750	calcineurin-like phosphoesterase family protein contains Pfam profile: PF00149 calcineurin-like phosphoesterase
Nuphar	165	195231	194634	0.3153	1.3017	At4g38620	At4g09460	myb family transcription factor (MYB4) contains Pfam profile: PF00249 myb-like DNA-binding domain
Nuphar	169	195119	194948	0.1531	0.462	At5g54680	At3g23210	basic helix-loop-helix (bHLH) family protein
Nuphar	171	195025	194674	0.0316	0.0514	At3g04910	At3g04910	"protein kinase family protein contains protein kinase domain, Pfam:PF00069"
Nuphar	174	194770	191804	0.0619	0.3293	At1g34750	At1g34750	"protein phosphatase 2C, putative"
Nuphar	175	194758	192353	0.1919	0.5376	At5g20950	At5g20950	"glycosyl hydrolase family 3 protein beta-D-glucan-exohydrolase, Nicotiana tabacum, EMBL:AB017502"
Nuphar	181	194640	192499	0.0945	0.8587	At3g54340		
Nuphar	182	194615	193739	0.2433	0.1423			
Nuphar	186	194489	191470	0.0456	0.0757	At1g63430	At1g63430	"leucine-rich repeat transmembrane protein kinase, putative contains Pfam profiles: PF00069 Eukaryotic protein kinase domain, PF00560 Leucine Rich Repeat"
Nuphar	188	194438	195505	0.0657	0.5583	At5g01320	At5g01320	"pyruvate decarboxylase, putative strong similarity to pyruvate decarboxylase 1 [Vitis vinifera] GI:10732644"
Nuphar	198	194128	191522	0.0141	0.6077	At3g04400	At3g04400	60S ribosomal protein L23 (RPL23C)
Nuphar	199	194125	193689	0.0306	0.3105	At4g12600	At5g20160	"ribosomal protein L7Ae/L30e/S12e/Gad45 family protein Similar to NHP2/L7Ae family proteins, see SWISSPROT:P32495 and PMID:2063628."
Nuphar	202	194056	190942	0.1183	0.0493	At1g69545	At1g69545	leucine-rich repeat family protein contains Pfam PF00560: Leucine Rich Repeat domains
Nuphar	204	193885	195506	0.0819	0.1539	At5g20720	At5g20720	"20 kDa chaperonin, chloroplast (CPN21) (CHCPN10) (CPN20)"
Nuphar	209	193694	193347	0.2082	1.7348	At1g54690	At1g54690	"histone H2A, putative strong similarity to histone H2A GI:3204129 SP O65759 from Cicer arietinum, Picea abies SP P35063"
Nuphar	221	193034	192534	0.0965	0.7979	At2g18050	At2g18050	histone H1-3 (HIS1-3)
Nuphar	222	192990	191090	0.0614	0.4087	At4g10140	At1g33490	expressed protein

Nuphar	223	192938	191829	0.0819	0.4124	At2g19860	At4g29130	hexokinase 2 (HXK2)
Nuphar	226	192799	191113	0.1011	0.307	At3g27540	At1g12990	glycosyl transferase family 17 protein
Nuphar	230	192504	190923	0.1054	0.4361	At3g60600	At3g60600	"vesicle-associated membrane protein, putative"
Nuphar	231	192445	190958	0.2615	1.5059	At2g33040	At2g33040	"ATP synthase gamma chain, mitochondrial (ATPC)"
Nuphar	232	192444	191461	0.0627	0.1683	At1g71310	At1g71310	expressed protein
Nuphar	235	192154	191161	0.0428	0.1438	At1g78570	At1g78570	NAD-dependent epimerase/dehydratase family protein
Nuphar	238	191733	191269	0.1186	0.3469	At1g23550	At1g32230	expressed protein
Nuphar	241	191390	191147	0.0449	0.6697	At5g27770	At3g05560	"60S ribosomal protein L22 (RPL22C) ribosomal protein L22 (cytosolic), Rattus norvegicus, PIR:S52084"
Nuphar	244	191336	191171	0.075	0.4473	At4g12710	At4g12710	armadillo/beta-catenin repeat family protein contains Pfam profile: PF00514 armadillo/beta-catenin-like repeat
Nuphar	247	191165	195532	0.1301	0.4425			
Nuphar	249	190938	190905	0	0.0009	At3g10160	At5g05980	dihydrofolate synthetase/folypolyglutamate synthetase (DHFS/FPGS3) nearly
