

SUPPLEMENTAL TABLE S3. Proteins from non-secretory organelles. NSAF normalized spectral abundance factor; SpC: spectral counts, Sorb: sorbitol addition; X: xylose addition. Blue cells: proteins over-represented on sorbitol; orange cells: proteins over-represented on xylose.

A. niger Locus	Description	SpC		NSAF.10 ⁴	
		Sorb	Xyl	Sorb	Xyl
NUCLEAR					
An06g01440	similarity to heterogeneous nuclear ribonucleoprotein (hnRNP) Tom34 - Saccharomyces cerevisiae	29	27	22.9	14.8
An11g11310	strong similarity to histone H2B - Aspergillus nidulans	9	11	17.5	14.7
An03g06670	weak similarity to myosin-like protein Mlp1 - Saccharomyces cerevisiae	122	248	15.3	21.6
An07g05820	strong similarity to hypothetical transmembrane protein usgS - Aspergillus nidulans	14	26	10.3	13.1
An15g06440	strong similarity to karyopherin alpha Srp1 - Saccharomyces cerevisiae	21	17	10.2	5.8
An16g01870	strong similarity to mRNA cleavage factor I 25 kDa subunit CFIM25 - Homo sapiens	8	7	8.0	4.9
An08g10060	strong similarity to small G-protein Gsp1 - Candida albicans	6	10	7.9	8.9
An15g00170	strong similarity to protein kinase skp1p - Schizosaccharomyces pombe	11	11	7.6	5.3
An08g06940	strong similarity to histone H4.1 - Aspergillus nidulans	2	3	6.3	6.1
An07g02990	similarity to RNA-binding protein AUF1 - Homo sapiens	7	13	6.2	7.7
An14g04940	strong similarity to mRNA turnover 4 protein Mrt4 - Saccharomyces cerevisiae	5	8	6.1	6.6
An11g11140	strong similarity to nuclear pore membrane protein Pom152 - Saccharomyces cerevisiae	28	48	5.9	7.0
An12g07790	strong similarity to transcription factor btf3p - Schizosaccharomyces pombe-	3	2	5.9	2.9
An12g08030	strong similarity to NADH oxidoreductase complex I subunit Sub2 - Saccharomyces cerevisiae	9	12	5.6	5.1
An07g02690	similarity to hypothetical regulational protein PBK1 - Homo sapiens-	8	4	5.4	2.0
An01g12230	strong similarity to nucleolar protein Nop1 - Saccharomyces cerevisiae	6	18	5.4	10.7
An14g00100	strong similarity to nucleoporin-interacting protein Nic96 - Saccharomyces cerevisiae	20	10	5.4	1.9
56745	strong similarity to pre-mRNA splicing factor (Srp1), putative [Neosartorya fischeri NRRL 181]	4	7	5.3	6.1
An07g01520	strong similarity to nucleoporin Nup170 - Saccharomyces cerevisiae	25	11	4.9	1.5
An12g00410	strong similarity to RNA binding protein 47 RBP47 - Nicotiana plumbaginifolia	7	6	4.9	2.9
An01g06040	strong similarity to hypothetical membrane protein YOL077c - Saccharomyces cerevisiae	6	6	4.7	3.3
An16g01810	strong similarity to histone H2A variant pht1p - Schizosaccharomyces pombe-	2	1	4.7	2.0
An14g02360	strong similarity to U2 snRNA-specific protein A - Homo sapiens	4	4	4.6	3.2
An01g14070	strong similarity to karyopherin β Kap95 - Saccharomyces cerevisiae-	15	19	4.6	4.0
An04g01520	similarity to nuclear envelope protein cut11p - Schizosaccharomyces pombe	9	6	4.4	2.1
An09g00500	weak similarity to transcription factor Arg81 - Saccharomyces cerevisiae	13	16	4.0	3.4
An02g08100	strong similarity to translin-like protein TRAX - Gallus gallus-	3	2	3.9	1.9
An02g09260	strong similarity to nucleolar protein Nop5 - Saccharomyces cerevisiae	8	11	3.8	3.6
An15g00140	similarity to transcription repressor Tup1 - Saccharomyces cerevisiae-	8	4	3.8	1.4
An08g00520	strong similarity to protein sonA - Aspergillus nidulans	4	4	3.3	2.3
An16g03090	strong similarity to small nucleolar RNP component Nop56 - Saccharomyces cerevisiae	6	9	3.3	3.3
An07g03430	strong similarity to hypothetical protein CAD70902.1 - Neurospora crassa	3	4	3.1	2.8
An17g02170	strong similarity to centromere/microtubule-binding protein Cbf5 - Saccharomyces cerevisiae	5	11	3.0	4.3
An15g00160	strong similarity to transcription regulator CaGCR3 - Candida albicans-	8	17	2.6	3.7
An02g03860	strong similarity to hypothetical protein B1D1.160 - Neurospora crassa-	12	9	2.6	1.4
An07g06730	strong similarity to cut3p - Schizosaccharomyces pombe-	12	3	2.5	0.5
An11g01510	similarity to the protein involved in sister chromatid segregation Src1 - Saccharomyces cerevisiae	6	3	2.3	0.9
An07g09830	strong similarity to hypothetical protein encoded by B19C19.110 - Neurospora crassa	4	5	2.3	1.9
An18g01170	strong similarity to poly(ADP-ribose) polymerase NAP protein from patent WO200004173-A1 - Zea mays-	5	0	2.2	0.1
An02g12640	strong similarity to RNA-binding protein 30 - Nicotiana plumbaginifolia-	4	7	2.2	2.5
An08g09010	strong similarity to spliceosomal protein SAP130 - Homo sapiens	9	14	2.0	2.2

An02g03940	strong similarity to glucose repression mediator protein Ssn6 - <i>Saccharomyces cerevisiae</i> -	6	1	2.0	0.3
An02g14750	strong similarity to actin-related protein - <i>Homo sapiens</i>	3	3	1.9	1.3
An16g05050	similarity to importin RanBP7 - <i>Homo sapiens</i>	7	6	1.9	1.1
An04g02130	similarity to U1 and U2 snRNPs component Smb - <i>Homo sapiens</i>	1	4	1.8	3.7
An02g03520	strong similarity to G protein-binding protein CRFG - <i>Homo sapiens</i>	3	9	1.4	2.6
An01g00150	strong similarity to nuclear protein Enp1 - <i>Saccharomyces cerevisiae</i>	2	5	1.3	2.0
An08g07050	strong similarity to 189 kD subunit of DNA-directed RNA polymerase I rpa190p - <i>Schizosaccharomyces pombe</i>	8	10	1.3	1.1
An15g01240	strong similarity to protein required for accurate mitotic chromosome segregation Cse1 - <i>Saccharomyces cerevisiae</i>	4	23	1.2	4.4
An16g09200	strong similarity to U5 snRNP-specific protein U5-116kD - <i>Mus musculus</i>	4	9	1.2	1.7
An07g07420	strong similarity to splicing factor PRP8 - <i>Homo sapiens</i>	10	15	1.1	1.2
An18g02480	strong similarity to DNA repair protein XAB2 - <i>Homo sapiens</i> -	3	1	1.1	0.3
An11g04870	strong similarity to ribonucleoprotein autoantigen Sm-D - <i>Homo sapiens</i>	0	4	1.1	6.7
An14g06530	similarity to nucleoporin Nup192 - <i>Saccharomyces cerevisiae</i> -	5	3	0.8	0.4