Amborella	4	195700	198738	0.0261	0.0003	At1g73230	At4g36250	nascent polypeptide-associated complex (NAC) domain-containing protein
Amborella	5	195715	197589	0.0517	0.2871	At2g21660	At2g21660	glycine-rich RNA-binding protein (GRP7) SPIQ03250 Glycine-rich RNA-binding protein 7 (Arabidopsis thaliana)
Amborella	6	195729	201048	0.0524	0.1372	At3g56230	At3g56230	speckle-type POZ protein-related contains Pfam PF00651 : BTB/POZ domain
Amborella	7	195757	196274	0.0492	0.7084	At1g13440	At1g13440	"glyceraledehyde 3-phosphate dehydrogenase, cytosolic, putative"
Amborella	8	195768	196478	0.1358	0.166	At3g19000	At3g19000	"oxidoreductase, 2OG-Fe(II) oxygenase family protein"
Amborella	9	195788	196475	0.03	0.4311	At5g59910	At5g59910	histone H2B nearly
Amborella	10	195794	196152	0.0134	0.3938	At5g60390	At5g60390	elongation factor 1-alpha
Amborella	12	195825	197052	0.0969	1.174	At1g14650	At1g14650	SWAP (Suppressor-of-White-Apricot)/surp domain-containing protein
Amborella	13	195836	201312	0.0003	0			
Amborella	16	195871	195897	0.0795	0.1974	At4g35090	At4g35090	catalase 2
Amborella	17	195909	196037	0.0825	0.1198	At5g20620		
Amborella	18	195911	198228	0	0.0026	At3g44110	At3g44110	"DNAJ heat shock protein, putative (J3)"
Amborella	19	195914	196091	0.0827	0.1492	At4g17890	At4g17890	human Rev interacting-like family protein
Amborella	20	195917	201513	0.0002	0.0003	At3g10300	At5g04170	calcium-binding EF hand family protein
Amborella	21	195927	195962	0.1235	0.3135	At5g19440	At5g19440	"cinnamyl-alcohol dehydrogenase, putative (CAD)"
Amborella	22	195936	200395	0	0.0011	At1g78380	At1g78380	"glutathione S-transferase, putative"
Amborella	23	195945	196796	0.0163	1.5862	At5g09810	At3g12110	actin 7 (ACT7)
Amborella	24	195966	196371	0.2086	0.7243	At5g06060	At2g29260	"tropinone reductase, putative"
Amborella	25	195968	196817	0.0949	0.1566	At3g46230	At1g53540	17.4 kDa class I heat shock protein (HSP17.4-CI)
Amborella	29	196022	198250	0	0.0016	At3g09790	At5g20620	polyubiquitin (UBQ8)
Amborella	30	196063	198918	0.1265	0.257	At5g16990	At5g16990	"NAD(P)-dependent oxidoreductase, putative strong similarity to probable NAD(P)-dependent oxidoreductase (zeta-crystallin homolog) P1 [SPIQ39172][gi:886428] and P2 [SPIQ39173][gi:886430], Arabidopsis thaliana"
Amborella	31	196110	196753	0.0247	1.7543	At2g34420	At2g34420	chlorophyll A-B binding protein
Amborella	32	196137	198796	0.322	0.8968	At1g43190	At1g43190	"polypyrimidine tract-binding protein, putative"
Amborella	33	196165	197990	0.0884	0.1657	At5g12020	At5g12020	17.6 kDa class II heat shock protein (HSP17.6-CII)
Amborella	35	196183	198559	0.3113	0.129	At2g34480	At2g34480	60S ribosomal protein L18A (RPL18aB)
Amborella	36	196192	199425	0	0.0268	At4g39230	At1g75280	"isoflavone reductase, putative"
Amborella	37	196212	196863	0.0011	1.0907	At3g62290	At5g14670	ADP-ribosylation factor
Amborella	38	196215	196292	0.0829	0.264	At5g59720	At5g59720	18.1 kDa class I heat shock protein (HSP18.1-CI)
Amborella	40	196309	197860	0.0865	0.1979	At5g58490	At5g58490	cinnamoyl-CoA reductase family
Amborella	41	196340	201086	0	0.0011	At3g12490	At3g12490	"cysteine protease inhibitor, putative"
Amborella	42	196345	201618	0.6083	0.7894			
Amborella	43	196362	199298	0.1944	0.275	At1g05570	At5g13000	callose synthase 1 (CALS1)
Amborella	45	196387	201221	0.0327	0.086	At4g16270	At4g16270	peroxidase 40 (PER40) (P40)