An02g05400	strong similarity to 146D nuclear protein - <i>Xenopus laevis</i>	3	5	0.8	0.8
An04g05870	strong similarity to E3 ubiquitin ligase Tom1 - <i>Saccharomyces cerevisiae</i>	11	17	0.7	0.8
An04g05630	similarity to nuclear pore complex subunit Nup100 - <i>Saccharomyces cerevisiae</i> -	5	1	0.7	0.1
An04g02640	strong similarity to protein pescadillo - <i>Homo sapiens</i>	1	11	0.6	3.1
An15g06390	strong similarity to ribosomal RNA processing protein Rrp5 - <i>Saccharomyces cerevisiae</i>	3	13	0.5	1.3
An07g10400	strong similarity to cell division control protein Cdc68 - <i>Saccharomyces cerevisiae</i>	1	5	0.4	1.0
An02g10200	strong similarity to protein TRRAP - <i>Homo sapiens</i>	3	4	0.2	0.2
An08g06090	similarity to nucleoporin nup184p - <i>Schizosaccharomyces pombe</i>	1	6	0.2	0.6
An11g01770	strong similarity to 135 kD subunit of DNA-directed RNA polymerase I - <i>Neurospora crassa</i>	0	8	0.1	1.3
An12g00720	strong similarity to 138 kD subunit of DNA-dependent RNA polymerase II rpb2p - <i>Schizosaccharomyces pombe</i>	0	4	0.1	0.6
An16g07120	strong similarity to regulator protein Sin3 - <i>Saccharomyces cerevisiae</i>	0	3	0.1	0.4
An17g00540	similarity to suppressor of <i>S.cerevisiae</i> sin4 mutation Rlr1 - <i>Saccharomyces cerevisiae</i>	0	5	0.1	0.4
MITOCHONDRIAL					
An18g04220	strong similarity to mitochondrial ADP/ATP carrier anc1p - <i>Schizosaccharomyces pombe</i>	114	207	93.4	117.3
An14g04180	strong similarity to H ⁺ -transporting ATP synthase β chain - <i>Neurospora crassa</i> [truncated ORF]	141	219	88.3	95.0
An01g13600	strong similarity to mitochondrial phosphate transport protein Mir1 - <i>Saccharomyces cerevisiae</i>	56	116	46.8	66.9
An09g06650	strong similarity to core protein II of ubiquinol--cytochrome c reductase CAA42214.1 - <i>Bos primigenius taurus</i>	80	103	45.7	40.8
An04g04060	strong similarity to cytochrome-c peroxidase precursor Ccp1 - <i>Saccharomyces cerevisiae</i>	63	67	45.4	33.5
An07g06840	strong similarity to precursor of dihydrolipoamide dehydrogenase Lpd1 - <i>Saccharomyces cerevisiae</i>	67	84	34.2	29.7
An16g07410	strong similarity to mitochondrial F1-ATPase alpha-subunit Atp1 - <i>Saccharomyces cerevisiae</i>	68	136	32.1	44.3
An09g05870	strong similarity to nucleoside-diphosphate kinase NDK-1 - <i>Neurospora crassa</i>	18	25	31.5	30.1
An02g01830	cytochrome c cyc - <i>Aspergillus niger</i>	13	16	31.4	26.6
203715	strong similarity to outer mitochondrial membrane protein porin [<i>Aspergillus clavatus</i> NRRL 1]	41	76	30.9	39.4
An07g02180	strong similarity to dihydrolipoamide acetyltransferase Lat1 - <i>Saccharomyces cerevisiae</i>	78	58	30.3	15.6
An12g04940	strong similarity to mitochondrial heat shock protein Hsp60 - <i>Saccharomyces cerevisiae</i>	60	146	26.8	45.0
An02g11910	similarity to mitochondrial pyruvate dehydrogenase complex protein Pdx1 - <i>Saccharomyces cerevisiae</i>	28	22	25.7	14.0
An14g04400	strong similarity to succinate dehydrogenase iron-sulfur protein subunit Sdh2 - <i>Saccharomyces cerevisiae</i>	27	40	23.9	24.4
An01g00100	strong similarity to pyruvate dehydrogenase β chain precursor Pdb1 - <i>Saccharomyces cerevisiae</i>	32	32	22.6	15.7
An02g12770	strong similarity to succinate dehydrogenase Sdh1 - <i>Saccharomyces cerevisiae</i>	54	123	22.0	34.5
An07g02160	strong similarity to mitochondrial malate dehydrogenase Mdh1 - <i>Saccharomyces cerevisiae</i>	28	55	21.8	29.4
An15g01710	strong similarity to F1Fo-ATP synthase subunit 7 ATP7 - <i>Kluyveromyces lactis</i>	14	38	21.8	40.1
An09g06680	citrate synthase citA - <i>Aspergillus niger</i>	38	57	21.1	21.9

An08g07360	strong similarity to mitochondrial import receptor TOM20 - <i>Neurospora crassa</i>	13	15	21.0	16.7
An02g09930	strong similarity to subunit VI of cytochrome c oxidase Cox6 - <i>Saccharomyces cerevisiae</i>	12	16	20.6	18.8
An09g03940	strong similarity to ketol-acid reductoisomerase ilv-2 - <i>Neurospora crassa</i>	31	46	20.4	20.9
An16g07290	strong similarity to F1Fo-ATP synthase subunit 4 ATP4 - <i>Kluyveromyces lactis</i>	17	40	18.7	29.9
An01g06180	strong similarity to cytochrome c1 of ubiquinol--cytochrome c reductase CYT-1 - <i>Neurospora crassa</i>	22	64	18.5	36.8
An16g08550	strong similarity to ATP synthase coupling factor (F0) subunit e Tim11 - <i>Saccharomyces cerevisiae</i>	6	11	18.4	22.5
An11g09390	strong similarity to 21 kD subunit of NADH:ubiquinone reductase nuo-21 - <i>Neurospora crassa</i>	14	33	17.2	27.6
An09g06850	strong similarity to 78 kD subunit of NADH:ubiquinone reductase NDUFS1 - <i>Bos taurus</i>	48	132	17.1	32.4
An14g04080	strong similarity to iron-sulfur subunit of ubiquinol--cytochrome c reductase rip1p - <i>Schizosaccharomyces pombe</i>	15	44	16.9	33.7
An01g03570	strong similarity to cytochrome-b5 reductase Mcr1 - <i>Saccharomyces cerevisiae</i>	20	64	16.6	36.1
An15g00190	strong similarity to mitochondrial import receptor MOM38 - <i>Neurospora crassa</i>	22	47	16.5	24.2
An11g10200	strong similarity to subunit VIa of cytochrome c oxidase Cox13 - <i>Saccharomyces cerevisiae</i>	8	13	15.7	17.3
An08g10690	strong similarity to 40 kD subunit of NADH-ubiquinone reductase NUO-40 - <i>Neurospora crassa</i>	21	54	15.0	26.4
An08g00210	strong similarity to glycerol-3-phosphate dehydrogenase gdm1 - <i>Mus musculus</i>	40	82	15.0	21.1
An02g05470	strong similarity to 49 kD subunit of NADH:ubiquinone reductase - <i>Neurospora crassa</i>	26	56	14.5	21.4
An08g04070	strong similarity to mitochondrial receptor complex chain MOM22 - <i>Neurospora crassa</i>	8	8	14.5	10.0
An01g12210	strong similarity to core protein I of ubiquinol--cytochrome-c reductase β -MPP - <i>Neurospora crassa</i>	25	98	13.9	37.1
An14g04170	cytochrome c oxidase subunit V cox5 - <i>Aspergillus niger</i>	10	26	13.8	24.1
An15g00690	strong similarity to 14.8 kD subunit of NADH:ubiquinone reductase - <i>Neurospora crassa</i>	6	11	13.8	16.9