Amborella	46	196414	196533	0.2262	0.8918	At5g13710	At5g13710	"sterol 24-C-methyltransferase, putative"
Amborella	47	196420	199969	0	0.0019	At5g14670	At3g62290	"ADP-ribosylation factor, putative"
Amborella	49	196422	196655	0.1345	0.1792	At3g19000	At3g19010	"oxidoreductase, 2OG-Fe(II) oxygenase family protein"
Amborella	50	196448	201179	0	0.0007			
Amborella	51	196471	196620	0.0718	0.8111	At1g13950	At1g13950	eukaryotic translation initiation factor 5A-1
Amborella	52	196496	196740	0.0365	0.1662	At3g45140	At3g45140	lipoygenase (LOX2)
Amborella	54	196499	200910	0.0488	1.9777	At4g33950	At5g66880	"protein kinase, putative"
Amborella	55	196563	198177	0.1208	0.9238	At5g67510	At5g67510	60S ribosomal protein L26 (RPL26B)
Amborella	56	196596	196676	0.0008	0.7664	At5g20620	At5g20620	polyubiquitin (UBQ4)
Amborella	57	196605	201623	0.011	1.7599	At1g78870	At1g16890	"ubiquitin-conjugating enzyme, putative nearly"
Amborella	59	196702	199720	0	0.0014	At3g19000	At3g19000	"oxidoreductase, 2OG-Fe(II) oxygenase family protein"
Amborella	60	196718	196934	0.0563	0.0759	At1g54290	At1g54290	"eukaryotic translation initiation factor SUI1, putative"
Amborella	61	196752	201716	0	0.0243	At1g79750	At1g79750	"malate oxidoreductase, putative"
Amborella	62	196775	200488	0.0388	0.017	At5g13700	At5g13700	"polyamine oxidase, putative"
Amborella	64	196822	200988	0.0313	0.08	At1g69620	At1g69620	60S ribosomal protein L34 (RPL34B)
Amborella	71	196927	198418	0	0.0009			
Amborella	72	196986	198799	0.1502	0.8305			
Amborella	74	197049	201229	0.0167	0.0308	At5g56590	At5g56590	glycosyl hydrolase family 17 protein
Amborella	76	197101	200686	0.0002	0.0005			
Amborella	78	197106	198383	0.0002	0.0005			
Amborella	85	197358	201689	0	0.0008	At1g74470	At1g74470	geranylgeranyl reductase
Amborella	88	197437	198223	0.0004	0.0009			
Amborella	99	197772	198352	0.1311	0.1322			
Amborella	109	198086	200762	0.0003	0.0006			
Amborella	113	198248	200492	0.0003	0.0006			
Amborella	114	198271	200032	0.0623	0.0756	At5g54640	At1g54690	histone H2A
Amborella	129	198609	198632	0.0003	0.0008	At1g01230	At4g32260	ORMDL family protein contains Pfam domain PF04061: ORMDL family
Amborella	131	198715	199326	0.4036	0.7655	At2g37110	At2g37110	"expressed protein contains Pfam profile PF04749: Protein of unknown function, DUF614"
Amborella	139	198977	199430	0.1488	0.6078	At4g27650	At4g27650	pelota (PEL1)
Amborella	151	199682	200013	0.0238	1.3369	At5g12250	At5g23860	tubulin beta-6 chain (TUB6) nearly
Amborella	152	199925	200922	0.0035	0	At4g27000	At4g27000	"RNA-binding protein 45 (RBP45), putative DNA binding protein ACBF - Nicotiana tabacum, PIR:G1989188"
Amborella	156	200179	200264	0.0049	0.0153			
Amborella	161	200334	200659	0.0584	0.3605	At5g02610	At5g02610	"60S ribosomal protein L35 (RPL35D) ribosomal protein L35- cytosolic, Arabidopsis thaliana, PIR:T00549"
Amborella	162	200861	201094	0.0038	0	At4g00660	At4g00660	"DEAD/DEAH box helicase, putative"
Amborella	165	201072	201253	0.3624	0.3206	At1g20390		
Amborella	167	201610	198019	0.0585	0.0776	At5g25900	At5g25900	"ent-kaurene oxidase, putative (GA3)"
Welwitschia	1	330950	330968	0.0024	0.684	At5g35530	At5g35530	40S ribosomal protein S3 (RPS3C)
Welwitschia	4	330989	330883	0.1243	1.0655	At1g15950	At1g98020	"cinnamoyl-CoA reductase, putative nearly"
Welwitschia	6	330998	335018	0.0036	0.7174	At5g14640	At5g14640	protein kinase family protein