An02g05900	similarity to hypothetical protein AA57718.1 - <i>Aspergillus nidulans</i>	6	9	13.6	13.8
An14g00220	strong similarity to hypothetical protein SPAC17C9.06 - <i>Schizosaccharomyces pombe</i>	26	44	13.4	15.6
An08g05580	strong similarity to precursor of isocitrate dehydrogenase (NAD ⁺) chain Idh2 - <i>Saccharomyces cerevisiae</i>	22	22	13.4	9.3
An06g01390	strong similarity to 21.3 kD subunit of NADH:ubiquinone reductase - <i>Neurospora crassa</i>	9	26	12.7	24.5
An16g05090	strong similarity to endonuclease SceI 75 kDa subunit Ens1 - <i>Saccharomyces cerevisiae</i>	30	39	11.9	10.7
An08g06540	strong similarity to antiproliferative protein prohibitin Phb1 - <i>Saccharomyces cerevisiae</i>	12	36	11.7	23.6
An11g06200	strong similarity to 31 kD subunit of NADH:ubiquinone reductase - <i>Neurospora crassa</i>	12	30	11.6	19.6
An02g05880	strong similarity to 29.9 kD subunit of NADH:ubiquinone reductase - <i>Neurospora crassa</i>	10	25	11.5	19.4
An07g09530	strong similarity to alpha subunit E1 of the pyruvate dehydrogenase complex Pda1 - <i>Saccharomyces cerevisiae</i>	17	14	11.3	6.5
An12g04750	strong similarity to prohibitin Phb2 - <i>Saccharomyces cerevisiae</i>	12	33	10.6	19.7
An14g00060	strong similarity to 20.9 kD subunit of NADH:ubiquinone reductase - <i>Neurospora crassa</i>	7	19	10.4	18.7
An04g05220	strong similarity to subunit 6 of ubiquinol--cytochrome-c reductase Qcr6 - <i>Saccharomyces cerevisiae</i>	6	9	10.1	10.3
An07g07390	strong similarity to subunit IV of cytochrome c oxidase Cox4 - <i>Saccharomyces cerevisiae</i>	7	29	10.1	27.4
An02g04520	strong similarity to H ⁺ -transporting ATP synthase delta chain precursor Atp5 - <i>Saccharomyces cerevisiae</i>	8	20	9.7	16.2
An03g03900	similarity to single-stranded DNA-binding protein Rim1 - <i>Saccharomyces cerevisiae</i>	5	5	9.7	6.7
An01g03480	strong similarity to sorbitol dehydrogenase gutB - <i>Bacillus subtilis</i>	12	18	9.6	9.8
An07g03070	strong similarity to mitochondrial carrier protein ARALAR2 - <i>Homo sapiens</i>	25	96	9.5	25.0
An12g00220	strong similarity to hypothetical protein EAA61911.1 - <i>Aspergillus nidulans</i>	5	6	9.3	7.6
An03g04790	strong similarity to mitochondrial outer membrane protein Tom70 - <i>Podospira anserina</i>	21	63	8.9	18.2
An08g04470	strong similarity to mitochondrial elongation factor Tu - <i>Arabidopsis thaliana</i>	14	16	8.6	6.8
An01g10880	similarity to F1Fo-ATP synthase subunit g homolog Atp20 - <i>Saccharomyces cerevisiae</i>	6	18	8.5	16.9
An17g01110	strong similarity to 17.2 kD subunit of NADH:ubiquinone reductase b17.2 - <i>Bos taurus</i>	4	6	8.4	8.4
An17g01670	strong similarity to succinyl coenzyme A synthase alpha subunit SYRTSA - <i>Rattus norvegicus</i>	10	9	8.2	5.2
An07g10010	strong similarity to mitochondrial carrier protein Yhm1 - <i>Saccharomyces cerevisiae</i>	9	37	8.0	21.9