Welwitschia	7	331000	332251	0.0071	1.1506	At5g60390	At5g60390	elongation factor 1-alpha
Welwitschia	8	331008	332286	0.0679	0.8472	At2g39700	At2g39700	"expansin, putative (EXP4)"

Welwitschia	9	331014	335754	0.008	0.0001	A14g29830	A14g29830	transducin family protein
Welwitschia	12	331033	331426	0.0556	0.9836	A15g52640	A15g52640	heat shock protein 81-1 (HSP81-1)
Welwitschia	14	331050	334356	0.1272	0.5129	A14g08150	A11g62360	homeobox protein knotted-1 like 1 (KNAT1)
Welwitschia	16	331072	331626	0.0159	1.1139	A15g13490	A14g28390	"ADP, ATP carrier protein 2, mitochondrial"
Welwitschia	17	331075	335565	0.1022	0.6257	A14g34230	A13g19450	"cinnamyl-alcohol dehydrogenase, putative"
Welwitschia	18	331076	333073	0.0008	0.7995	A15g65360	A15g65360	histone H3
Welwitschia	20	331091	334093	0.0065	1.4129	A15g65360	A15g65360	histone H3
Welwitschia	21	331095	334198	0.1786	0.8281	A15g22920	A15g22920	"zinc finger (C3HC4-type RING finger) family protein contains Pfam profiles:PF05495 CHY zinc finger, PF00097 zinc finger, C3HC4 type (RING finger)"
Welwitschia	22	331120	331738	0.0273	1.0648	A14g01850	A13g17390	S-adenosylmethionine synthetase 2 (SAM2)
Welwitschia	23	331121	334478	0.0387	1.1669	A14g26100	A14g26100	"casein kinase, putative"
Welwitschia	24	331135	331304	0	0.0333	A11g50010	A14g14960	tubulin alpha-2/alpha-4 chain (TUA2)
Welwitschia	25	331138	333177	0.0709	1.2855	A14g32295	A14g32295	expressed protein
Welwitschia	27	331157	331214	0.0129	0.6939	A15g13930	A15g13930	chalcone synthase
Welwitschia	28	331165	331262	0.0289	0.8657	A15g17920	A13g03780	5-methyltetrahydropteroyltrimethylglutamate-homocysteine methyltransferase
Welwitschia	29	331167	336730	0	0.0022	A14g24340	A14g24350	phosphorylase family protein contains Pfam PF01048: Phosphorylase family
Welwitschia	30	331176	331902	0.0348	0.012	A13g29090	A13g29090	pectinesterase family protein
Welwitschia	31	331186	335973	0.0423	0.2976	A11g78380	A11g78380	"glutathione S-transferase, putative"
Welwitschia	32	331188	332736	0.0316	0.8034	A12g32670	A12g32670	synaptobrevin family protein
Welwitschia	34	331208	331497	0.0015	1.5081	A14g05050	A15g20620	polyubiquitin (UBQ11)
Welwitschia	35	331212	332001	0.0024	0.8115	A13g62290	A13g62290	ADP-ribosylation factor
Welwitschia	36	331218	332460	0.026	0.847	A11g26910	A11g26910	60S ribosomal protein L10 (RPL10B) Nearly
Welwitschia	37	331226	333657	0.007	0.0001	A13g12580	A13g12580	"heat shock protein 70, putative"
Welwitschia	38	331227	332498	0.1148	0.7977	A12g01970	A11g14670	"endomembrane protein 70, putative"
Welwitschia	40	331234	333915	0.1001	0.5241	A13g56150	A13g56150	eukaryotic translation initiation factor 3 subunit 8
Welwitschia	41	331235	335797	0.0003	0.0006	A11g72370		40S ribosomal protein SA (RPSaA)
Welwitschia	42	331237	331862	0.0016	1.5657	A13g04400	A13g04400	60S ribosomal protein L23 (RPL23C)
Welwitschia	43	331241	333858	0.1252	0.7869	A13g01280	A13g01280	"porin, putative"
Welwitschia	44	331245	332492	0.0575	1.6733	A14g00430		plasma membrane intrinsic protein 1B (PIP1B)
Welwitschia	46	331249	331747	0	0.0028	A12g28900	A12g28900	mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 family protein contains Pfam PF02466: Mitochondrial import inner membrane translocase subunit Tim17
Welwitschia	48	331254	331488	0.0516	0.4017	A11g27390	A13g27080	mitochondrial import receptor subunit TOM20-2 (TOM20-2)
Welwitschia	50	331270	332236	0.1344	0.2455	A14g24340	A14g24340	phosphorylase family protein contains Pfam PF01048: Phosphorylase family
Welwitschia	52	331279	332835	0.0049	0	A15g48930	A15g41040	transferase family protein
Welwitschia	54	331299	333816	0.0406	0.1232	A15g58490	A15g58490	cinnamoyl-CoA reductase family
Welwitschia	55	331306	331666	0.0197	0.8149	A12g01140	A12g01140	"fructose-bisphosphate aldolase, putative"
Welwitschia	57	331338	333715	0.0786	1.1837	A13g25560	A11g60800	protein kinase family protein contains Prosite:PS00108: Serine/Threonine protein kinases active-site signature and PS00107: Protein kinases ATP-binding region signature
Welwitschia	58	331341	331567	0.0304	0.9564	A11g22410	A11g22410	"2-dehydro-3-deoxyphosphoheptonate aldolase, putative"
Welwitschia	59	331343	333370	0.1119	0.575	A13g50830	A13g50830	"stress-responsive protein, putative"
Welwitschia	60	331350	336002	0.0514	0.381	A12g37250	A12g37250	adenylate kinase family protein contains Pfam profile: PF00406 adenylate kinase
Welwitschia	61	331356	331802	0.0632	1.5777	A13g14240	A13g14240	subtilase family protein contains similarity to SBT1 Gl:1771160 from [Lycopersicon esculentum]
Welwitschia	62	331360	334785	0.0284	1.0362	A13g44110	A13g44110	"DNAJ heat shock protein, putative (J3)"
Welwitschia	64	331369	335907	0.0473	1.416	A11g30970	A11g30970	"zinc finger (C2H2 type) family protein contains Pfam domain PF00086: Zinc finger, C2H2 type"
Welwitschia	67	331385	334418	0	0.0013			
Welwitschia	69	331395	331486	0.0024	0.7648	A13g12110	A13g12110	actin 11 (ACT11)
Welwitschia	70	331407	333156	0.0512	1.0398	A13g12390	A13g12390	"nascent polypeptide associated complex alpha chain protein, putative"
Welwitschia	71	331414	333427	0.0244	0.1848	A14g09800	A14g09800	40S ribosomal protein S18 (RPS18C)
Welwitschia	72	331418	332619	0.108	0.3123	A13g19000	A13g19000	"oxidoreductase, 2OG-Fe(II) oxygenase family protein"
Welwitschia	73	331424	335358	0.0393	0.0612	A15g09810	A15g09810	actin 7 (ACT7)
Welwitschia	74	331425	333972	0.024	1.2507	A14g35080	A14g35080	catelase 2
Welwitschia	75	331430	333971	0.0294	0.9649	A12g32280	A12g32280	"cholinephosphate cytidyltransferase, putative"
Welwitschia	76	331432	334057	0.3539	0.4302	A11g06680	A12g30790	photosystem II oxygen-evolving complex 23 (OEC23) JBC 14:211-238 (2002)
Welwitschia	78	331460	333544	0.0095	0.0183	A11g56450	A11g56450	20S proteasome beta subunit G1 (PBG1) (PRCH)
Welwitschia	79	331481	331709	0.0189	1.1129	A13g13670	A13g13670	"protein kinase family protein contains Pfam domains, PF00089: Protein kinase domain"
Welwitschia	80	331487	332283	0.0055	1.2303	A14g17530	A11g02130	"Ras-related GTP-binding protein, putative very strong similarity to RAB1C [Lotus corniculatus var. japonicus] Gl: 1370166"
Welwitschia	81	331493	332285	0.2533	0.315	A12g38530		nonspecific lipid transfer protein 2 (LTP2)
Welwitschia	82	331501	332425	0.0021	0.0584	A15g20620	A15g20620	polyubiquitin (UBQ4)
Welwitschia	83	331506	335281	0.0184	0.517	A11g56075	A11g56075	
Welwitschia	84	331507	331903	0.008	1.3142	A13g12580	A15g02500	"heat shock protein 70, putative"
Welwitschia	85	331515	334851	0.0674	1.3961	A12g19800	A12g19800	expressed protein
Welwitschia	86	331517	332094	0.1766	0.4343	A14g24340	A14g24340	phosphorylase family protein contains Pfam PF01048: Phosphorylase family