An14g02250	strong similarity to flavocytochrome b2 L-lactate dehydrogenase CYB2 - <i>Pichia anomala</i>	14	8	7.5	3.1
An18g01590	strong similarity to carnitine O-acetyltransferase cat2 - <i>Candida tropicalis</i>	18	10	7.5	2.9
An12g04780	strong similarity to 24 kD subunit of NADH:ubiquinone reductase Nuo24 - <i>Neurospora crassa</i>	7	18	7.3	12.4
An08g01370	strong similarity to Oxodicarboxylate carrier Odc2 - <i>Saccharomyces cerevisiae</i>	8	24	7.3	14.5
An15g01780	strong similarity to 2-methylcitrate dehydratase PrpD - <i>Salmonella typhimurium</i>	13	9	7.0	3.4

An04g02460	strong similarity to heart muscle protein mitofilin HMP - Homo sapiens	16	59	6.8	17.0
An13g00670	strong similarity to mitochondrial protein Mia1 - Saccharomyces cerevisiae-	3	2	6.7	3.3
An18g05890	similarity to pyruvate dehydrogenase phosphatase isoenzyme 1 PDP1 - Rattus norvegicus	15	24	6.7	7.3
An04g05640	mitochondrial proton-pumping NADH:ubiquinone reductase nuo51 - Aspergillus niger	12	67	6.6	24.5
An07g09920	strong similarity to NADH-dependent glutamate synthase NADH-GOGAT - Medicago sativa	50	76	6.2	6.5
An04g04750	strong similarity to oxoglutarate dehydrogenase (lipoamide) Kgd1 - Saccharomyces cerevisiae	24	71	6.0	12.2
An02g12430	precursor of mitochondrial isocitrate dehydrogenase icdA - Aspergillus niger	9	10	6.0	4.6
An15g01920	strong similarity to methylcitrate synthase mcsA - Aspergillus nidulans	10	6	5.9	2.5
An08g04910	strong similarity to 22 kD subunit NADH:ubiquinone reductase - Neurospora crassa	3	5	5.7	6.2
An03g03640	strong similarity to mitochondrial sulfide dehydrogenase (coenzyme Q2) SPBC2G5.06c - Schizosaccharomyces pombe [putative sequencing error]	11	27	5.7	9.4
An09g06670	strong similarity to suppressor gene of mitochondrial histone Yhm2 - Saccharomyces cerevisiae	6	30	5.4	17.4
An01g09840	strong similarity to hypothetical protein AN0630.2 - Aspergillus nidulans	1	5	5.3	13.4
An18g05670	strong similarity to 23 kD subunit of NADH:ubiquinone reductase - Bos taurus	4	14	5.2	11.7
An04g00110	strong similarity to 21/29 kD subunit of NADH:ubiquinone reductase - Neurospora crassa	5	17	5.1	11.3
An03g04660	weak similarity to hypothetical protein YGR165w - Saccharomyces cerevisiae-	7	11	5.0	5.4
An01g04630	strong similarity to gamma chain precursor of the H ⁺ -transporting ATP synthase Atp3 - Saccharomyces cerevisiae	5	14	4.8	8.8
An02g07320	strong similarity to AU-specific RNA-binding protein / enoyl-CoA hydratase AUH - Homo sapiens-	5	3	4.7	2.1
An11g11280	strong similarity to dihydrolipoamide succinyltransferase kgd2 - Aspergillus fumigatus	8	19	4.7	7.5
An11g05700	similarity to hypothetical membrane protein YGR235c - Saccharomyces cerevisiae	4	11	4.6	8.2
An18g02990	similarity to mitochondrial ribosomal protein Mrp20 - Saccharomyces cerevisiae-	3	3	4.6	3.2
An16g07110	strong similarity to acetyl-CoA hydrolase Ach1 - Saccharomyces cerevisiae	8	9	4.2	3.3
An08g01590	similarity to membrane associated protein SLP-2 - Homo sapiens	6	24	3.9	10.1