Welwitschia	87	331527	335495	0.1232	1.148	A11g57860	A11g57860	60S ribosomal protein L21
Welwitschia	88	331529	332345	0.234	1.308	A15g03820	A15g03820	GDSL-motif lipase/hydrolase family protein
Welwitschia	90	331538	335538	0.0156	1.2199	A14g02080	A13g62560	GTP-binding protein (SAR1A)
Welwitschia	91	331539	332199	0.0327	0.5113	A12g37270	A12g37270	40S ribosomal protein S5 (RPS5A)
Welwitschia	92	331547	333312	0.0614	0.2165	A11g02650	A11g26560	glycosyl hydrolase family 1 protein contains Pfam PF00232 : Glycosyl hydrolase family 1 domain
Welwitschia	95	331569	336882	0	0.0023	A13g60530		zinc finger (GATA type) family protein
Welwitschia	98	331603	334547	0	0.0013	A13g04520	A13g04520	threonine aldolase family protein
Welwitschia	99	331606	332334	0.0523	1.6533	A11g78300	A11g78300	14-3-3 protein GF14 omega (GRF2)
Welwitschia	101	331627	336009	0.0037	0	A14g39090	A14g16190	cysteine proteinase RD19a (RD19A)
Welwitschia	102	331630	335060	0.0755	0.8696	A11g26880	A11g26880	60S ribosomal protein L34 (RPL34A)
Welwitschia	105	331659	333680	0.0718	0.1044	A13g18490	A13g18490	"aspartyl protease family protein contains Pfam domain, PF00026: eukaryotic aspartyl protease"
Welwitschia	106	331683	332383	0.0232	0.0791	A11g24020	A15g14030	Bet v I allergen family protein
Welwitschia	107	331688	334956	0.1766	0.2904			
Welwitschia	108	331705	334210	0.0013	1.3193	A15g59970	A15g59970	histone H4
Welwitschia	109	331716	331745	0.0556	0.5225	A15g46110	A15g46110	"phosphate/triose-phosphate translocator, putative"
Welwitschia	111	331733	335561	0.0031	0.9101	A13g52580	A13g52580	"40S ribosomal protein S14 (RPS14C) ribosomal protein S14 -Zea mays.PIR2:A30097"
Welwitschia	113	331750	336903	0.1081	0.6854	A12g31240	A12g31240	tetratricopeptide repeat (TPR)-containing protein contains Pfam profile PF00515: TPR Domain
Welwitschia	116	331792	336764	0.0091	0.0001	A15g13050		5-formyltetrahydrofolate cyclo-ligase (5-FCL) nearly
Welwitschia	117	331832	331892	0.046	1.37	A14g00680	A14g00680	"actin-depolymerizing factor, putative strong similarity to SPIP30175 Actin-depolymerizing factor (ADF) [Lilium longiflorum]"
Welwitschia	118	331864	334570	0.0217	0.6524	A11g54290	A11g54290	"eukaryotic translation initiation factor SU11, putative"
Welwitschia	119	331867	332326	0.1488	1.9263	A14g34670	A14g34670	40S ribosomal protein S3A (RPS3aB)
Welwitschia	120	331873	335851	0.0064	0.0001	A15g47900	A15g27730	hypothetical protein

Welwitschia	121	331879	332851	0	0.001	At1g79750	At2g19900	"malate oxidoreductase, putative"
Welwitschia	123	331906	333445	0.0482	0.1977	At5g13930	At5g13930	chalcone synthase
Welwitschia	125	331915	332599	0.0043	0.0344	At5g63860	At3g02630	UVB-resistance protein (UVR8)
Welwitschia	127	331935	332320	0.075	1.3409	At4g36960	At4g36960	RNA recognition motif (RRM)-containing protein
Welwitschia	129	331966	336230	0	0.0051	At5g55190	At5g55190	Ras-related GTP-binding protein (RAN3)
Welwitschia	130	331969	336222	0	0.0139	At4g14420	At4g14420	lesion inducing protein-related
Welwitschia	131	331999	332754	0.008	0.4402	At3g53020	At2g36620	"60S ribosomal protein L24 (RPL24B) 60S ribosomal protein L24, Arabidopsis thaliana, EMBL:AC006282"
Welwitschia	132	332020	333548	0.0527	1.4614	At1g13950	At1g13950	eukaryotic translation initiation factor 5A-1
Welwitschia	133	332022	333303	0	0.0123	At4g14320	At4g14320	60S ribosomal protein L36a/L44 (RPL36aB)