An08g05500	strong similarity to mitochondrial ribosomal protein of the large subunit Yml3 - Saccharomyces cerevisiae	5	5	3.9	2.7
An02g07600	strong similarity to succinate dehydrogenase Sdh1 - Saccharomyces cerevisiae	9	11	3.8	3.2
An03g03360	strong similarity to carnitine/acyl carnitine carrier acuH - Aspergillus nidulans	4	16	3.6	9.2
An16g02130	similarity to novel cell death-regulatory protein GRIM19 - Mus musculus	1	12	3.6	20.7
An12g04110	strong similarity to precursor of mitochondrial nuclease Nuc1 - Saccharomyces cerevisiae	4	14	3.5	7.8
An08g04880	strong similarity to hypothetical protein CAD27304.1 - Aspergillus fumigatus	3	9	3.5	6.5
An04g01200	strong similarity to 14 kD subunit of ubiquinol--cytochrome c reductase Qcr7 - Saccharomyces cerevisiae	1	5	3.2	8.1
An08g10530	strong similarity to mitochondrial aconitate hydratase Aco1 - Saccharomyces cerevisiae	9	56	3.2	13.1
An02g11200	similarity to 13 kD subunit of NADH:ubiquinone reductase - Bos taurus	3	7	3.1	4.6
An18g06760	strong similarity to NAD(+)-isocitrate dehydrogenase subunit I idh1 - Ajellomyces capsulatus	4	4	3.0	2.1
An13g03940	strong similarity to long-chain-acyl-CoA dehydrogenase precursor LCAD - Rattus norvegicus	4	5	2.8	2.4
An01g03110	similarity to ribosomal protein of the small subunit Rsm7 - Saccharomyces cerevisiae-	4	1	2.8	0.6
An07g07880	similarity to ORFX ORF2689 polypeptide sequence SEQ ID NO:5378 from patent WO200058473-A2 - Homo sapiens	5	12	2.8	4.4
An02g01750	strong similarity to chaperone involved in mitochondrial protein import Mge1 - Saccharomyces cerevisiae	2	10	2.7	7.9
An17g01530	alcohol-dehydrogenase adhA from patent WO8704464-A - Aspergillus niger-	3	1	2.6	0.8
An08g04240	strong similarity to alternative NADH:ubiquinone reductase NDH2 - Yarrowia lipolytica	5	33	2.5	10.7
An07g07000	strong similarity to mitochondrial m-AAA protease subunit Yta12 - Saccharomyces cerevisiae	8	27	2.5	5.5
An07g02770	strong similarity to hypothetical protein YKL195w - Saccharomyces cerevisiae	2	5	2.4	3.7
An16g08740	strong similarity to 17.8 kD subunit of NADH:ubiquinone reductase Nuo-17.8 - Neurospora crassa	1	7	2.3	7.9
An04g00220	strong similarity to methionine-N-acetyltransferase Nat2 - Saccharomyces cerevisiae	2	4	2.3	2.8
An07g09550	strong similarity to mitochondrial ribosomal protein Nam9 - Saccharomyces cerevisiae	3	5	2.1	2.3
An06g01730	strong similarity to mtRNA splice defect-suppressing mitochondrial carrier Mrs3 - Saccharomyces cerevisiae	2	4	2.0	2.5

An04g09030	strong similarity to mitochondrial succinate-fumarate transporter Sfc1 - <i>Saccharomyces cerevisiae</i>	2	8	2.0	4.7
An02g06530	strong similarity to protein required for dispersion of mitochondria cluA - <i>Dictyostelium discoideum</i>	9	20	2.0	3.0
53140	strong similarity to mitochondrial cytochrome b2, putative [<i>Aspergillus flavus</i> NRRL3357]	3	4	1.9	1.7
An07g09110	similarity to monooxygenase VioC - <i>Chromobacterium violaceum</i>	3	4	1.8	1.6
An01g13930	similarity to succinate dehydrogenase - <i>Saccharomyces cerevisiae</i>	1	7	1.8	6.1
An12g00130	strong similarity to mRNA processing protein of cytochrome c oxidase Mss51 - <i>Saccharomyces cerevisiae</i>	3	6	1.7	2.2
An16g04170	strong similarity to acetolactate synthase protein from patent EP257993-A - <i>Saccharomyces cerevisiae</i> -	4	5	1.7	1.4
An04g00060	strong similarity to 19.3 kD subunit of NADH:ubiquinone reductase - <i>Neurospora crassa</i>	1	6	1.7	5.1
An05g00110	strong similarity to hypothetical protein YNR020c - <i>Saccharomyces cerevisiae</i>	1	8	1.6	6.5
An01g06370	strong similarity to hypothetical protein YKR065c - <i>Saccharomyces cerevisiae</i>	1	5	1.6	4.0
An04g04970	strong similarity to Yta11 - <i>Saccharomyces cerevisiae</i>	4	28	1.5	6.4
An15g00980	strong similarity to maintaining mitochondrial morphology protein MMM1 - <i>Neurospora crassa</i>	2	4	1.3	1.7
An07g03130	strong similarity to mitochondrial cation transporter Mmt1 - <i>Saccharomyces cerevisiae</i>	2	10	1.3	3.9
An18g05590	strong similarity to mitochondrial carrier protein Ymc1 - <i>Saccharomyces cerevisiae</i>	1	6	1.3	3.9
An08g04250	strong similarity to dynamin-related protein msp1p - <i>Schizosaccharomyces pombe</i>	4	7	1.3	1.5
An11g10070	strong similarity to hypothetical protein Afu3g06270 - <i>Aspergillus fumigatus</i>	1	5	1.2	3.1
An01g10190	similarity to mitochondrial tricarboxylate carrier - <i>Rattus sp.</i>	1	7	1.1	3.7
An12g07580	strong similarity to acetylglutamate kinase/N-acetyl-gamma-glutamyl-phosphate reductase precursor arg-6 - <i>Neurospora crassa</i> -	3	5	1.0	1.1
An11g09350	strong similarity to mitochondrial NADH dehydrogenase ndh64 - <i>Neurospora crassa</i>	2	9	0.9	2.4
An04g08800	strong similarity to mitochondrial carrier Leu5 - <i>Saccharomyces cerevisiae</i>	1	3	0.9	1.5
An02g04000	strong similarity to pyruvate dehydrogenase kinase isoform 2 - <i>Zea mays</i>	1	3	0.9	1.4
An04g07060	strong similarity to peptide ABC transporter protein Mdl1 - <i>Saccharomyces cerevisiae</i>	1	6	0.5	1.5
An11g11230	strong similarity to citrate transport protein Ctp1 - <i>Saccharomyces cerevisiae</i>	0	7	0.4	4.6
An14g00810	strong similarity to hypothetical protein EAA61688.1 - <i>Aspergillus nidulans</i>	0	3	0.4	1.8
An15g02490	similarity to 3-isopropylmalate dehydrogenase leuB - <i>Sulfolobus sp.</i>	0	3	0.4	1.7
An01g06960	strong similarity to hypothetical phosphatidyl synthase SPAC22A12.08c - <i>Schizosaccharomyces pombe</i>	0	5	0.4	2.7
An02g12070	strong similarity to mitochondrial phosphate transport protein G7 - <i>Glycine max</i>	0	7	0.3	3.6
An01g07190	strong similarity to component of the translocase of mitochondrial inner membrane Tim54 - <i>Saccharomyces cerevisiae</i>	0	3	0.3	1.4
An01g07200	similarity to N-acetylglucosaminyltransferases chain p110 - <i>Rattus norvegicus</i>	0	19	0.2	4.2