Welwitschia	134	332042	335708	0.0181	0.2422	At5g13930	At5g13930	chalcone synthase
Welwitschia	135	332044	336445	0.1082	0.7097	At5g22440	At2g27530	60S ribosomal protein L10A (RPL10aC)
Welwitschia	137	332048	334131	0.0283	1.9027	At3g49010	At3g49010	60S ribosomal protein L13 (RPL13B)
Welwitschia	139	332065	333184	0.0397	1.5499	At1g08200	At1g08200	expressed protein
Welwitschia	140	332085	333635	0.0842	1.4139	At3g52590	At3g52590	ubiquitin extension protein 1 (UBQ1)
Welwitschia	142	332098	333733	0.0035	0	At5g62930	At5g62930	GDSL-motif lipase/hydrolase family protein
Welwitschia	143	332111	335151	0.0355	0.4933	At3g05590	At3g05590	60S ribosomal protein L18 (RPL18B)
Welwitschia	144	332137	335066	0	0.0021	At5g08590	At4g33950	serine/threonine protein kinase (ASK2)
Welwitschia	146	332150	332677	0.0199	1.2975	At3g13920	At1g54270	eukaryotic translation initiation factor 4A-1
Welwitschia	147	332166	333645	0.0058	0.0001	At1g35720	At1g35720	annexin 1 (ANN1)
Welwitschia	148	332179	333373	0.032	0.9219	At1g09630	At1g09630	"Ras-related GTP-binding protein, putative"
Welwitschia	151	332207	332338	0.0867	0.5078	At1g60710	At1g60710	"aldo/keto reductase family protein contains Pfam profile PF00248: oxidoreductase, aldo/keto reductase family"
Welwitschia	152	332219	336945	0.0204	0.7464	At4g32530	At4g32530	"vacuolar ATP synthase, putative"
Welwitschia	155	332248	334174	0.0012	1.1951	At5g20290	At5g20290	"40S ribosomal protein S8 (RPS8A) ribosomal protein S8 - Zea mays, PIR:T04088"
Welwitschia	156	332253	332047	0.0058	0.2438			
Welwitschia	158	332268	336967	0.0744	0.6036	At2g32720	At2g32720	"cytochrome b5, putative"
Welwitschia	159	332273	336613	0.0285	0.7493	At3g43810	At5g37780	calmodulin-7 (CAM7) almost
Welwitschia	160	332279	333131	0.0258	0.0879			
Welwitschia	161	332288	336988	0.1466	1.2068	At4g27440	At2g40590	"protochlorophyllide reductase B, chloroplast"
Welwitschia	162	332291	334442	0.0029	0.0235	At5g55180	At2g05790	glycosyl hydrolase family 17 protein
Welwitschia	164	332308	334044	0.0677	1.0082	At5g14670	At1g10630	"ADP-ribosylation factor, putative"
Welwitschia	168	332352	335744	0.0161	1.1809	At5g28840	At5g28840	NAD-dependent epimerase/dehydratase family protein
Welwitschia	169	332393	333449	0.0002	0.0004	At5g20950	At5g20950	"glycosyl hydrolase family 3 protein beta-D-glucan: exohydrolase, Nicotiana tabacum, EMBL:AB017502"
Welwitschia	170	332406	334429	0.0414	1.275	At2g27600	At2g27600	AAA-type ATPase family protein
Welwitschia	171	332411	333072	0.045	1.1368	At5g60860	At5g60860	"Ras-related GTP-binding protein, putative"
Welwitschia	173	332436	332741	0.017	0.1554	At4g21450		
Welwitschia	175	332468	333006	0.0003	0.0009	At5g59720	At5g59720	17.4 kDa class I heat shock protein (HSP17.4-CI)
Welwitschia	180	332540	336825	0.0407	0.2791	At3g57270	At3g57270	glycosyl hydrolase family 17 protein
Welwitschia	182	332573	333728	0.0309	1.6153	At3g03740	At3g03740	speckle-type POZ protein-related contains Pfam PF00651 : BTB/POZ domain
Welwitschia	184	332580	336277	0.1389	0.1713	At4g00100	At4g00100	40S ribosomal protein S13 (RPS13A)
Welwitschia	185	332585	332796	0.0039	0.5362	At5g47370	At5g62300	"40S ribosomal protein S20 (RPS20B) 40S RIBOSOMAL PROTEIN S20 - ARABIDOPSIS THALIANA,PID:g1350956"
Welwitschia	187	332609	334488	0.0127	1.4945	At1g36240	At1g77940	60S ribosomal protein L30 (RPL30A)
Welwitschia	190	332672	332692	0.0003	0.0006			
Welwitschia	192	332720	334692	0.0176	0.0357	At4g27830	At5g44640	glycosyl hydrolase family 1 protein contains Pfam PF00232 : Glycosyl hydrolase family 1 domain
Welwitschia	195	332729	336767	0	0.0008			
Welwitschia	201	332813	333021	0.0021	0.0264	At1g17370	At1g17370	"oligouridylate-binding protein, putative"
Welwitschia	203	332840	333805	0.0571	0.2728	At5g20090	At5g20090	"expressed protein contains Pfam domain, PF03650: Uncharacterized protein family (UPF0041)"
Welwitschia	206	332917	335013	0	0.0057	At5g02100	At5g59420	oxysterol-binding family protein
Welwitschia	207	332961	334293	0.063	0.2053	At5g58230	At5g58230	WD-40 repeat protein (MS1) contains 6 WD-40 repeats (PF0400)
Welwitschia	211	333005	335603	0.0357	0.0106	At4g25750		"ABC transporter family protein Bactrocera tryoni membrane transporter (white) gene, PID:g367629g"
Welwitschia	212	333037	335385	0	0.0023	At3g62260	At3g62260	"protein phosphatase 2C, putative"
Welwitschia	214	333120	334327	0.1546	0.2988	At5g57480	At3g28600	AAA-type ATPase family protein contains Pfam profile: PF00004 ATPase family
Welwitschia	216	333130	336462	0.0704	1.5349	At1g57720	At1g57720	"elongation factor 1B-gamma, putative"
Welwitschia	222	333313	335748	0.1186	0.0609	At1g72370	At1g72370	40S ribosomal protein S4 (RPSaA)
Welwitschia	225	333397	335915	0.0002	0.0004	At2g47110	At2g47110	ubiquitin extension protein 6 (UBQ6)
Welwitschia	227	333431	336482	0.014	0.725	At5g58420	At5g58420	"40S ribosomal protein S4 (RPS4D) ribosomal protein S4, Arabidopsis thaliana, PIR:T48480"
Welwitschia	233	333609	334976	0.039	1.1499	At3g09770	At3g09770	"zinc finger (C3HC4-type RING finger) family protein contains Pfam domain, PF00097: Zinc finger, C3HC4 type (RING finger)"
Welwitschia	236	333640	335154	0	0.0201	At1g31812	At1g31812	acyl-CoA binding protein
Welwitschia	241	334060	335681	0	0.0021			
Welwitschia	243	334143	335535	0.0984	0.1625	At2g29590		
Welwitschia	244	334158	335725	0.006	0.0472	At2g39630	At2g39630	glycosyl transferase family 2 protein
Welwitschia	259	334826	335383	0.018	1.0104	At5g35320	At3g29360	"UDP-glucose 6-dehydrogenase, putative very strong similarity to SPI06558 UDP-glucose 6-dehydrogenase (EC 1.1.1.22) (UDP-Glc dehydrogenase) (UDP-GlcDH) (UDPGDH) (Glycine max)"
Welwitschia	260	334827	335905	0.03	1.5653	At5g53140	At5g53140	"protein phosphatase 2C, putative"
Welwitschia	263	334945	336150	0.0246	0.9185	At1g36730	At1g36730	"eukaryotic translation initiation factor 5, putative"
Welwitschia	265	335103	335771	0.0082	0.0001	At2g41460	At2g41460	apurinic endonuclease-redox protein
Welwitschia	268	335195	335608	0	0.0027	At1g42480	At1g42480	expressed protein
Welwitschia	273	335509	335432	0.1073	0.8931	At4g34460	At4g34460	guanine nucleotide-binding protein beta subunit (GB1)
Welwitschia	276	335520	336654	0.0819	0.4858	At5g05520	At5g05520	"outer membrane OMP85 family protein contains Pfam profile PF01103: outer membrane protein, OMP85 family"
Welwitschia	281	335689	336947	0.5263	0.6803			
Welwitschia	282	335853	336693	0.1203	0.8636	At1g55320	At1g55320	acyl-activating enzyme 18 (AAE18) nearly
Welwitschia	284	335965	336343	0.0587	1.2018	At2g35635	At2g35635	ubiquitin family protein contains INTERPRO:IPR000626 ubiquitin domain
Welwitschia	289	336685	336571	0.1456	0.6354	At5g65910	At5g65910	BSD domain-containing protein contains Pfam profile PF03909: BSD domain